PTO-1542
(4-85)

U.S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICE

ONLINE SEARCH REQUEST FORM

USER Spector U.S. SERIAL NUMBER 243545

ART UNIT 1812 PHONE 308-1793 DATE 4/3/95

Please give a detailed statement of requirements. Describe as specifically as possible the subject matter to be searched. Define any terms that may have special meaning. Give examples or relevant citations, authors, or keywords, if known.

You may include a copy of the broadest and or relevant claim(s).

→ See CRF for parent 08/162407
Please search Seq ID 145,
also ~~a~~ ~~b~~ reverse translate
& search aa 28-182 of ID6.

Thanks!

STAFF USE ONLY

4-23

COMPLETED 4/5
SEARCHER Idalo 4058
ONLINE TIME 32 TOTAL TIME ____
(in minutes)
NO. OF DATABASES ____

SYSTEMS
____ CAS ONLINE
____ DARC/QUESTEL
____ DIALOG
____ SDC
✓ OTHER JG

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq1.res made by  on Wed 5 Apr 95 19:41:35-PDT.


Query sequence being compared:US-08-162-407-1 (1-879)
Number of sequences searched:                  313646
Number of scores above cutoff:                   4589

      Results of the initial comparison of US-08-162-407-1 (1-879) with:
   Data bank : EMBL-NEW 1, all entries
   Data bank : GenBank 86, all entries
   Data bank : GenBank-NEW 1, all entries
   Data bank : UEMBL 41_86, all entries

1000000-
      -
N     -
U00000-
M     -
B     -
E     -
R     -
      -
O     -**
F00000-
      -
S     -  *
E50000-
Q     -
U     -
E     -
N     -   *
C     *
E     -
S10000-
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      -    *
  5000-
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      -
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Spector 243543/162407

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   100-        *
     -
     -
    50-
     -
     -
     -          *
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    10-
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     5-            *
     -              *
     -                              *
     -
     -
     -                                                 *             *
     0------------------------------------------------------------------------
      ||   |||||  || |     |      |      |      |      |      |      |
SCORE 0|   ||92|  |184    276    368    461    553    645    737    829
STDEV -1       6   9

                             PARAMETERS

Similarity matrix       Unitary     K-tuple                  4
Mismatch penalty              1     Joining penalty         30
Gap penalty                1.00     Window size             32
Gap size penalty           0.33
Cutoff score                  2
Randomization group           0

Initial scores to save       45     Alignments to save      15
Optimized scores to save      0     Display context         10

                             SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            31           30          13.25

Times:                     CPU                     Total Elapsed
                       00:38:23.03                 00:38:32.00

Number of residues:               288682119
Number of sequences searched:        313646
Number of scores above cutoff:         4589

Cut-off raised to 23.
Cut-off raised to 27.
Cut-off raised to 30.
Cut-off raised to 33.
Cut-off raised to 36.
Cut-off raised to 39.
Cut-off raised to 42.
Cut-off raised to 45.
Cut-off raised to 48.
Cut-off raised to 52.
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Cut-off raised to 55.
Cut-off raised to 58.
Cut-off raised to 61.
Cut-off raised to 64.
Cut-off raised to 67.
Cut-off raised to 70.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                   Init. Opt.
Sequence Name      Description               Length Score Score  Sig. Frame
----------------------------------------------------------------------------
                   **** 60 standard deviations above mean ****
  1. MUSLIGAND     Mouse flt3 ligand mRNA, compl    829   829   829  60.20   0
                   **** 45 standard deviations above mean ****
  2. MMU04807      Mus musculus FLT3/FLK2 ligand   1152   630   807  45.19   0
                   **** 26 standard deviations above mean ****
  3. HSU04806      Human FLT3/FLK2 ligand mRNA,     859   378   591  26.18   0
  4. HSU03858      Human flt3 ligand mRNA, compl   1080   378   608  26.18   0
                   **** 10 standard deviations above mean ****
  5. HSC1RCP       Human complement C1r mRNA, co   2493   173   397  10.71   0
  6. HUMIRBPG      Human interstitial retinol-bi   9711   172   391  10.64   0
  7. HUMIRBPG      Human interstitial retinol-bi   9711   172   391  10.64   0
                   ****  9 standard deviations above mean ****
  8. HSCGPDEG2     Human rod cGMP-phosphodiester   2417   162   392   9.88   0
  9. HSC1R         Human mRNA for complement com   2386   160   398   9.73   0
 10. HUMC1R        Human complement C1r mRNA, co   2493   160   397   9.73   0
 11. HUMCEL        Human carboxyl ester lipase (  11502   156   395   9.43   0
 12. HSCEL         Human carboxyl ester lipase (  11502   156   395   9.43   0
 13. DDU03413      Dictyostelium discoideum AX2    1679   155   369   9.36   0
 14. HSNUMAU4G     H.sapiens NuMA gene (Clone U4   2832   153   403   9.20   0
 15. HSNUMAU6G     H.sapiens NuMA gene (Clone U6   4762   153   403   9.20   0
 16. HSNUMAMR      H.sapiens mRNA for NuMA prote   7154   153   403   9.20   0
 17. SSENDOGA      S.scrofa endoglin mRNA, compl   2908   151   390   9.05   0
                   ****  8 standard deviations above mean ****
 18. OCAPOAI       Rabbit apo-AI mRNA for apolip    892   149   330   8.90   0
 19. MUSACTR2B     Mouse activin receptor (ActR    1708   148   389   8.83   0
 20. LEMINVOL      Lemur (ring-tailed) involucri   1380   147   396   8.75   0
 21. HUMIRBPM      Human interstitial retinol bi   4124   146   352   8.68   0
 22. HUMIRBPM      Human interstitial retinol bi   4124   146   352   8.68   0
 23. MUSTRANONC    Mus musculus ERP mRNA, comple   2211   145   400   8.60   0
 24. AD4POLTP2     Adenovirus type 4 Pol gene, e   5541   145   386   8.60   0
 25. HUMMEVKIN     Homo sapiens mevalonate kinas   1967   144   407   8.53   0
 26. MMNETRN       M.musculus net mRNA.            2658   144   398   8.53   0
 27. SCSECYDNA     S.coelicolor secY locus DNA.    4794   143   411   8.45   0
 28. SCSECYDNA     S.coelicolor secY locus DNA     4794   143   411   8.45   0
 29. HSAE1ERY      Human anion exchanger (AE1) g  21319   140   396   8.22   0
 30. AGMUVDAMBP    Cercopithecus aethiops UV-dam   4181   138   382   8.07   0
                   ****  7 standard deviations above mean ****
 31. HRSIFNB       Horse interferon-beta gene, c   2467   135   349   7.85   0
 32. S70756S3      Tlx-1=homeobox gene HOX11 hom    771   134   339   7.77   0
 33. OCCALPH13     O.cuniculus gene for C alphal   1422   134   393   7.77   0
 34. CRATP2        C.reinhardtii atp2 (atpB) mRN   2664   134   404   7.77   0
 35. MUSACMHCB     Mouse alpha cardiac myosin he   5817   133   383   7.70   0
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 36. I08072        Sequence 4 from patent EP 029   1698   132   407   7.62   0
 37. PIGA2AR       Porcine alpha2A-adrenergic re   1728   132   397   7.62   0
 38. HUMGLUT5      Human glucose transport-like    2218   132   395   7.62   0
 39. HUMGCK        Human glucokinase (GCK) gene,   7807   132   385   7.62   0
 40. HUMIHRP       Human placental ribonuclease    1682   131   407   7.54   0
 41. HUMIHRP       Human placental ribonuclease    1682   131   407   7.54   0
 42. HUMRAI        Human ribonuclease/angiogenin   1920   131   407   7.54   0
 43. HUMRAI        Human ribonuclease/angiogenin   1920   131   407   7.54   0
 44. HSRAI         Human mRNA for ribonuclease/a   1921   131   407   7.54   0
 45. NEUAMG        N.crassa am (NADP-specific gl   2643   131   389   7.54   0


1. US-08-162-407-1 (1-879)
   MUSLIGAND     Mouse flt3 ligand mRNA, complete cds.

  LOCUS       MUSLIGAND     829 bp ss-mRNA            ROD       04-JAN-1994
  DEFINITION  Mouse flt3 ligand mRNA, complete cds.
  ACCESSION   L23636
  KEYWORDS    ligand.
  SOURCE      Mus musculus (strain SJL/J) cDNA to mRNA.
    ORGANISM  Mus musculus
              Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
              Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
  REFERENCE   1  (bases 1 to 829)
    AUTHORS   Lyman,S.D., James,L., VandenBos,T., deVries,P., Brasel,K.,
              Gliniak,B., Hollingsworth,L., Picha,K.S., McKenna,H.J.,
              Splett,R.R., Fletcher,F.A., Maraskovsky,E., Farrah,T.,
              Foxworthe,D., Williams,D.E. and Beckmann,M.P.
    TITLE     Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
              receptor -- a proliferative factor for primitive hematopoietic
              cells
    JOURNAL   Cell 75, 1157-1167 (1993)
    STANDARD  full automatic
  COMMENT     NCBI gi: 439441
  FEATURES             Location/Qualifiers
       source          1..829
                       /organism="Mus musculus"
                       /strain="SJL/J"
                       /sequenced_mol="cDNA to mRNA"
       sig_peptide     32..109
                       /codon_start=1
       CDS             32..727
                       /note="NCBI gi: 439442"
                       /codon_start=1
                       /product="flt3 ligand"
                       /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
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                       NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQ
                       CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR
                       GELHPGVPLPSHP"
       mat_peptide     110..724
                       /codon_start=1
  BASE COUNT      163 a    265 c    221 g    180 t
  ORIGIN

 Initial Score     =    829  Optimized Score    =    829  Significance = 60.20
 Residue Identity =   100%  Matches            =    829  Mismatches   =     0
 Gaps              =      0  Conservative Substitutions              =     0

         20       X 30        40        50        60        70        80
   ACGACCTGCTCTGTCACAGGCATGAGGGGTCCCCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
             CTGTCACAGGCATGAGGGGTCCCCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAA
             X       10        20        30        40        50        60

    90       100       110       120       130       140       150
   ATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCC
         70        80        90       100       110       120       130

 160       170       180       190       200       210       220       230
   ACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAG
      140       150       160       170       180       190       200

         240       250       260       270       280       290       300
   TCACTGTGGCCGTCAATCTTCAGGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TCACTGTGGCCGTCAATCTTCAGGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCT
    210       220       230       240       250       260       270

       310       320       330       340       350       360       370
   GGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATAC
  280       290       300       310       320       330       340       350

     380       390       400       410       420       430       440
   ATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACC
          360       370       380       390       400       410       420

  450       460       470       480       490       500       510
   TCCTGAAGGACACCTGCACACAGCTGCTTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TCCTGAAGGACACCTGCACACAGCTGCTTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTC
        430       440       450       460       470       480       490

 520       530       540       550       560       570       580       590
   GGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAG
      500       510       520       530       540       550       560

         600       610       620       630       640       650       660
   CCACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCCTCTCACACTGGTGC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CCACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCCTCTCACACTGGTGC
    570       580       590       600       610       620       630

       670       680       690       700       710       720       730
   TGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGAGCTCCACCCTGGGGTGCCCC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGAGCTCCACCCTGGGGTGCCCC
  640       650       660       670       680       690       700       710

     740       750       760       770       780       790       800
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   TCCCCTCCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCCAGGGTCTTATCTCGGTTACACCTG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TCCCCTCCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCCAGGGTCTTATCTCGGTTACACCTG
         720       730       740       750       760       770       780

   810       820       830       840       850   X   860
   TAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTCGT
   |||||||||||||||||||||||||||||||||||||||||||||||
   TAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGG
        790       800       810       820        X


2. US-08-162-407-1 (1-879)
   MMU04807      Mus musculus FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS       MMU04807      1152 bp    mRNA            ROD       11-MAY-1994
 DEFINITION  Mus musculus FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION   U04807
 KEYWORDS    .
 SOURCE      mouse.
   ORGANISM  Mus musculus
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Rodentia; Myomorpha; Muridae; Mus.
 REFERENCE   1  (bases 1 to 921)
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1152)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483846
 FEATURES             Location/Qualifiers
      source          1..1152
                      /clone="mouse Flt3/Flk2 ligand T110"
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      CDS             256..954
                      /note="NCBI gi: 483847"
                      /codon_start=1
                      /product="FLT3/FLK2 ligand"
                      /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
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                      NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQ
                      CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARR
                      RGELHPGVPLPSHP"
 BASE COUNT      238 a    346 c    324 g    244 t
 ORIGIN

Initial Score     =    630  Optimized Score  =    807  Significance = 45.19
Residue Identity =    90%  Matches          =    828  Mismatches   =    48
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Gaps              =      35  Conservative Substitutions            =      0

            X         10         20                    30        40
            GT-CGA-CTGGA-ACGAGACGACCTG---CT---------CTGTCACAGGCATGAGGGGTCC
            ||  || |  || ||  | |  ||||   ||         ||||||||||||||||||||||
  GGGCTGCAGGGTATGAGCCCGAGACCTGCCCTCCTGTCACTTCCAAGAACCTGTCACAGGCATGAGGGGTCC
     180    X  190        200       210       220       230       240

   50        60        70        80        90        100       110
  CCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  CCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTG
   250       260       270       280       290       300       310

120       130       140       150       160       170       180       190
  AGTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  AGTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAG
 320       330       340       350       360       370       380       390

        200       210       220       230       240       250       260
  TTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAG
         400       410       420       430       440       450       460

      270       280       290       300       310       320       330
  CACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCT
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  CACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCT
       470       480       490       500       510       520       530

     340       350       360       370       380       390       400
  AAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  AAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTA
     540       550       560       570       580       590       600

   410       420       430       440       450       460       470
  CCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGCT
  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
  CCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGGT
    610       620       630       640       650       660       670

480       490       500       510       520       530       540       550
  CTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  CTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCC
 680       690       700       710       720       730       740       750

        560       570       580       590       600       610       620
  TCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAG
         760       770       780       790       800       810       820

      630          640       650       660       670       680       690
  CTGTTGCTC---CTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGG
  |||||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  CTGTTGCTCCTGCTGCTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGG
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       830       840       850       860       870       880       890

       700       710       720       730       740       750       760
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  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
  CAAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGCCCCTCCCCTCCCATCCCTAGGATGCGAGCCTT
     900       910       920       930       940       950       960

     770       780       790       800       810                 820
  GTGCATCGTTGACTCAGCCAGGGTCTTATCTCGGTTACACCTGTA-AT----CTCA----GCCCTTGGGAGC
  ||||||||||||||||||||||||||||||||| | |   ||  | ||    | ||    | | |||  | |
  GTGCATCGTTGACTCAGCCAGGGTCTTATCTCGATGAGGTCTCAATATGTTGCCCAAACTGACTTTGAAAAC
   970       980       990      1000      1010      1020      1030

  830          840       850       860         870        X
  CCAGA-GCAGGAT--TGCTGAATGGTCTGGAGCAGGTCGTCTCG--TTCCAGTCGAC
  |  || |||   |  |||   |    ||    ||   |  || |  || | | |
  CTCGATGCACCTTCCTGCCCCACAAACT--TCCA-AACAGCTGGGCTTACGGGCATGCTATATACAA
1040      1050      1060        1070      1080      1090  X    1100


3. US-08-162-407-1 (1-879)
   HSU04806      Human FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS       HSU04806       859 bp    mRNA            PRI       11-MAY-1994
 DEFINITION  Human FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION   U04806
 KEYWORDS    .
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 798)
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 859)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483844
 FEATURES             Location/Qualifiers
      source          1..859
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                      /clone_lib="SV48 cDNA"
                      /organism="Homo sapiens"
                      /cell_line="SV48 thymic stroma"
      CDS             93..800
                      /note="NCBI gi: 483845"
                      /codon_start=1
                      /product="FLT3/FLK2 ligand"
                      /translation="MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVK
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Same as 2

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                      TEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
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 BASE COUNT      147 a    318 c    246 g    148 t
 ORIGIN

Initial Score     =    378  Optimized Score  =    591  Significance = 26.18
Residue Identity  =    72%  Matches          =    613  Mismatches   =   200
Gaps              =     32  Conservative Substitutions               =     0

              X       10         20        30         40        50        60
              GTCGACTGGAACGAGAC-GACCTGCTCTGTCA-CAGGCATGAGGGGTCCCCGGCAGAGATGA
                | |||||  | || | ||||  |   | ||  |||||||||||| ||||||| || ||||
    CCCTTCCACACCCAACTGGGGCAAGCCTGACC--CGGCGACAGGAGGCATGAGGGGCCCCCGGCCGAAATGA
      30      X 40        50          60        70        80        90

            70        80        90       100       110       120       130
    CAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCCTTGCCTGC
    |||||||||||||||||||||||||||   |||  |   | || ||| |||||||||||||  |  | ||
    CAGTGCTGGCGCCAGCCTGGAGCCCAACAACCTATC---TCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCA
     100       110       120       130          140       150       160

         140       150       160       170       180       190       200
    GGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTTGA
    | ||||| |  ||||| | ||||   ||||| |||||||||||| |||||   || ||  |  | ||| ||
    GTGGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGT
      170       180       190       200       210       220       230

       210       220       230       240       250       260       270
    CTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAGCACTGCAAGGCCT
    ||||| |||||||| |||||||||||||||| ||||||  ||| || ||||||||| ||| ||||  |||
    CTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCGC
    240       250       260       270       280       290       300

     280       290       300       310       320       330       340
    TGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAACGC
    | ||| | ||  |||| || ||||||||||| ||||  || |||||||| || ||||| ||||||| || ||
    TCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGC-AAGGC
  310       320       330       340       350       360       370        380

   350        360       370       380       390       400       410
    TT-CTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTG
    || ||||||  ||| ||||| |||||||| |||||||||  |||| |||| |||||||  ||    |||||
    TTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTT
           390       400       410       420       430       440       450

  420       430       440       450       460       470       480       490
    CGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGCTCTGAAGCCCTGT
    || |||||||||||||||||||||| ||||||| |||| |||| |   |||||| | || |||||||||||
    CGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGG
         460       470       480       490       500       510       520

          500       510       520       530       540       550       560
    ATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTG
    |||    |  |  ||||||| ||||| |||||||||||| ||||||| ||||| |||||||| |||||||
    ATC----ACTC--GCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCA
           530         540       550       560       570       580       590

        570       580       590       600       610       620       630
```

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|||||| ||||||||    |||| || |||||  ||| || | |||| ||   ||| |  ||  |||||||
CCCCCATGGAGTCCCCGGCCCCTGGAGGCCAC--AGCCCCGACAGCCCCG---CAGCCCCCT-CTGCTCCTC
       600       610       620         630          640        650

  640       650       660       670       680       690       700
CTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGG
|| |||||||||||  |    ||  |||||||||| || |||||| |||| | |||||| ||| |  |  ||
CTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCGG
 660       670       680       690       700       710       720

710       720       730           740         750       760       770
AGGGGGGAGCTCCACCCTGGGGTGC----CCCTCCCCTCCC--ATCCCTAGGATTCGAGCCTTGTGCATCGT
|  ||  | | || |||||||| ||     || ||| ||||   |||| ||||   |   |||||| | |
A--GGACACC-CCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCAC
 730        740       750       760       770       780       790

    780       790        800       810       820       830    X  840
TGACTCAGCCAGGGTCTTAT-CTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTG
||||   |||| || || || || ||    |   |||  | || |    ||||| |   |||
TGACCTGGCCAAGGCCTCATCCTGGGGAGGATACGTAGGCACA-CAGAGGGGAGTCACCAGCC
800       810       820       830       840        850        X


A


4. US-08-162-407-1 (1-879)
   HSU03858      Human flt3 ligand mRNA, complete cds.

 LOCUS       HSU03858      1080 bp    mRNA             PRI       19-JUL-1994
 DEFINITION  Human flt3 ligand mRNA, complete cds.
 ACCESSION   U03858
 KEYWORDS    .
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 1080)
   AUTHORS   Lyman,S.D., James,L., Johnson,L., Brasel,K., de Vries,P.,
             Escobar,S.S., Downey,H., Splett,R.R., Beckmann,M.P. and
             McKenna,H.J.
   TITLE     Cloning of the human homologue of the murine flt3 ligand: a growth
             factor for early hematopoietic progenitor cells
   JOURNAL   Blood 83, 2795-2801 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1080)
   AUTHORS   Lyman,S.D.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-NOV-1993) Stewart D. Lyman, Immunex Research and
             Development Corporation, 51, University St., Seattle, WA 98101, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 494978
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                      /organism="Homo sapiens"
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      5'UTR           1..83
      CDS             84..791
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                      /note="ATTTA mRNA instability motif"
      polyA_signal    1059..1064
      polyA_site      1080
                      /note="32 A residues"
 BASE COUNT      204 a    384 c    290 g    202 t
 ORIGIN

Initial Score    =     378 Optimized Score  =     608 Significance = 26.18
Residue Identity =     70% Matches          =     644 Mismatches   =   212
Gaps             =      60 Conservative Substitutions              =     0

              X          10            20          30           40        50
              GTC---GACTGGAAC----GAGACGACC-TG-CTCTGTCAC---AGGCATGAGGGGTCCCCG
              |||   |||| |  |    |   |  ||  | | | |  ||   |||||||||||| |||||
    GGGCATGAGGGTCCGAGACTTGTTCTTCTGTCCCTTCCAAGACCCGGCGACAGGAGGCATGAGGGGCCCCCG
       10     X  20        30        40        50        60        70

            60        70        80        90       100       110       120
    GCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGT
    || || |||||||||||||||||||||||||||||||   |||  |   | || ||| |||||||||||||
    GCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAACAACCTATC---TCCTCCTGCTGCTGCTGCTGAGC
     80        90       100       110       120          130       140

         130       140       150       160       170       180       190
    CCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTT
     |  | ||  | ||||| |  ||||| | ||||   ||||| |||||||||||| |||||   || ||  |
    TCGGGACTCAGTGGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATC
     150       160       170       180       190       200       210

       200       210       220       230       240       250       260
    AGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAGCAC
     | ||| || ||||| |||||||| |||||||||||||||| ||||||  ||| || ||||||||| ||| |
    CGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC
   220       230       240       250       260       270       280       290

     270       280       290       300       310       320       330
    TGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAG
    |||  || | | ||| | ||  |||| || ||||||||||| ||||  || |||||||| || ||||| |||
    TGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAG
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           300       310       320       330       340       350       360

   340       350        360       370       380       390       400
    ATGCAAACGCTT-CTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACC
    |||| || |||| ||||||  ||| ||||| |||||||| |||||||||  |||| |||| |||||||  ||
    ATGC-AAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCC
          370       380       390       400       410       420       430

  410       420       430       440       450       460       470       480
    AGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGCTCT
        ||||| || |||||||||||||||||||||| ||||||| |||| |||| |   |||||| | || ||
    CAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCT
        440       450       460       470       480       490       500

          490       500       510       520       530       540       550
    GAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTC
    ||||||||| |||    |  |  ||||||| ||||| |||||||||||| ||||||| ||||| ||||||||
    GAAGCCCTGGATC----ACTC--GCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTC
      510           520         530       540       550       560       570

        560       570       580       590       600       610       620
    CACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCT
     |||||||  |||||| ||||||||    |||| || |||||  ||| || | |||| ||   ||| |  ||
    AACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCAC--AGCCCCGACAGCCCCG---CAGCCCCCT
          580       590       600       610         620          630

      630       640       650       660       670       680       690
    GTTGCTCCTGCTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAG
      ||||||| || |||||||||||  |    ||  |||||||||| || |||||| |||| | |||||| ||
    -CTGCTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAG
    640       650       660       670       680       690       700

    700       710       720       730           740         750       760
    GGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGC----CCCTCCCCTCCC--ATCCCTAGGATTCGAGCCT
    | |  |  |||  ||  | | || |||||||| ||     || ||| ||||   |||| ||||   |   ||
    GACGCGGCGGA--GGACACC-CCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCT
  710       720          730       740       750       760       770

        770       780       790             800           810       820
    TGTGCATCGTTGACTCAGCCAGGGTCTTATC--TCGG----TTACAC----CTGTAATCTCAGCCCT-TGGG
    |||| | |  ||||   |||| || || |||   |||    ||| ||    | || |   ||| | | |
    TGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGA-GACAGACATCTATC
   780       790       800       810       820       830        840

              830       840       850       860       870        X
    AGCC-------CAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTCGTCTCGTTCCAGTCGAC
    | ||       ||| | |||| | ||||  ||     ||  ||  ||| |   ||||  ||
    ATCCCATTTTACAGGGGAGGA-TACTGA--GGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTG
  850       860       870          880       890       900       910

5. US-08-162-407-1 (1-879)
   HSC1RCP      Human complement C1r mRNA, complete cds.

 ID   HSC1RCP    standard; RNA; PRI; 2493 BP.
 XX
 AC   M14058;
 XX
 DT   02-APR-1988 (Rel. 15, Created)
 DT   16-DEC-1994 (Rel. 42, Last updated, Version 3)
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XX
DE   Human complement C1r mRNA, complete cds.
XX
KW   .
XX
OS   Homo sapiens (human)
OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC   Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
XX
RN   [1]
RP   1-2493
RA   Leytus S.P., Kurachi K., Sakariassen K.S., Davie E.W.;
RT   "Nucleotide sequence of the cDNA coding for human complement C1r";
RL   Biochemistry 25:4855-4863(1986).
XX
DR   SWISS-PROT; P00736; C1R_HUMAN.
XX
CC   NCBI gi: 179643
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FT   source          1..2493
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Initial Score    =    173  Optimized Score  =    397  Significance = 10.71
Residue Identity =    51%  Matches          =    486  Mismatches  =   342
Gaps             =    123  Conservative Substitutions             =      0

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              GTCGACT--GGAACGAGACGACC-TGCTCTG----TCA--CAGGCATG-AGGGGTCCCCGGC
              | | |||   |  |  | || ||  ||| ||    |||   || || | |    | || |||
    CTACGTTGGAGGCTACTTCTGTTCCTGCCGTCCAGGCTATGAGCTTCAGGAAGACAGGCATTCCTGCCAGGC
        570   X   580       590       600       610       620       630

          60            70        80          90       100       110
    AGAGATGA-CA--GTGCTG-GCGC-CAGCCTGGAGCCCAAAT-TCCTCCCTGTTGCTGCTGTTGCTGCTGCT
     |||   | ||  | ||||  | |  || |   || | | || |||  ||||  | | |  | | | || |
    TGAGTGCAGCAGCGAGCTGTACACGGAGGCATCAGGCTACATCTCCAGCCTGGAG-TACCCTCGGTCCTAC-
      640       650       660       670       680       690        700

   120       130           140       150         160       170       180
    GAGTCCTTGCCTGCGGGG----GACACCTGACTGTT--ACTTCAGCCACAGTCCCATCTCCTCCAACTTCAA
        |||  ||||||  |     ||| |   | | | |  |     ||| ||  |||  | ||| ||| |||
    -CCCCCTGACCTGCGCTGCAACTACAGCATCCGGGTGGAGCGGGGCCTCA--CCCTGCACCT-CAAGTTC--
       710       720       730       740       750         760        770
```

```
   190         200       210       220       230       240           250
AGTGAAG--TTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTC----AATCT
  || ||  ||| || | |||| |||||||| ||   |||  ||| | | | || || ||  |     ||||
-CTGGAGCCTTTTGATA-TTGA-TGACCACCAGC---AAG--TACACTGCCCCTATGACCAGCTACAGATCT
       780        790        800            810       820       830

        260          270        280       290       300        310
-TCAGGACGAGAAG--CACTG-CAAGGCCT-TGTGGAGCCTCTTCCTAGCCCAGCGCTGGATA-GAGCAACT
 |    ||| ||||  || || | ||  || || | |||     ||   ||| |  || || |  |||| |
ATGCCAACGGGAAGAACATTGGCGAGTTCTGTGGGAAGCAAAGGCC---CCCCGACCTCGACACCAGCAGC-
  840       850       860       870       880          890       900

 320        330       340       350       360       370       380
GAAGACTGTGG-CAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCT
 ||  ||||||    | | |      || | |  || || ||||  |     |  ||  |       ||||
-AATGCTGTGGATCTGCTGTTCTTCACAGATGAGTC-GGGGGACAGCCGGGGCTGGAAGCTGCGCTACACCA
     910       920       930        940       950       960       970

390       400         410       420       430       440       450
CATGTACCTTCCA--GCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGA
|    | | || |  ||||| | |  || | |  |   | | | ||  || ||||  |||   |||| ||
CCGAGATCATCAAGTGCCCCCAGCCCAA-GAC--C--CTAGACGAGTTCACCATCATCCAGAACCTGCAG--
    980       990      1000           1010      1020      1030

  460       470         480           490       500       510       520
  CACCTGCACACAGCTGCTTG-CT-CTGAA--GC--CCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTG
  |  | | || ||| | | || || ||  |  ||  |||| |   | |||| || ||||    |     ||
  CCTCAGTAC-CAGTTCCGTGACTACTTCATTGCTACCTGCA--AGCAAGG-CTACCAGCTCATAGAGGGGAA
1040       1050      1060      1070        1080       1090      1100

    530         540       550       560       570         580       590
CCTGGAGGTGCAGTGC--CAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGA--GTCCCATAGCCCTAGAAG
|| || | |||| | |  || | |   ||  |||   || || | |   | |  || |||| |||| ||| |
CCAGGTGCTGCATTCCTTCA-CAGCTGTCTGCCAGGATGATGGCACGTGGCATCGTGCCAT-GCCC-AGATG
1110      1120       1130      1140      1150      1160       1170

      600       610          620       630        640        650
CCACGGAGCTCCCAGAGCCT---CGGCCCAGGCAGCTGTTGCTCCTGCTG-CTGCTGCTGC-CTCTCACACT
| |  ||  ||   ||   |   | |||| |  | |||   ||  || || || | | | | |   |||| |
CAA--GA--TCAAGGACTGTGGGCAGCCCCGAAACCTG--CCTAATGGTGACTTCCGTTACACCACCACAAT
   1180        1190      1200        1210      1220      1230      1240

  660         670         680           690         700       710
G---GTG--CTGCTGGCAG--CCGCCTGGGG-CCTTC-GC--TG-GC-AAAGGGCAAGAAGGAGGGGGGAGC
|   |||  |  ||   ||  |||  |   |  || | ||  || || | |   ||||| | ||    ||||
GGGAGTGAACACCTACAAGGCCCGTATCCAGTACTACTGCCATGAGCCATATTACAAGATGCAGACCAGAGC
     1250      1260      1270      1280      1290      1300      1310

 720         730       740          750       760       770       780
T-CCACCCTGGGG--TGCCCCTCCCCT---CCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCC
|  || |  || |  ||  |      |   | | | |  || |   | || || || |    |||  |||
TGGCAGCAGGGAGTCTGAGCAAGGGGTGTACACCTGCACAGCA-CAGGGCATT-TGGAAGAATGA-ACAG-A
   1320      1330      1340      1350       1360       1370       1380

    790       800       810       820       830       840       850
AGGGTCTTATCTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGA
||||    |    | || | |      |  |||    |||||  || | | |     |  |||  |   | |
AGGGAGAGA---AGATTCCTCGGTGCTTGCCAGTGTGTGGGAAGCCCGTG-AACCCCGTGGAACAG-AGGCA
     1390         1400      1410      1420       1430      1440
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      860        870        X
    GCAGGTCGTC-TCGTTCCAGTCGAC
    ||   |  ||   |  | |   | |
    GCGCATAATCGGAGGGCAAAAAGCCAAGATGGGCA
  1450      1460      1470  X   1480


6. US-08-162-407-1 (1-879)
   HUMIRBPG     Human interstitial retinol-binding protein (IRBP)

LOCUS       HUMIRBPG     9711 bp ds-DNA             PRI       06-JAN-1995
DEFINITION  Human interstitial retinol-binding protein (IRBP) gene, complete
            cds.
ACCESSION   J05253
KEYWORDS    interstitial retinol-binding protein.
SOURCE      Human DNA, clone HGL.3.
  ORGANISM  Homo sapiens
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE   1  (bases 1 to 9711)
  AUTHORS   Fong,S.L., Fong,W.B., Morris,T.A., Kedzie,K.M. and Bridges,C.D.
  TITLE     Characterization and comparative structural features of the gene
            for human interstitial retinol-binding protein
  JOURNAL   J. Biol. Chem. 265, 3648-3653 (1990)
  STANDARD  full automatic
COMMENT     NCBI gi: 186534
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                     /note="precursor;  NCBI gi: 386835"
                     /codon_start=1
                     /product="interstitial retinol-binding protein"
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                     ALTSLSEEELLAWLQRGLRHEVLEGNVGYLRVDSVPGQEVLSMMGEFLVAHVWGNLMG
                     TSALVLDLRHCTGGQVSGIPYIISYLHPGNTILHVDTIYNRPSNTTTEIWTLPQVLGE
                     RYGADKDVVVLTSSQTRGVAEDIAHILKQMRRAIVVGERTGGGALDLRKLRIGESDFF
                     FTVPVSRSLGPLGGGSQTWEGSGVLPCVGTPAEQALEKALAILTLRSALPGVVHCLQE
                     VLKDYYTLVDRVPTLLQHLASMDFSTVVSEEDLVTKLNAGLQAASEDPRLLVRAIGPT
                     ETPSWPAPDAAAEDSPGVAPELPEDEAIRQALVDSVFQVSVLPGNVGYLRFDSFADAS
                     VLGVLAPYVLRQVWEPLQDTEHLIMDLRHNPGGPSSAVPLLLSYFQGPEAGPVHLFTT
                     YDRRTNITQEHFSHMELPGPRYSTQRGVYLLTSHRTATAAEEFAFLMQSLGWATLVGE
                     ITAGNLLHTRTVPLLDTPEGSLALTVPVLTFIDNHGEAWLGGGVVPDAIVLAEEALDK
                     AQEVLEFHQSLGALVEGTGHLLEAHYARPEVVGQTSALLRAKLAQGAYRTAVDLESLA
                     SQLTADLQEVSGDHRLLVFHSPGELVVEEAPPPPPAVPSPEELTYLIEALFKTEVLPG
                     QLGYLRFDAMAELETVKAVGPQLVRLVWQQLVDTAALVIDLRYNPGSYSTAIPLLCSY
                     FFEAEPRQHLYSVFDRATSKVTEVWTLPQVAGQRYGSHKDLYILMSHTSGSAAEAFAH
                     TMQDLQRATVIGEPTAGGALSVGIYQVGSSPLYASMPTQMAMSATTGKAWDLAGVEPD
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                     ITVPMSEALSIAQDIVALRAKVPTVLQTAGKLVADNYASAELGAKMATKLSGLQSRYS
                     RVTSEVALAEILGADLQMLSGDPHLKAAHIPENAKDRIPGIVPMQIPSPEVFEELIKF
                     SFHTNVLEDNIGYLRFDMFGDGELLTQVSRLLVEHIWKKIMHTDAMIIDMRFNIGGPT
                     SSIPILCSYFFDEGPPVLLDKIYSRPDDSVSELWTHAQVVGERYGSKKSMVILTSSVT
                     AGTAEEFTYIMKRLGRALVIGEVTSGGCQPPQTYHVDDTNLYLTIPTARSVGASDGSS
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                     /number=1
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                     /note="IRBP intron A"
     exon            4966..5156
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     intron          5157..7016
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     exon            7017..7159
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     exon            8766..>9121
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BASE COUNT     2246 a   2672 c   2641 g   2152 t
ORIGIN      Chromosome 10q11.2.

Initial Score    =    172  Optimized Score   =    391  Significance = 10.64
Residue Identity =    50%  Matches           =    481  Mismatches   =   348
Gaps             =    125  Conservative Substitutions               =     0

          X       10        20         30        40        50
          GTCGACTGGAACGAGACGACCTGCTCTG-TCACAGGCATGAGGGGTCCCCGG--CAGAGA-T
          |   |  ||    || | | |||| | |  ||  | || |    |  | | |  ||| ||
CAGCTGAGAAGGACAAGGGCGGAAGGC-AGCTGCACAGAGCAGGGCCACGGCTTGCACACAGTCCAGGGAGC
       30 X      40         50        60        70        80        90

60        70         80        90       100       110       120
GACAGTGCTGGCGCCA-GCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGA-GTCCTTGC
    |||| || |||| ||||    |||    ||| || || ||      | | | ||||| | |||| |||
TTTTGTGCAGGAGCCAGGCCT---CCCCCTGGTCC-CCATGATGAGAGAATGGGTTCTGCTCATGTCCGTGC
     100       110          120        130       140       150       160

   130            140       150       160       170       180       190
----CTGCGG---GG--GACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAG
    ||| ||    ||  | | ||  ||   |  | |||||| ||  ||   | ||  |    ||  |  |||
TGCTCTGTGGCCTGGCTGGCCCCACACACCTGTTCCAGCCA-AG--CCTGGTGCTGGA----CATGGCCAAG
       170       180       190       200          210           220

      200       210        220          230       240       250
TTTAGAGAGTTGACTGACCACCTGCTT-AAAGATTACC--C-AGTCACTGTGGCCGTCAATCTTCAGGACGA
 |       |||  | || | ||||||    ||  |||  |  | ||    ||  | ||  |  |||| |
GT---CCTCTTGGATAACTA-CTGCTTCCCGGAGAACCTGCTGGGCATGCAGGAAGCCATCCAGCAGGCCAT
     230       240        250       260       270       280       290
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260       270       280       290         300       310        320
  GAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCC-CAG-CGCTGGATAGAGCAACTGA-AGACTGTG-G
   |||  |  || |   || | |||| || ||  | || ||| ||||||  || |   |||| || | | | |
  CAAGAGC--CATGAGATTCT-GAGCATC-TCAGACCCGCAGACGCTGGCCAGTG-TGCTGACAGCCGGGGTG
      300         310         320       330       340        350       360

  330            340           350           360       370       380
  CAG-GGTC--TAA--GATGCAAAC--GCT--TCT----GGAGGACGTCAACACCGAGATACATTTTGTCACC
  ||| | ||  | |  ||| |   |  | |  |||     |||  |  || | |||||   |          |
  CAGAGCTCCCTGAACGATCCTCGCCTGGTCATCTCCTATGAGCCCAGCACCCCCGAGCCTCCCCCACAAGTC
         370       380       390       400       410       420       430

   390       400        410       420          430       440          450
  TCATGTACCTTCCAGCCCCT-ACCAGAATGTCTGC--GATTCG-TCCAGACCAACATCTCCC---ACCTCCT
   || | ||   |||||| || |  |||    ||||  |  | | | || |    | ||  ||   |  | ||
  CCA-GCACTCACCAGCCTCTCAGAAGAGGAACTGCTTGCCTGGCTGCAAAGGGGCCTCCGCCATGAGGTTCT
        440       450       460       470       480       490       500

         460       470         480       490       500       510
  -GAAGGACACCTGCACACAGCTGC--TTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAAT-TTCTCTC
   || ||  |  ||  |  | ||||   ||  | |  | || |   | ||| |  |||  || ||  |
  GGAGGGTAATGTGGGC-TACCTGCGGGTGGACAG-CGTCCCGGGCCAGGAGGTGCTG--AGCATGATGGGGG
      510        520       530        540       550         560       570

520       530        540       550       560       570       580       590
  GGTGCCTGGAGGTGCA-GTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAA
   || ||||| ||  || |||   |  ||| | |||     ||  || ||   |     || |||  || | |
  AGTTCCTGGTGGCCCACGTG--TGGGGGAAT-CTC----ATG-GGCACCTCCG-----CCTTAGTGCT-GGA
        580       590         600             610            620

         600          610       620       630       640         650
  GCCACGGAGCT-CCCA-GAG-CCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCT-GCTGCTGCC-TCTCACAC
   |  |||  || | || ||| ||  | | | ||||     | |  |  || ||  |||| ||     ||||
  TCTCCGGCACTGCACAGGAGGCCAGGTCTCTGGCATTCCCTACATCATCTCCTACCTGCACCCAGGGAACAC
630       640       650       660       670       680       690       700

    660       670       680       690       700        710           720
  --TGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAG-GGGGGA----GCTCCA-
    |  |||   |||   |   ||    ||  | ||  | ||   ||  | ||||    |||    || |||
  CATCCTGCACGTGGACACTATCTACAACCGCCCCT--CCAACACCACCACGGAGATCTGGACCTTGCCCCAG
        710       720       730         740       750       760       770

         730       740       750        760        770       780
  -CCCTGGGGTGCCCCTCCCCTCCCATCCCTAGGAT-TCGAG-CCTTGTGCATCGTTGACTCAG-CCAGGGTC
    ||||||       | |  | ||    | ||||| | | |  | |   || |    |  ||| |||||| |
  GTCCTGGGAGAAAGGTACGGTGCC--GACAAGGATGTGGTGGTCCTCACCAGC----AGCCAGACCAGGGGC
        780       790         800       810       820           830

790       800         810         820        830       840       850
  TTATCTCGGTTACA-CCTGTA-ATC--TCAGCCCTTG-GGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAG
   |  | ||   ||| |  | | |||  | |||   || | ||  |  | |  | | |  ||  || |||| |
  GTGGC-CGAGGACATCGCGCACATCCTTAAGCAGATGCGCAGGGC-CATCGTGGTGGGCGAGCGGACTGGGG
  840        850       860       870       880        890       900

   860         870           X
  CAGGTCGTCTCG--TTCC---AGTCGAC
   |||    || |   |||   ||  ||
  GAGGGGCCCTGGACCTCCGGAAGCTGAGGATAGGCGAG
  910       920       930    X  940
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7. US-08-162-407-1 (1-879)
   HUMIRBPG     Human interstitial retinol-binding protein (IRBP)

 LOCUS       HUMIRBPG      9711 bp ds-DNA             PRI       14-SEP-1994
 DEFINITION  Human interstitial retinol-binding protein (IRBP) gene, complete
             cds.
 ACCESSION   J05253
 KEYWORDS    interstitial retinol-binding protein.
 SOURCE      Human DNA, clone HGL.3.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 9711)
   AUTHORS   Fong,S.-L., Fong,W.-B., Morris,T.A., Kedzie,K.M. and Bridges,C.D.B.
   TITLE     Characterization and comparative structural features of the gene
             for human interstitial retinol-binding protein
   JOURNAL   J. Biol. Chem. 265, 3648-3653 (1990)
   STANDARD  full automatic
 COMMENT     NCBI gi: 186534
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                      /cell_type="leukocyte"
                      /sequenced_mol="DNA"
                      /clone="HGL3"
      prim_transcript 1..>9505
                      /note="IRBP mRNA and introns (alt.)"
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                      /note="IRBP mRNA and introns (alt.)"
      CDS             join(130..3180,4966..5156,7017..7159,8766..9121)
                      /gene="IRBP"
                      /map="chromosome 10"
                      /note="precursor;  NCBI gi: 386835"
                      /codon_start=1
                      /product="interstitial retinol-binding protein"
                      /translation="MREWVLLMSVLLCGLAGPTHLFQPSLVLDMAKVLLDNYCFPENL
                      LGMQEAIQQAIKSHEILSISDPQTLASVLTAGVQSSLNDPRLVISYEPSTPEPPPQVP
                      ALTSLSEEELLAWLQRGLRHEVLEGNVGYLRVDSVPGQEVLSMMGEFLVAHVWGNLMG
                      TSALVLDLRHCTGGQVSGIPYIISYLHPGNTILHVDTIYNRPSNTTTEIWTLPQVLGE
                      RYGADKDVVVLTSSQTRGVAEDIAHILKQMRRAIVVGERTGGGALDLRKLRIGESDFF
                      FTVPVSRSLGPLGGGSQTWEGSGVLPCVGTPAEQALEKALAILTLRSALPGVVHCLQE
                      VLKDYYTLVDRVPTLLQHLASMDFSTVVSEEDLVTKLNAGLQAASEDPRLLVRAIGPT
                      ETPSWPAPDAAAEDSPGVAPELPEDEAIRQALVDSVFQVSVLPGNVGYLRFDSFADAS
                      VLGVLAPYVLRQVWEPLQDTEHLIMDLRHNPGGPSSAVPLLLSYFQGPEAGPVHLFTT
                      YDRRTNITQEHFSHMELPGPRYSTQRGVYLLTSHRTATAAEEFAFLMQSLGWATLVGE
                      ITAGNLLHTRTVPLLDTPEGSLALTVPVLTFIDNHGEAWLGGGVVPDAIVLAEEALDK
                      AQEVLEFHQSLGALVEGTGHLLEAHYARPEVVGQTSALLRAKLAQGAYRTAVDLESLA
                      SQLTADLQEVSGDHRLLVFHSPGELVVEEAPPPPPAVPSPEELTYLIEALFKTEVLPG
                      QLGYLRFDAMAELETVKAVGPQLVRLVWQQLVDTAALVIDLRYNPGSYSTAIPLLCSY
                      FFEAEPRQHLYSVFDRATSKVTEVWTLPQVAGQRYGSHKDLYILMSHTSGSAAEAFAH
                      TMQDLQRATVIGEPTAGGALSVGIYQVGSSPLYASMPTQMAMSATTGKAWDLAGVEPD
                      ITVPMSEALSIAQDIVALRAKVPTVLQTAGKLVADNYASAELGAKMATKLSGLQSRYS
                      RVTSEVALAEILGADLQMLSGDPHLKAAHIPENAKDRIPGIVPMQIPSPEVFEELIKF
                      SFHTNVLEDNIGYLRFDMFGDGELLTQVSRLLVEHIWKKIMHTDAMIIDMRFNIGGPT
                      SSIPILCSYFFDEGPPVLLDKIYSRPDDSVSELWTHAQVVGERYGSKKSMVILTSSVT
                      AGTAEEFTYIMKRLGRALVIGEVTSGGCQPPQTYHVDDTNLYLTIPTARSVGASDGSS
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                      /number=1
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                      /product="interstitial retinol-binding protein"
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      intron          5157..7016
                      /note="IRBP intron B"
      exon            7017..7159
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      intron          7160..8765
                      /note="IRBP intron C"
      exon            8766..>9121
                      /gene="IRBP"
                      /number=4
 BASE COUNT    2246 a    2672 c    2641 g   2152 t
 ORIGIN      Chromosome 10q11.2.

Initial Score    =    172  Optimized Score  =    391  Significance = 10.64
Residue Identity =    50%  Matches          =    481  Mismatches   =   348
Gaps             =    125  Conservative Substitutions          =     0

              X       10        20         30        40        50
              GTCGACTGGAACGAGACGACCTGCTCTG-TCACAGGCATGAGGGGTCCCCGG--CAGAGA-T
              |   |  ||    || | | |||| | |  ||  | || |    |  | | |  ||| ||
    CAGCTGAGAAGGACAAGGGCGGAAGGC-AGCTGCACAGAGCAGGGCCACGGCTTGCACACAGTCCAGGGAGC
           30 X      40         50        60        70        80        90

    60        70         80        90        100       110       120
    GACAGTGCTGGCGCCA-GCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGA-GTCCTTGC
        |||| || |||| ||||    |||    ||| || || ||      | | | ||||| | |||| |||
    TTTTGTGCAGGAGCCAGGCCT---CCCCCTGGTCC-CCATGATGAGAGAATGGGTTCTGCTCATGTCCGTGC
         100       110          120         130       140       150       160

       130            140       150       160       170       180       190
    ----CTGCGG---GG--GACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAG
        ||| ||   ||  | | ||  ||   |  | |||||| ||  ||   | ||  |    ||  |  |||
    TGCTCTGTGGCCTGGCTGGCCCCACACACCTGTTCCAGCCA-AG--CCTGGTGCTGGA----CATGGCCAAG
           170       180       190       200          210          220

          200       210        220           230       240       250
    TTTAGAGAGTTGACTGACCACCTGCTT-AAAGATTACC--C-AGTCACTGTGGCCGTCAATCTTCAGGACGA
     |       |||  | || | ||||||    ||  |||  |  | ||    ||  | ||  |  |||| |
    GT---CCTCTTGGATAACTA-CTGCTTCCCGGAGAACCTGCTGGGCATGCAGGAAGCCATCCAGCAGGCCAT
         230       240         250       260       270       280       290

  260       270       280       290         300       310        320
    GAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCC-CAG-CGCTGGATAGAGCAACTGA-AGACTGTG-G
     |||  |  || |   || | |||| || ||  | || ||| ||||||   |||   |||| || | | | |
    CAAGAGC--CATGAGATTCT-GAGCATC-TCAGACCCGCAGACGCTGGCCAGTG-TGCTGACAGCCGGGGTG
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        300         310         320       330       340        350       360

    330            340           350           360       370       380
    CAG-GGTC--TAA--GATGCAAAC--GCT--TCT----GGAGGACGTCAACACCGAGATACATTTTGTCACC
    ||| | ||  | |  ||| |   |  | |  |||     |||  |  || | |||||   |          |
    CAGAGCTCCCTGAACGATCCTCGCCTGGTCATCTCCTATGAGCCCAGCACCCCCGAGCCTCCCCCACAAGTC
           370       380       390       400       410       420       430

     390       400        410       420          430       440          450
    TCATGTACCTTCCAGCCCCT-ACCAGAATGTCTGC--GATTCG-TCCAGACCAACATCTCCC---ACCTCCT
     || | ||   |||||| || |  |||    ||||  |  | | | || |    | ||  ||   |  | ||
    CCA-GCACTCACCAGCCTCTCAGAAGAGGAACTGCTTGCCTGGCTGCAAAGGGGCCTCCGCCATGAGGTTCT
          440       450       460       470       480       490       500

           460       470         480       490       500       510
    -GAAGGACACCTGCACACAGCTGC--TTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAAT-TTCTCTC
     || ||  |  ||  |  | ||||   ||  | |  | || |   | ||| |  |||  || ||  |
    GGAGGGTAATGTGGGC-TACCTGCGGGTGGACAG-CGTCCCGGGCCAGGAGGTGCTG--AGCATGATGGGGG
        510        520       530        540       550         560       570

  520       530        540       550       560       570       580       590
    GGTGCCTGGAGGTGCA-GTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAA
     || ||||| ||  || |||   |  ||| | |||     ||  || ||   |     || |||  || | |
    AGTTCCTGGTGGCCCACGTG--TGGGGGAAT-CTC----ATG-GGCACCTCCG-----CCTTAGTGCT-GGA
          580       590         600             610            620

           600          610       620       630       640         650
    GCCACGGAGCT-CCCA-GAG-CCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCT-GCTGCTGCC-TCTCACAC
     |  |||  || | || ||| ||  | | | ||||     | |  |  || ||  ||||  ||     ||||
    TCTCCGGCACTGCACAGGAGGCCAGGTCTCTGGCATTCCCTACATCATCTCCTACCTGCACCCAGGGAACAC
  630       640       650       660       670       680       690       700

      660       670       680       690       700        710           720
    --TGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAG-GGGGGA----GCTCCA-
      |  |||   |||   |   ||    ||  | ||  | ||   ||  | ||||    |||    || |||
    CATCCTGCACGTGGACACTATCTACAACCGCCCCT--CCAACACCACCACGGAGATCTGGACCTTGCCCCAG
          710       720       730         740       750       760       770

           730       740       750        760        770       780
    -CCCTGGGGTGCCCCTCCCCTCCCATCCCTAGGAT-TCGAG-CCTTGTGCATCGTTGACTCAG-CCAGGGTC
      ||||||       | |  | ||    | ||||| | | |  | |   || |    |  ||| |||||| |
    GTCCTGGGAGAAAGGTACGGTGCC--GACAAGGATGTGGTGGTCCTCACCAGC----AGCCAGACCAGGGGC
          780       790         800       810       820           830

  790       800         810         820        830       840       850
    TTATCTCGGTTACA-CCTGTA-ATC--TCAGCCCTTG-GGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAG
     |  | ||   ||| |  | | |||  | |||   || | ||  |  | |  | | |  ||  || |||| |
    GTGGC-CGAGGACATCGCGCACATCCTTAAGCAGATGCGCAGGGC-CATCGTGGTGGGCGAGCGGACTGGGG
    840        850       860       870       880        890       900

     860         870           X
    CAGGTCGTCTCG--TTCC---AGTCGAC
     |||    || |   |||   ||  ||
    GAGGGGCCCTGGACCTCCGGAAGCTGAGGATAGGCGAG
    910       920       930    X  940


8.  US-08-162-407-1 (1-879)
   HSCGPDEG2    Human rod cGMP-phosphodiesterase gamma-subunit (PD
LOCUS       HSCGPDEG2    2417 bp    DNA             PRI       20-DEC-1993
DEFINITION  Human rod cGMP-phosphodiesterase gamma-subunit (PDEG) gene, exon 2.
ACCESSION   U00481
KEYWORDS    .
SEGMENT     2 of 3
SOURCE      human.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2417)
  AUTHORS   Hahn,L.B., Berson,E.L. and Dryja,T.P.
  TITLE     Evaluation of the gene encoding the gamma subunit of rod
            phosphodiesterase in retinitis pigmentosa
  JOURNAL   Unpublished
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 2417)
  AUTHORS   Cotran,P.R., Bruns,G.A., Berson,E.L. and Dryja,T.P.
  TITLE     Genetic analysis of patients with retinitis pigmentosa using a
            cloned cDNA probe for the human gamma subunit of cyclic GMP
            phosphodiesterase
  JOURNAL   Exp. Eye Res. 53, 557-564 (1991)
  STANDARD  full automatic
REFERENCE   3  (bases 1 to 2417)
  AUTHORS   Tuteja,N., Danciger,M., Klisak,I., Tuteja,R., Inana,G.,
            Mohandas,T., Sparkes,R.S. and Farber,D.B.
  TITLE     Isolation and characterization of cDNA encoding the gamma-subunit
            of cGMP phosphodiesterase in human retina
  JOURNAL   Gene 88, 227-232 (1990)
  STANDARD  full automatic
REFERENCE   4  (bases 1 to 2417)
  AUTHORS   Dryja,T.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-1993) Thaddeus P. Dryja, Massachusetts Eye and
            Ear Infirmary, Harvard Medical School, Room CB621, 243 Charles
            Street, Boston, MA 02114-3096, USA
  STANDARD  full automatic
COMMENT     NCBI gi: 409400
FEATURES             Location/Qualifiers
     source          1..2417
                     /map="17q(approx.21.1)"
                     /organism="Homo sapiens"
                     /cell_line="normal human lymphoblast line"
     repeat_unit     1..236
                     /rpt_family="Alu-class IV(sense)"
                     /evidence=experimental
     repeat_unit     321..601
                     /rpt_family="Alu-class II(sense)"
                     /evidence=experimental
     repeat_unit     complement(886..1173)
                     /rpt_family="Alu-classIII(sense)"
                     /evidence=experimental
     exon            1637..1841
                     /gene="PDEG"
                     /note="1637..1695 is noncoding; initiation codon at 1696"
                     /number=2
                     /evidence=experimental
                     /product="gamma-subunit of rod cGMP phosphodiesterase"
     misc_feature    1682..1683
                     /note="C deletion polymorphism"
     repeat_unit     2088..2371
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                        /rpt_family="Alu-classII(sense)"
                        /evidence=experimental
 BASE COUNT       621 a    598 c    810 g    388 t
 ORIGIN

Initial Score    =    162  Optimized Score  =    392  Significance =  9.88
Residue Identity =    49%  Matches          =    462  Mismatches   =   376
Gaps             =     97  Conservative Substitutions              =     0

              X       10        20          30        40         50
              GTCGACTGGAACGAGACGACC--TGCTCTGTCACAGGCATGAGGGGTC-CCCGGCAGAGATG
               ||  ||||  |  |  | ||  | | | | ||   ||   || || |   | |||||| |
    AGGCAGGCTCCTCTGCTGGGCCTGGCAGGCCCATTCCCAG-CAGGAGCCACAGAGGACTTTCAGCAGAG-TA
   810       820       830       840        850       860       870

   60            70         80         90         100       110
    ACAG-TG---CTGGCGC-CAGCCTGGAGCC-CAAATTCC-TCCCTGT-TGCTGCTGTTGCTGCTG----CTG
     ||| ||   | || ||   | ||   |||   ||| ||  | || |  |  ||||  || | ||     ||
    GCAGCTGGGCCGGGTGCGGTGGCTCACGCCTGTAATACCAGCACTTTGGGAGGCTGAGGCGGGTGGATCATG
   880       890       900       910       920       930       940       950

  120       130       140        150       160       170       180       190
    AGTCCTTGCCTGCGGGGGACACCT-GACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAA
    ||  |  |  | || |  | |||| | |       | |  | | |||   ||| ||  || | ||||   ||
    AGGTCAGGAGTTCGAGACA-ACCTCGTCAACATGGTGAAACCCCGTC---TCTACTAAAAATGCAAA---AA
           960        970       980       990         1000      1010

           200       210       220        230       240       250        260
    GTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTAC-CCAGTCACTGTGGCCGTCAATCTTCAGG-ACGAG
     |  | ||| | | | |    | || |   |||   |   | || | |  || |   |   | ||| | |||
    -TGCAAAGATTAGCCGG---GCATGGTGGCAGACGCCGGTAATCCCAGCTGCTGGGGAGGCTGAGGCAGGAG
      1020      1030         1040      1050      1060      1070      1080

           270       280       290       300       310       320       330
    AAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGG
    || ||||  ||  ||  | || |    || | ||   ||| |  ||||| || |||| |  |     ||||
    AATCACTTGAA-CCCGGGAGGCGGAGGTTGC-AG-TGAGC-CGAGATAGTGCCACTGCACTCCAGCCCAGGC
       1090       1100      1110        1120       1130      1140      1150

         340        350         360       370       380       390       400
    TCTAAGATGCAAACGCT-TCTGGAGGAC--GTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAG
       ||||   |||| || |||  |  ||    ||| ||  | | | |    |      ||  ||  | ||
    AACAAGAGCAAAACTCTGTCTCAAAAACAAAACAAAACAAAAAAAAACCCAG-AGTAGCAGTTAAATGCCGA
         1160      1170      1180      1190      1200       1210      1220

          410        420          430       440       450        460
    CCCCTACCA-GAATGTCTGCGATTCG---TCCAGACCAACATCTCCCACCTCCTGA-AGGACACCTGCACAC
    |      || |  |  ||| | |  |     |||   ||        |  |  | |  || ||||  ||||
    CGGGAGTCACGCTTCCCTGGGGTGGGAACGCAGGGGAAGGGGCAGGAAGTTGTCAGTGGTCACC--CACAG
        1230      1240      1250      1260      1270      1280        1290

   470       480       490       500       510       520        530
    AGCTGCTTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGT-GCCTGGAGGTGCAGTGC
     |  |  || |  | |  || |  || |||   ||||||| |  ||     | | |  | |  ||| | ||
    GGAGG--TGGTGAGGACTCCAGGCTCAGGA---CCTGCCACAGGTTGGGAGGCTAGGTTTGCTGTGGATTGT
          1300      1310      1320         1330      1340      1350

  540        550       560       570       580        590        600
    CAGCC-GGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCT-AGAAGCCA-CGGAGCTCCCAGAG
      ||| || |        || |  | |     ||||| ||  |||  |  |  |||| ||  ||     | |
    GGGCCGGGGCGAGGGAGGCCAG--GACAGGGGGAGT-CCGGAGCTGTGTGTGGCCAGCGTTGC-AGGGGGG
 1360      1370      1380        1390       1400      1410      1420

   610       620       630        640       650        660       670
    CCTCGGCCCAGGCAGCTGTTGCTCCTGC-TGCTGCTGCTGCCTCTCACA-CTGGTGCTGCTGGCAGCCGCCT
    | ||   | |||||   |        || ||| | ||   ||   || | ||||    |||||   || ||
    CATC-CACTAGGCAAGGGGAATGGGAGCGTGCGGGTGGACCCAAGCAAAGCTGG-CAGGCTGGTTACC-CCA
   1430       1440      1450      1460      1470      1480       1490

   680       690        700       710         720       730       740
    GGGGCCTTCGCTGGCAAAG-GGCAAGAAGGAGGGGGGAGCT--CCACCCTGGGGTGCCCCTCCCCTCCCATC
    |||    | || ||    |  |   | | || |  ||||||  |    |||||.  | |  ||||| ||| |
    GGGCGGATTGCAGGGGCTGCTGTCTGGATGACGCTGGAGCTGGCGGGGCTGGG--TCTCAGCCCCT-CCACC
    1500      1510      1520      1530      1540        1550      1560

    750       760                     770       780        790       800
    CCTAGGATTCGAGCC---------TTG--TGC---ATCGTTGACTCAG-CCAGGGTCTTATCTCGGTTACAC
      | || |  || ||         |||   ||   |  | |||||  | || ||| ||  ||    |  | |
    GGTGGGTTGAGACCCCCACAAGGGTTGGAAGCAGGAGGGCTGACTGGGACCCGGGCCTGGTC----TGCCCC
     1570      1580      1590      1600      1610      1620          1630

      810       820       830         840       850        860       870
    CTGTAATCTCAGCCCTTGGGAGCCCA-GAG-CAGGATTGCTGAATGGTCTGGAGCAG-GTCGTCTCGTTCC-
    | |  | | ||||    ||||| ||| ||| || | |||| |    ||||    |||  ||  |  |  ||
    CAG--ACCGCAGCAGGAGGGAGTCCAGGAGCCAAGGTTGCCGCGGTGTCTCCGTCAGCCTCACCATGAACCT
         1640      1650      1660      1670      1680      1690      1700

            X
    --AGTCGAC
      |  || |
    GGAACCGCCCAAGGCTGAG
       1710 X    1720


9. US-08-162-407-1 (1-879)
   HSC1R          Human mRNA for complement component C1r.

 LOCUS       HSC1R         2386 bp    RNA             PRI       12-SEP-1993
 DEFINITION  Human mRNA for complement component C1r.
 ACCESSION   X04701
 KEYWORDS    complement protein C1r.
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2386)
   AUTHORS   Journet,A. and Tosi,M.
   TITLE     Cloning and sequencing of full-length cDNA encoding the precursor
             of human complement component C1r
   JOURNAL   Biochem. J. 240, 783-787 (1986)
   STANDARD  full automatic
 COMMENT     NCBI gi: 29538
 FEATURES             Location/Qualifiers
      source          1..2386
                      /organism="Homo sapiens"
      CDS             52..102
                      /note="signal peptide (AA -17 to -1);  NCBI gi: 29540"
                      /codon_start=1
                      /translation="MWLLYLLVPALFCRAGG"
      CDS             52..2169
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                      /note="precursor of C1r (AA -17 to 688);  NCBI gi: 29539"
                      /codon_start=1
                      /translation="MWLLYLLVPALFCRAGGSIPIPQKLFGEVTSPLFPKPYPNNFET
                      TTVITVPTGYRVKLVFQQFDLEPSEGCFYDYVKISADKKSLGRFCGQLGSPLGNPPGK
                      KEFMSQGNKMLLTFHTDFSNEENGTIMFYKGFLAYYQAVDLDECASRSKLGEEDPQPQ
                      CQHLCHNYVGGYFCSCRPGYELQEDRHSCQAECSSELYTEASGYISSLEYPRSYPPDL
                      RCNYSIRVERGLTLHLKFLEPFDIDDHQQVHCPYDQLQIYANGKNIGEFCGKQRPPDL
                      DTSSNAVDLLFFTDESGDSRGWKLRYTTEIIKCPQPKTLDEFTIIQNLQPQYQFRDYF
                      IATCKQGYQLIEGNQVLHSFTAVCQDDGTWHRAMPRCKIKDCGQPRNLPNGDFRYTTT
                      MGVNTYKARIQYYCHEPYYKMQTRAGSRESEQGVYTCTAQGIWKNEQKGEKIPRCLPV
                      CGKPVNPVEQRQRIIGGQKAKMGNFPWQVFTNIHGRGGGALLGDRWILTAAHTLYPKE
                      HEAQSNASLDVFLGHTNVEELMKLGNHPIRRVSVHPDYRQDESYNFEGDIALLELENS
                      VTLGPNLLPICLPDNDTFYDLGLMGYVSGFGVMEEKIAHDLRFVRLPVANPQACENWL
                      RGKNRMDVFSQNMFCAGHPSLKQDACQGDSGGVFAVRDPNTDRWVATGIVSWGIGCSR
                      GYGFYTKVLNYVDWIKKEMEED"
      CDS             103..2169
                      /note="C1r zymogenic form (AA 1-688);  NCBI gi: 579717"
                      /codon_start=1
                      /translation="XIPIPQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYRVKLVFQ
                      QFDLEPSEGCFYDYVKISADKKSLGRFCGQLGSPLGNPPGKKEFMSQGNKMLLTFHTD
                      FSNEENGTIMFYKGFLAYYQAVDLDECASRSKLGEEDPQPQCQHLCHNYVGGYFCSCR
                      PGYELQEDRHSCQAECSSELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLK
                      FLEPFDIDDHQQVHCPYDQLQIYANGKNIGEFCGKQRPPDLDTSSNAVDLLFFTDESG
                      DSRGWKLRYTTEIIKCPQPKTLDEFTIIQNLQPQYQFRDYFIATCKQGYQLIEGNQVL
                      HSFTAVCQDDGTWHRAMPRCKIKDCGQPRNLPNGDFRYTTTMGVNTYKARIQYYCHEP
                      YYKMQTRAGSRESEQGVYTCTAQGIWKNEQKGEKIPRCLPVCGKPVNPVEQRQRIIGG
                      QKAKMGNFPWQVFTNIHGRGGGALLGDRWILTAAHTLYPKEHEAQSNASLDVFLGHTN
                      VEELMKLGNHPIRRVSVHPDYRQDESYNFEGDIALLELENSVTLGPNLLPICLPDNDT
                      FYDLGLMGYVSGFGVMEEKIAHDLRFVRLPVANPQACENWLRGKNRMDVFSQNMFCAG
                      HPSLKQDACQGDSGGVFAVRDPNTDRWVATGIVSWGIGCSRGYGFYTKVLNYVDWIKK
                      EMEED"
      misc_feature    424..426
                      /note="N-linked glycosylation site"
      misc_feature    550..552
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      misc_feature    1440..1441
                      /note="zymogen cleavage site"
      misc_feature    1591..1593
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      misc_feature    1792..1794
                      /note="N-linked glycosylation site"
      misc_feature    2264..2269
                      /note="polyadenylation signal"
      polyA_site      2282
                      /note="polyadenylation site"
 BASE COUNT      587 a    661 c    648 g    490 t
 ORIGIN

Initial Score     =    160  Optimized Score  =    398  Significance =  9.73
Residue Identity  =    51%  Matches          =    487  Mismatches   =   341
Gaps              =    123  Conservative Substitutions             =     0

              X         10        20             30           40        50
              GTCGACT--GGAACGAGACGACC-TGCTCTG----TCA--CAGGCATG-AGGGGTCCCCGGC
              | | |||   |  |  | || ||  ||| ||    |||   || || | |    | || |||
    CTACGTTGGAGGCTACTTCTGTTCCTGCCGTCCAGGCTATGAGCTTCAGGAAGACAGGCATTCCTGCCAGGC
          560 X     570       580       590       600       610       620

          60            70         80         90       100       110
    AGAGATGA-CA--GTGCTG-GCGC-CAGCCTGGAGCCCAAAT-TCCTCCCTGTTGCTGCTGTTGCTGCTGCT
    |||   | ||  | ||||  | |  || |   || | | || |||  ||||  | | |  | | | || |
   TGAGTGCAGCAGCGAGCTGTACACGGAGGCATCAGGCTACATCTCCAGCCTGGAG-TACCCTCGGTCCTAC-
       630       640       650       660       670        680       690

  120       130           140       150         160       170       180
   GAGTCCTTGCCTGCGGGG----GACACCTGACTGTT--ACTTCAGCCACAGTCCCATCTCCTCCAACTTCAA
       |||  ||||||  |     ||| |   | | |  |     ||| ||  |||  | ||| ||| |||
   -CCCCCTGACCTGCGCTGCAACTACAGCATCCGGGTGGAGCGGGGCCTCA--CCCTGCACCT-CAAGTTC--
        700       710       720       730       740         750

      190         200       210       220       230       240          250
   AGTGAAG--TTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTC----AATCT
     || ||  ||| || | |||| |||||||| ||   |||  ||| | | | || || ||  |     ||||
   -CTGGAGCCTTTTGATA-TTGA-TGACCACCAGC---AAG--TACACTGCCCCTATGACCAGCTACAGATCT
  760       770         780       790           800        810        820

           260          270        280       290       300        310
   -TCAGGACGAGAAG--CACTG-CAAGGCCT-TGTGGAGCCTCTTCCTAGCCCAGCGCTGGATA-GAGCAACT
    |    ||| ||||  || || | ||  || || | |||     ||   ||| |  || || |  |||| |
   ATGCCAACGGGAAGAACATTGGCGAGTTCTGTGGGAAGCAAAGGCC---CCCCGACCTCGACACCAGCAGC-
       830       840       850       860          870       880       890

    320        330       340       350       360       370       380
   GAAGACTGTGG-CAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCT
    ||  ||||||    | | |      || | |  || || ||||  |     |  ||  |       ||||
   -AATGCTGTGGATCTGCTGTTCTTCACAGATGAGTC-GGGGGACAGCCGGGGCTGGAAGCTGCGCTACACCA
          900       910       920        930       940       950       960

   390       400         410       420       430       440       450
   CATGTACCTTCCA--GCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGA
   |    | | || |  ||||| | |  || | |  |   | | | ||  || ||||  |||   |||| ||
   CCGAGATCATCAAGTGCCCCCAGCCCAA-GAC--C--CTAGACGAGTTCACCATCATCCAGAACCTGCAG--
         970       980        990          1000      1010      1020

   460       470         480          490       500       510       520
   CACCTGCACACAGCTGCTTG-CT-CTGAA--GC--CCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTG
   |  | | || ||| | | || || ||  |  ||  |||| |   | |||| || ||||    |     ||
   CCTCAGTAC-CAGTTCCGTGACTACTTCATTGCTACCTGCA--AGCAAGG-CTACCAGCTCATAGAGGGGAA
   1030       1040      1050      1060        1070       1080      1090

       530         540       550       560       570         580       590
   CCTGGAGGTGCAGTGC--CAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGA--GTCCCATAGCCCTAGAAG
   || || | |||| | |  || | |   ||  |||   || || | |   | |  || |||| |||| ||| |
   CCAGGTGCTGCATTCCTTCA-CAGCTGTCTGCCAGGATGATGGCACGTGGCATCGTGCCAT-GCCC-AGATG
     1100      1110       1120      1130      1140      1150        1160

         600       610          620       630        640        650
   CCACGGAGCTCCCAGAGCCT---CGGCCCAGGCAGCTGTTGCTCCTGCTG-CTGCTGCTGC-CTCTCACACT
   | |  ||  ||   ||   |   | |||| |  | |||   ||  || || || | | | | |   |||| |
   CAA--GA--TCAAGGACTGTGGGCAGCCCCGAAACCTG--CCTAATGGTGACTTCCGTTACACCACCACAAT
          1170      1180      1190        1200      1210      1220

     660         670          680           690         700       710
   G---GTG--CTGCTGGCAG--CCGCCTGGGG-CCTTC-GC--TG-GC-AAAGGGCAAGAAGGAGGGGGGAGC
   |   |||  |  ||   ||  |||  |   |  || | ||  || || | |   ||||| | ||    ||||
   GGGAGTGAACACCTACAAGGCCCGTATCCAGTACTACTGCCATGAGCCATATTACAAGATGCAGACCAGAGC
1230      1240      1250      1260      1270      1280      1290      1300

    720         730       740          750       760       770       780
   T-CCACCCTGGGG--TGCCCCTCCCCT---CCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCC
```

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   |  || |  || |  ||  |      |   | | | |  || |   | || || || |    |||  |||
   TGGCAGCAGGGAGTCTGAGCAAGGGGTGTACACCTGCACAGCA-CAGGGCATT-TGGAAGAATGA-ACAG-A
        1310      1320      1330      1340       1350       1360

       790       800       810       820       830       840       850
   AGGGTCTTATCTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGA
   ||||    |    | || | |      |  |||    |||||  || | | |     |  |||  |   | |
   AGGGAGAGA---AGATTCCTCGGTGCTTGCCAGTGTGTGGGAAGCCCGTG-AACCCCGTGGAACAG-AGGCA
1370         1380      1390      1400      1410       1420      1430

     860        870        X
   GCAGGTCGTC-TCGTTCCAGTCGAC
   ||   || ||   |  | |   | |
   GCGCATCATCGGAGGGCAAAAAGCCAAGATGGGCA
   1440      1450      1460      1470


10. US-08-162-407-1 (1-879)
    HUMC1R         Human complement C1r mRNA, complete cds.

 LOCUS       HUMC1R       2493 bp ss-mRNA            PRI       31-OCT-1994
 DEFINITION  Human complement C1r mRNA, complete cds.
 ACCESSION   M14058
 KEYWORDS    .
 SOURCE      Human, cDNA to mRNA.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2493)
   AUTHORS   Leytus,S.P., Kurachi,K., Sakariassen,K.S. and Davie,E.W.
   TITLE     Nucleotide sequence of the cDNA coding for human complement C1r
   JOURNAL   Biochemistry 25, 4855-4863 (1986)
   STANDARD  full automatic
 COMMENT     NCBI gi: 179643
 FEATURES             Location/Qualifiers
      source          1..2493
                      /organism="Homo sapiens"
      mat_peptide     64..1452
                      /note="C1r A chain"
                      /codon_start=1
      CDS             64..2181
                      /gene="C1R"
                      /map="12p13"
                      /note="human complement C1r;  NCBI gi: 179644"
                      /codon_start=1
                      /gdb_xref="G00-119-729"
                      /translation="MWLLYLLVPALFCRAGGSIPIPQKLFGEVTSPLFPKPYPNNFET
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                      KEFMSQGNKMLLTFHTDFSNEENGTIMFYKGFLAYYQAVDLDECASRSKSGEEDPQPQ
                      CQHLCHNYVGGYFCSCRPGYELQEDRHSCQAECSSELYTEASGYISSLEYPRSYPPDL
                      RCNYSIRVERGLTLHLKFLEPFDIDDHQQVHCPYDQLQIYANGKNIGEFCGKQRPPDL
                      DTSSNAVDLLFFTDESGDSRGWKLRYTTEIIKCPQPKTLDEFTIIQNLQPQYQFRDYF
                      IATCKQGYQLIEGNQVLHSFTAVCQDDGTWHRAMPRCKIKDCGQPRNLPNGDFRYTTT
                      MGVNTYKARIQYYCHEPYYKMQTRAGSRESEQGVYTCTAQGIWKNEQKGEKIPRCLPV
                      CGKPVNPVEQRQRIIGGQKAKMGNFPWQVFTNIHGRGGALLGDRWILTAAHTLYPKE
                      HEAQSNASLDVFLGHTNVEELMKLGNHPIRRVSVHPDYRQDESYNFEGDIALLELENS
                      VTLGPNLLPICLPDNDTFYDLGLMGYVSGFGVMEEKIAHDLRFVRLPVANPQACENWL
                      RGKNRMDVFSQNMFCAGHPSLKQDACQGDSGGVFAVRDPNTDRWVATGIVSWGIGCSR
                      GYGFYTKVLNYVDWIKKEMEEED"
      mat_peptide     1453..2178
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                      /note="C1r B chain serine protease"
                      /codon_start=1
 BASE COUNT      619 a    680 c    662 g    532 t
 ORIGIN      Chromosome 12p13.

Initial Score    =    160  Optimized Score =    397  Significance =  9.73
Residue Identity =    51%  Matches         =    486  Mismatches   =   342
Gaps             =    123  Conservative Substitutions              =     0

              X         10        20             30           40        50
              GTCGACT--GGAACGAGACGACC-TGCTCTG----TCA--CAGGCATG-AGGGGTCCCCGGC
              | | |||   |  |  | || ||  ||| ||    |||   || || | |    | || |||
    CTACGTTGGAGGCTACTTCTGTTCCTGCCGTCCAGGCTATGAGCTTCAGGAAGACAGGCATTCCTGCCAGGC
        570   X   580       590       600       610       620       630

          60            70         80         90        100       110
    AGAGATGA-CA--GTGCTG-GCGC-CAGCCTGGAGCCCAAAT-TCCTCCCTGTTGCTGCTGTTGCTGCTGCT
     |||   | ||  | ||||  | |  || |   || | | || |||  ||||  | | |  | | | || |
    TGAGTGCAGCAGCGAGCTGTACACGGAGGCATCAGGCTACATCTCCAGCCTGGAG-TACCCTCGGTCCTAC-
      640       650       660       670       680       690        700

   120      130           140       150         160       170       180
    GAGTCCTTGCCTGCGGGG----GACACCTGACTGTT--ACTTCAGCCACAGTCCCATCTCCTCCAACTTCAA
        |||  ||||||  |     ||| |   | | | |  |     ||| ||  |||  | ||| ||| |||
    -CCCCCTGACCTGCGCTGCAACTACAGCATCCGGGTGGAGCGGGGCCTCA--CCCTGCACCT-CAAGTTC--
       710       720       730       740       750         760        770

       190         200       210       220       230       240           250
    AGTGAAG--TTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTC----AATCT
      || ||  ||| || | |||| |||||||| ||   |||  ||| | | | || || ||  |     ||||
    -CTGGAGCCTTTTGATA-TTGA-TGACCACCAGC---AAG--TACACTGCCCCTATGACCAGCTACAGATCT
           780        790        800            810       820       830

            260          270        280       290       300        310
    -TCAGGACGAGAAG--CACTG-CAAGGCCT-TGTGGAGCCTCTTCCTAGCCCAGCGCTGGATA-GAGCAACT
     |    ||| ||||  || || | ||  || || | |||     ||   ||| |  || || |  |||| |
    ATGCCAACGGGAAGAACATTGGCGAGTTCTGTGGGAAGCAAAGGCC---CCCCGACCTCGACACCAGCAGC-
      840       850       860       870       880          890       900

     320        330       340       350       360       370       380
    GAAGACTGTGG-CAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCT
     ||  ||||||    | | |      || | |  || || ||||  |     |  ||  |       ||||
    -AATGCTGTGGATCTGCTGTTCTTCACAGATGAGTC-GGGGGACAGCCGGGGCTGGAAGCTGCGCTACACCA
         910       920       930        940       950       960       970

    390       400         410       420       430       440       450
    CATGTACCTTCCA--GCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGA
    |    | | || |  ||||| | |  || | |  |   | | | ||  || ||||  |||   |||| ||
    CCGAGATCATCAAGTGCCCCCAGCCCAA-GAC--C--CTAGACGAGTTCACCATCATCCAGAACCTGCAG--
        980       990      1000           1010      1020      1030

    460       470         480           490       500       510       520
    CACCTGCACACAGCTGCTTG-CT-CTGAA--GC--CCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTG
    |  | | || ||| | | || || ||  |  ||  |||| |   | |||| || ||||    |     ||
    CCTCAGTAC-CAGTTCCGTGACTACTTCATTGCTACCTGCA--AGCAAGG-CTACCAGCTCATAGAGGGGAA
  1040      1050      1060      1070        1080       1090      1100

        530         540       550       560       570         580       590
    CCTGGAGGTGCAGTGC--CAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGA--GTCCCATAGCCCTAGAAG
    || || | |||| | |  || | |   ||  |||   || || | |   | |  || |||| |||| ||| |
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    CCAGGTGCTGCATTCCTTCA-CAGCTGTCTGCCAGGATGATGGCACGTGGCATCGTGCCAT-GCCC-AGATG
    1110      1120       1130      1140      1150      1160       1170

          600       610          620       630        640        650
    CCACGGAGCTCCCAGAGCCT---CGGCCCAGGCAGCTGTTGCTCCTGCTG-CTGCTGCTGC-CTCTCACACT
    | |  ||  ||   ||   |   | |||| |  | |||   ||  || || || | | | | |   |||| |
    CAA--GA--TCAAGGACTGTGGGCAGCCCCGAAACCTG--CCTAATGGTGACTTCCGTTACACCACCACAAT
       1180        1190      1200        1210      1220      1230      1240

      660         670         680           690         700       710
    G---GTG--CTGCTGGCAG--CCGCCTGGGG-CCTTC-GC--TG-GC-AAAGGGCAAGAAGGAGGGGGGAGC
    |   |||  |  ||   ||  |||  |   |  || | ||  || || | |   ||||| | ||    ||||
    GGGAGTGAACACCTACAAGGCCCGTATCCAGTACTACTGCCATGAGCCATATTACAAGATGCAGACCAGAGC
         1250      1260      1270      1280      1290      1300      1310

     720         730       740          750       760       770       780
    T-CCACCCTGGGG--TGCCCCTCCCCT---CCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCC
    |  || |  || |  ||  |      |   | | | |  || |   | || || || |    |||  |||
    TGGCAGCAGGGAGTCTGAGCAAGGGGTGTACACCTGCACAGCA-CAGGGCATT-TGGAAGAATGA-ACAG-A
       1320      1330      1340      1350       1360       1370       1380

        790       800       810       820       830       840       850
    AGGGTCTTATCTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGA
    ||||    |    | || | |      |  |||    |||||  || | | |     |  |||  |   | |
    AGGGAGAGA---AGATTCCTCGGTGCTTGCCAGTGTGTGGGAAGCCCGTG-AACCCCGTGGAACAG-AGGCA
         1390         1400      1410      1420       1430      1440

      860        870        X
    GCAGGTCGTC-TCGTTCCAGTCGAC
    ||   |  ||   |  | |   | |
    GCGCATAATCGGAGGGCAAAAAGCCAAGATGGGCA
  1450      1460      1470  X   1480


11. US-08-162-407-1 (1-879)
    HUMCEL       Human carboxyl ester lipase (CEL) gene, complete c

 LOCUS       HUMCEL      11502 bp ds-DNA             PRI       01-NOV-1994
 DEFINITION  Human carboxyl ester lipase (CEL) gene, complete cds.
 ACCESSION   M94579
 KEYWORDS    carboxyl ester lipase.
 SOURCE      Homo sapiens (individual_isolate 1) (tissue library: lambda-DASH)
             male DNA.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 11502)
   AUTHORS   Lidberg,U., Nilsson,J., Stromberg,K., Stenman,G., Sahlin,P.,
             Enerback,S. and Bjursell,G.
   TITLE     Genomic organization, sequence analysis, and chromosomal
             localization of the human carboxyl ester lipase (CEL) gene and a
             CEL-like (CELL) gene
   JOURNAL   Genomics 13, 630-640 (1992)
   STANDARD  full automatic
 COMMENT     NCBI gi: 180243
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Initial Score    =    156  Optimized Score =    395  Significance =  9.43
Residue Identity =    51%  Matches         =    492  Mismatches   =   319
Gaps             =    151  Conservative Substitutions             =     0

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             GTCGACTGGAACGAGAC-GACCTG--CTCTGTCACAGGCATGAGGGGTCCCCGGCAGAGATG
             |||||| | |  | ||| ||| ||  |||||   ||||       |||||| ||||
   ACCGGCTGTGGTCGACAGAAGAGGGACAGACGTGGCCTCTG---CAGGTCCACTCGGTCCCTGGCA------
      550    X  560       570       580          590       600

  60        70        80        90       100       110       120
   ACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCC---TTGC
         | |||  || |  || | |  ||  |     ||| | || ||| |  |  ||  || ||    ||
   -----CCCGGCCGCA-CGGGGTGGCAGAA--CGGGAGTGTGGTTGGTGTGG--GAAGCACAGGCCCCAGTGT
        610        620       630         640       650         660

  130        140       150          160        170         180       190
   CTGC-GGGGGACACCTGACTGTTA---CTTCAGCCACAGTC-CCATCTCCTCCA--ACTTCAAAGTGAAGTT
   || | |||||||   ||  ||  |   ||   ||  |  || || | | | |||  ||| || || |  ||
   CTCCTGGGGGACTGTTGGGTGGGAAGGCTCTGGCTGCCCTCACCCTGTTC-CCATCACTGCAGAGGGCTGT-
 670       680       690       700       710        720       730

       200       210       220        230       240       250        260
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   --GCG-GTGGCCTG--GAGCTGC-CACTGAGTGTCTCGGTGAGGGTGACC-TCACACTGGCTGAGCTTAAAG
   740        750          760       770       780        790       800

            270           280            290        300       310       320
   ----CA-CTGCAAGGCCTT----GTGGAG-CCT----CTTCCTAG-CCCAGCGCTGGATAGAGCAACTGAAG
       || ||| ||| | ||    |||| |  ||    ||||  ||  ||    |||| |  || |  | ||
   GCCCCATCTG-AAGACTTTGTTCGTGGTGTTCTTTCACTTCTCAGAGCCTTTCCTGGCTCCAGGA--TTAAT
      810        820       830       840       850       860         870

            330       340       350       360        370       380
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   GGCCTCTTTCCCTCCCCTTCTGTCACTCTGCCTGGGCATGCCCCAGGGCCTCGGCTGGGCCCTTTGTTTCCA
      950       960       970       980       990      1000      1010

         460       470       480        490       500       510       520
   GAAGGACACCTGCACACAGCTGCTTGCTCT-GAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGT
    | ||| |||| ||      || |||  || || |||     || | |   ||  |||      | | | |
   CAGGGAAACCTACA------TGGTTGGGCTAGATGCC-----TCCGCA--CCCCCCCACCCACACCCCCTGA
   1020      1030            1040           1050        1060      1070

        530       540        550       560       570       580        590
   GCCTGGAGGTGCAGTGCCAGCC-GGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCT-AGAAG-
   ||||  | || |  | ||  || ||||   ||   |  | ||    |    ||| ||| |||| | ||  |
   GCCTCTA-GTCC--TCCCTCCCAGGACAGATCAGGCTGGATGGTGAC----AGTTCCACAGCCTTGAGTGGG
    1080         1090      1100      1110          1120      1130      1140

            600        610       620       630        640       650
   -CCAC--GGAGCT-CCCAGAGCCTCGGCCCAGGCAGCTGTTGCT-CCTGCTGCTGCTGCTGCCTCTCACACT
    |  |   | ||| | | | |  |||   ||  |||||    || || ||| |    ||  |     |  ||
   ACTGCCTTGTGCTGCTCTGGGATTCG---CACCCAGCTTGGACTACCCGCTCCACGGGCCCCAGGAAAAGCT
         1150      1160         1170      1180      1190      1200

 660           670             680            690          700        710
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    || | | |  || ||||| | ||      |||||| |     |||| |      |  | |||||  | | |
   CGTACAGATAAGGTCAGCCACATGAGTGGAGGGCCTGCAGCATGCTGCCCTTTCTGTCCCAGAAGTCACGTG
1210      1220      1230      1240      1250      1260      1270      1280

        720       730       740         750       760        770       780
   GGAGCTCCACCCTGGGGTGCCCCTCCCCTCCCA--TCCCTAGGATTCGAGCCTTGTG-CATCGTTGACTCAG
      | ||  ||||  |  ||||||     || |     | || |   | || | | | ||| |  |||  ||
   CTCGGTC--CCCTCTGAAGCCCCTTTGGACCTAGGGGACAAGCA---GGGCATGGAGACAT-GGAGACAAAG
          1290      1300      1310      1320         1330        1340

         790       800       810       820          830           840
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     | |  ||| ||||  | |||  || |  |  ||||| || || |   |||||  |||||  | || || |
   -TATGCCCTTTTCTC--TGACA-GTG-ACACCAAGCCC-TGTGAACAAACCAGAAGGCAGGGCACTG-TGCA
   1350      1360          1370      1380       1390      1400       1410

       850       860       870        X
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12. US-08-162-407-1 (1-879)
    HSCEL          Human carboxyl ester lipase (CEL) gene, complete c

 ID   HSCEL        standard; DNA; PRI; 11502 BP.
 XX
 AC   M94579;
 XX
 DT   15-JUL-1992 (Rel. 32, Created)
 DT   16-DEC-1994 (Rel. 42, Last updated, Version 6)
 XX
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DE   Human carboxyl ester lipase (CEL) gene, complete cds.
XX
KW   carboxyl ester lipase.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC   Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
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RN   [1]
RP   1-11502
RA   Lidberg U., Nilsson J., Stromberg K., Stenman G., Sahlin P.,
RA   Enerback S., Bjursell G.;
RT   "Genomic organization, sequence analysis, and chromosomal
RT   localization of the human carboxyl ester lipase (CEL) gene and a
RT   CEL-like (CELL) gene";
RL   Genomics 13:630-640(1992).
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DR   CPGISLE; HSCEL; Release 2.0.
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Initial Score     =    156  Optimized Score   =    395  Significance =  9.43
Residue Identity  =    51%  Matches           =    492  Mismatches   =   319
Gaps              =    151  Conservative Substitutions                =     0

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              |||||| | |  | ||| ||| ||  |||||   ||||       |||||| ||||
    ACCGGCTGTGGTCGACAGAAGAGGGACAGACGTGGCCTCTG---CAGGTCCACTCGGTCCCTGGCA------
       550    X  560       570       580          590       600

   60        70        80        90       100       110       120
    ACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCC---TTGC
          | |||  || |  || | |  ||  |     ||| | || ||| |  |  ||  || ||    ||
    -----CCCGGCCGCA-CGGGGTGGCAGAA--CGGGAGTGTGGTTGGTGTGG--GAAGCACAGGCCCCAGTGT
         610        620       630         640       650         660

   130        140       150          160        170         180       190
    CTGC-GGGGGACACCTGACTGTTA---CTTCAGCCACAGTC-CCATCTCCTCCA--ACTTCAAAGTGAAGTT
    || | |||||||   ||  ||  |   ||   ||  |  || || | | | |||  ||| || || |  ||
    CTCCTGGGGGACTGTTGGGTGGGAAGGCTCTGGCTGCCCTCACCCTGTTC-CCATCACTGCAGAGGGCTGT-
  670       680       690       700       710        720       730

        200       210       220        230       240       250        260
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   --GCG-GTGGCCTG--GAGCTGC-CACTGAGTGTCTCGGTGAGGGTGACC-TCACACTGGCTGAGCTTAAAG
   740        750          760       770       780        790       800

            270           280            290        300       310       320
   ----CA-CTGCAAGGCCTT----GTGGAG-CCT----CTTCCTAG-CCCAGCGCTGGATAGAGCAACTGAAG
       || ||| ||| | ||    |||| |  ||    ||||  ||  ||    |||| |  || |  | ||
   GCCCCATCTG-AAGACTTTGTTCGTGGTGTTCTTTCACTTCTCAGAGCCTTTCCTGGCTCCAGGA--TTAAT
      810        820       830       840       850       860         870

            330       340       350       360        370       380
   A-CTG-TGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCA-ACACCGAGATACATTTTGTCACCTCA
   | ||| |  |||    || ||  |     || ||  |  || ||| ||  |    | | ||   || || |
   ACCTGTTCACAGAAAATACGAGTCGCCTCCTCCTCCACAACCTCACACGACCTTCTCCCTTCCCTC-CCGCT
       880       890       900       910       920       930        940

 390       400          410       420       430       440             450
   TG-TACCTTCCAGCCCCTAC---CAGAATGTCTGCGATTCGTCCAGACCAACATCT---CCC---ACCTCCT
    |   | ||||  ||||| |   ||   || ||| |  |   ||||  |  |  ||   |||      |||
   GGCCTCTTTCCCTCCCCTTCTGTCACTCTGCCTGGGCATGCCCCAGGGCCTCGGCTGGGCCCTTTGTTTCCA
      950       960       970       980       990      1000      1010

         460       470       480        490       500       510       520
   GAAGGACACCTGCACACAGCTGCTTGCTCT-GAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGT
    | ||| |||| ||      || |||  || || |||     || | |   ||  |||      | | | |
   CAGGGAAACCTACA------TGGTTGGGCTAGATGCC-----TCCGCA--CCCCCCCACCCACACCCCCTGA
   1020      1030            1040           1050        1060      1070

        530       540        550       560       570       580        590
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   ||||  | || |  | ||  || ||||   ||   |  | ||    |    ||| ||| |||| | ||  |
   GCCTCTA-GTCC--TCCCTCCCAGGACAGATCAGGCTGGATGGTGAC----AGTTCCACAGCCTTGAGTGGG
    1080         1090      1100      1110          1120      1130      1140

            600        610       620       630        640       650
   -CCAC--GGAGCT-CCCAGAGCCTCGGCCCAGGCAGCTGTTGCT-CCTGCTGCTGCTGCTGCCTCTCACACT
    |  |   | ||| | | | |  |||   ||  |||||    || || ||| |    ||  |     |  ||
   ACTGCCTTGTGCTGCTCTGGGATTCG---CACCCAGCTTGGACTACCCGCTCCACGGGCCCCAGGAAAAGCT
         1150      1160         1170      1180      1190      1200

  660          670             680            690          700        710
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    || | | |  || ||||| | ||      |||||| |     |||| |      |  | |||||  | | |
   CGTACAGATAAGGTCAGCCACATGAGTGGAGGGCCTGCAGCATGCTGCCCTTTCTGTCCCAGAAGTCACGTG
1210      1220      1230      1240      1250      1260      1270      1280

        720       730       740         750       760        770       780
   GGAGCTCCACCCTGGGGTGCCCCTCCCCTCCCA--TCCCTAGGATTCGAGCCTTGTG-CATCGTTGACTCAG
      | ||  ||||  |  ||||||     || |     | || |   | || | | | ||| |  |||  ||
   CTCGGTC--CCCTCTGAAGCCCCTTTGGACCTAGGGGACAAGCA---GGGCATGGAGACAT-GGAGACAAAG
          1290      1300      1310      1320         1330       1340

         790       800       810       820          830           840
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     | |  ||| ||||  | |||  || |  |  ||||| || || |   |||||  |||||  | || || |
   -TATGCCCTTTTCTC--TGACA-GTG-ACACCAAGCCC-TGTGAACAAACCAGAAGGCAGGGCACTG-TGCA
   1350      1360          1370      1380       1390      1400       1410

       850       860       870        X
    ---TGGTCTGGAGCAGGTCGTCTCGTTCCAGTCGAC
       ||  | |   ||      | | | ||| || |
    CCCTGCCCGGCCCCACCATCCCCCTTACCACCCGCCACCTTGCCAC
        1420      1430      1440      1450


13. US-08-162-407-1 (1-879)
    DDU03413     Dictyostelium discoideum AX2 calcium binding prote

 LOCUS       DDU03413     1679 bp    mRNA            INV       21-NOV-1993
 DEFINITION  Dictyostelium discoideum AX2 calcium binding protein mRNA, complete
             cds.
 ACCESSION   U03413
 KEYWORDS    .
 SOURCE      slime mold.
   ORGANISM  Dictyostelium discoideum
             Eucaryotae; Protozoa; Sarcomastigophora; Sarcodina; Rhizopoda;
             Eumycetozoa; Dictyostelia; Dictyosteliida; Dictyostelium.
 REFERENCE   1  (sites)
   AUTHORS   Wennington,R., Greenwood,M. and Tsang,A.
   JOURNAL   Unpublished
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1679)
   AUTHORS   Wennington,R.
   TITLE     Direct Submission
   JOURNAL   Submitted (11-NOV-1993) Wennington R., Concordia University, 1455
             De Maisonneuve Blvd. West, Montreal, Quebec, H3G 1M8, Canada
   STANDARD  full automatic
 COMMENT     NCBI gi: 416312
 FEATURES             Location/Qualifiers
      source          1..1679
                      /organism="Dictyostelium discoideum"
                      /strain="AX2"
                      /dev_stage="vegetative"
      CDS             124..1527
                      /note="NCBI gi: 416313"
                      /codon_start=1
                      /product="calcium binding protein"
                      /translation="MQNPQNPPPAGSAADFYSQMPVKVMGTPGAPGSQSTPGAPGAPG
                      QYPPQQPGAPGSNLPPYPGTQQPGAPGAPGQYPPQQPGQYPPQQPGAPGQYPPQQPGQ
                      PGYPPQQPGQSGQYPPQQPGQPGYPPQQPGAPGQYPPQQGQPGQYPPQQPGQPGQYPP
                      QQQGQYPPQQPGQPGAYPPQQPGQPGAYPPQQGVQNTLAKTGAPGQPGVPPPQGAYPG
                      QPGVPPQQGAYPGQQPPMGAYPPQGQPGAYPPQGQPGAYPPQQQQVAYPGQQPPMGAY
                      PPQQGAYPGQQGAYPGQQGAYPGQQGAYPGQPPMGAYPGQQQYGVSAYSQTTAAYQTG
                      AYPGQTPMGVYPGQTTAYAAYQTTAIGYGATSTYSYTRPTYSYATPYSRTAAFVVPVG
                      LPPHVVQKMMAASAAFRIHDSNCSGTLSKKEFKKLIKHLGYYFSKGQTKMLFHSIDRD
                      YSGSLSEREFVDWWSMQ"
      misc_feature    1357..1395
                      /note="calcium binding site"
 BASE COUNT      567 a    429 c    251 g    432 t
 ORIGIN

Initial Score    =     155  Optimized Score  =     369  Significance =  9.36
Residue Identity =     48%  Matches          =     463  Mismatches   =   349
Gaps             =     140  Conservative Substitutions               =     0

              X       10        20        30            40            50
              GTCGACTGGAACGAGACGACCTGCTCTGTCA--CAGG-CA-TGAGGGG----TCCCCGGCA-
              ||| ||    | | | | |||  |     ||  |||| ||   ||| |    ||| |  ||
    CAACAACCAGGTCAAC---CAGGTGCCTACCCACCACAACAACCAGGTCAACCAGGTGCCTATCCACCACAA
```

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  630       640          650       660       670       680       690

         60          70         80        90       100       110       120
  -GAGATG-AC--AGTGCTGGCGCC-AGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGA
    || || ||  | | |    ||| || | || || | |  ||  |       | | |||| |  |  |  |
  CAAGGTGTACAAAATACACTTGCCAAGACAGGTGCTCCAGGTCAAC-------CAGGTGTTCCACCACC--A
   700       710       720       730       740              750

         130       140       150       160         170            180
  GTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACA--GTCCCATCTCC---TC--CAACTTCAAA
       |||||     || || |    |||| |  || | |||  || || | |||   ||  ||||  | ||
  CAAGGTGCCTATCCAGGTCAACCAGGTGTTCCACCA-CAACAAGGTGCC-TATCCAGGTCAACAACCACCAA
760       770       780       790        800        810       820

    190       200       210       220       230       240         250
  GTGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCA--ATCTTCAGG
    |  | |||   |    |  | | ||| |     || ||| |||  |||   | |   ||  | |||
  TGGGTGCTTATCCACCACAAGGTCAACCAG----GAGCTTATCCA-CCACAAGGTCAACCAGGAGCTTATCC
830       840       850           860       870        880       890

    260       270          280       290       300       310       320
  ACGAGAAGCACTGCAAG--GCCT-TGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTG
  || | ||  ||  ||||  || | |   |  |  |  ||   || |  | ||  ||   || |  || |  |
  ACCACAACAACAACAAGTAGCATATCCAGGTCAACAACC--ACCAATGGGTGCTTA-TCCACCACAACAAGG
   900       910       920       930         940       950        960

     330       340       350       360       370          380       390
  TGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTT---TGTCACCTCATGTA
  | |||   ||  || |  | | | | ||     | |||||||   || | ||| |    |||| |  | ||
  T-GCA-TATC-CAGGTCAACAAGGTGCTTATCCAGGTCAACA---AGGTGCATATCCAGGTCAAC-AAGGTG
      970        980       990      1000         1010      1020       1030

       400       410        420       430       440       450        460
  CCT-TCCAGCCCCTACCA-GAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGA-CACCT
  | | |||||   | ||||  ||||  ||| ||   |||||  |||||    | |  |  || |  | ||  |
  CATATCCAG-GTCAACCACCAATGGGTGC-AT--ATCCAGGTCAACA---ACAATATGGTGTATCAGCATAT
         1040      1050       1060        1070         1080      1090

            470       480       490             500       510       520
  GCAC-----ACAGCTGCTTGCTCTGAAGCCCTG--TATC--GG--GAAGGCCTGCCAGAATTTCTCTCGGT-
   |||     || |||||||  ||  ||    ||  ||||  ||   ||  ||     |  ||| ||  |||
  TCACAAACTACCGCTGCTT-ATC-AAACTGGTGCTTATCCAGGTCAAACACCAATGGGTGTTTATCCAGGTC
   1100      1110        1120      1130      1140      1150      1160

           530       540       550            560         570       580
  ----GCCTGGAGGTGCAGTGCCAGCCGGACTCCT-CCACC----CTGCTGC--CCCCAAGGAGTCCCATAGC
        ||| |  |||  ||||   |  ||  || | | |     || |||  |  |||    |  | || |
  AAACTACTGCATATGC--TGCCTATCAAACAACTGCTATCGGTTATGGTGCAACATCAACTTAT-TCTTA-C
   1170      1180        1190      1200      1210      1220       1230

      590       600       610       620          630       640       650
  CCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGC-AG--CTGTTGCTCCTGCTGCTGCTGCTGCCTCT
   |||| | | ||  | |||  |  ||  |  |  |  | ||  | | ||||  ||  | | | | ||  |
  ACTAG-ACCAACTTA-CTCTTA-TGCAACTCCATATTCTAGAACCGCTGCTTTTGTAGTTCCAGTTGGTTTA
      1240       1250       1260      1270      1280      1290      1300

       660       670       680       690         700       710       720
  CACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGG--GCAAGAAGGAGGGGGGAGCTCCAC
  |   |   || ||    ||         ||||       ||||  |  |||   || |     ||  ||||
  CCACCACATGTTG--TACAAAAAATGATGGCC-------GCAAGTGCTGCATTCAGAATTCATGA-TTCCA-
```

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        1310        1320      1330             1340      1350       1360

         730       740       750       760       770       780        790
    CCTGGGGTGCCCCTCCCCTCCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCCAGGGT-CT-TA
      ||  |||   ||    ||  |     || |||  |          || || |  ||   ||| | || |
    ATTGTAGTGGTACT-TTATCTAA--AAAAGAATTTAA-----AAAACTCATT-AAACATTTAGGTTACTATT
       1370       1380      1390             1400      1410       1420

             800       810       820          830          840        850
    TCTC----GGTTACACCTGTAATCTCAGCCCTTGGGA--GCCC-AGA--GCAG-GATTGCTGAA-TGGTCTG
    ||||    ||| | | ||  ||| | |  || |   |  |  |  ||   ||| | ||  | || ||  |
    TCTCTAAAGGTCA-AACTAAAATGTTATTCCATTCAATTGATCGTGATTACAGTGGTTCATTAAGTGAACGT
    1430       1440      1450      1460      1470      1480      1490

        860       870        X
    GAGCAGGTCGTCTCGTTCCAGTCGAC
    ||    || | || | |  |||   |
    GAATTTGTTGACT-GGTGGAGTATGCAATAAATTAA
   1500      1510       1520 X    1530
```

14. US-08-162-407-1 (1-879)
    HSNUMAU4G   H.sapiens NuMA gene (Clone U4).

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LOCUS       HSNUMAU4G     2832 bp    RNA             PRI       15-APR-1993
DEFINITION  H.sapiens NuMA gene (Clone U4).
ACCESSION   Z14228
KEYWORDS    alternative splicing; NuMA gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE   1  (bases 1 to 2832)
  AUTHORS   Tang,T.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-AUG-1992) to the EMBL/GenBank/DDBJ databases. Tang T.
            K., Institute of Biomedical Sciences, Laboratory of Cell Biology,
            Section 2, Academy Road, Taipei, Taiwan, Republic of China, 115
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 2832)
  AUTHORS   Tang,T.K., Tang,C.J., Chen,Y.L. and Wu,C.W.
  TITLE     Nuclear proteins of the bovine esophageal epithelium. II. The NuMA
            gene gives rise to multiple mRNAs and gene products reactive with
            monoclonal antibody W1
  JOURNAL   J. Cell. Sci 104, 249-260 (1993)
  STANDARD  full automatic
COMMENT     NCBI gi: 296119
FEATURES             Location/Qualifiers
     source          1..2832
                     /organism="Homo sapiens"
                     /cell_line="U251"
                     /clone_lib="U251 cDNA library"
                     /clone="Clone U4"
     mRNA            <1..2409
                     /gene="NuMA"
                     /note="alternative splice product"
                     /evidence=experimental
BASE COUNT      690 a    724 c    987 g    431 t
ORIGIN
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Initial Score      =    153  Optimized Score     =    403  Significance =  9.20
Residue Identity   =    51%  Matches             =    491  Mismatches   =   334
Gaps               =    128  Conservative Substitutions                =     0

              X        10            20           30        40        50
              GTC-GACTGGAACG-AG--ACGA-CCTGCTCTG---TCACAGGCATGAGGGGTCCCCGGCAG
              | | | |||||||| ||   |||  |||  | |   || | ||| |||| ||  |   ||
    GGAGCAGGCTGACAGCCTGGAACGCAGCCTCGAGGCTGAGCGGGCCTCCCGGGC-TGAGCGGGACAGTGCTC
    500       510       520       530       540       550        560

        60        70        80        90       100       110       120
    AGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGT-CCT
     |  |||  ||| || |||||  | |||   ||      ||| |  |||   |   | |   | |||| |||
    TGGAGACTCTGCAGG-GCCAG-TTAGAGGAGAA----GGCCCAGGAGCT-AGGGCACAG--TCAGAGTGCCT
   570       580         590           600       610        620         630

       130       140         150         160       170       180        190
    T-GCCTGCGGGGGACACCTGACT--GTT-ACTTCAGC-CACAGTCCCATCTCCTCCAACTTCAAAG-TGAAG
    | |||| |||   | ||  || |  | |  |||| || |  ||   ||   ||    ||  ||| | |||||
    TAGCCT-CGGCCCA-ACGGGAGTTGGCTGCCTTCCGCACCAAGGTACAAGACC----ACAGCAAGGCTGAAG
           640        650       660       670       680            690

           200          210           220       230       240       250
    TTTAGAGAGTTGAC----TGACC----ACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCA--
     | || |    | |    || ||     || ||   | | | |   ||  |   | ||| || |||  ||
    ATGAGTGGAAGGCCCAGGTGGCCCGGGGCCGGCAAGAGGCTGA--GAGGAAAAATAGCC-TC-ATCAGCAGC
    700       710       720       730       740         750         760

          260       270       280       290      300        310
    --GGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAA----CTGAA
      ||| ||| ||   | ||   || ||    |||   |||| |   || |  ||  |||||||     ||||
    TTGGAGGAGGAGGTGTCCA--TCC-TGAATCGCCAGGTCCTGGAGAAG-GAGGGGGAGAGCAAGGAGTTGAA
      770       780       790          800       810        820       830

    320           330       340       350        360       370       380
    --GACTG----TGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGA-CGTCAACACCGAGATACATTTTGTCA
      | |||    |||| | |||  ||| |     |   ||||||||  | |  | ||  | | ||    |  |
    GCGGCTGGTGATGGCCGAGTCAGAGAAGAGCCAGAAGCTGGAGGAGAGGCTGCGCC-TGCTGCAGGCAGAGA
      840         850       860       870       880        890       900

       390         400       410           420       430       440      450
    CCTCATGTACC--TTCCAGCCCCTACCAGAATG----TCTGCGATTCGTCCAGACCAACATCTCCCACCTCC
    |  |  | | |  | ||||   || | ||||| |    |||||  | ||    ||    ||       |||||
    CAGCCAGCAACAGTGCCAG-AGCTGC-AGAACGCAGCTCTGCTCTGCGGGAGGAGGTGCA----GAGCCTCC
       910       920         930       940       950       960          970

           460       470        480       490       500        510      520
    TGAAGGACACCTGCACACAGCTGCTTGC-TCTGAAGCCCTGTATCGGGAAGGCCTG-CCAGAATTTCTCTCG
     | ||||  |    | ||||| | | || || ||   ||||   ||| | |  ||| ||  |    ||
    GGGAGGAGGCTGAGAAACAGCGGGTGGCTTCAGAGAACCTG---CGGCAGGAGCTGACCTCACAGGCTGAGC
           980       990      1000      1010         1020      1030

           530       540          550            560       570       580
    GTGCCTGGAGGTGCAGTGCC---AGCCGGACTCCT-CCA----CCCTGCTGCCCCCAAGGAGTCCCATAGCC
    ||||  ||||| || | |||   |   | |  | |  ||       | ||  ||  || |||   ||  |||
    GTGC--GGAGGAGCTGGGCCAAGAATTGAAGGCGTGGCAGGAGAAGTTCT-TCCAGAAAGAG---CA-GGCC
 1040        1050      1060      1070      1080       1090         1100

       590       600         610       620       630       640          650
    CTAGAAGCCACGGAGCTC--CCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTG-CTGCT--GCCTC
```

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||     ||  | |||||   || | ||    | |||||  ||| ||     ||||||| | |||  ||  |
CTCTCCACCCTGCAGCTCGAGCACA-CCAGCACACAGGC-CCTGGTGAGTGAGCTGCTGCCAGCTAAGCACC
  1110      1120       1130      1140       1150      1160      1170

      660       670         680       690       700           710
TCACACTGGTGCTGCTGGC--AGCCGCCTGGGGCCTTCGCTGGCAAAGGGCA--AGAAGGAG--GGGGGAGC
||   | |  ||||| |||  ||| | | |  |||       || |  |  |  ||  ||||  | |  |||
TCTGCCAGCAGCTGCAGGCCGAGCAGGCCGCTGCCGAGAAACGCCACCGTGAGGAGCTGGAGCAGAGCAAGC
  1180      1190      1200      1210      1220      1230      1240

720          730        740         750       760       770        780
TCCACCCTGGGG---TGC-CCCTCCCCTCC--CATCCCTAGGATTCGAGCCTTGTGCATC-GTTGACTCAGC
    | ||||||   |||   |    || |  |   || ||     ||| |||| | | | | |  ||| ||
AGGCCGCTGGGGGACTGCGGGCAGAGCTGCTGCGGGCCCAG--CGGGAG-CTTGGGGAGCTGATTCCTCTGC
1250      1260      1270      1280        1290       1300      1310

       790       800       810       820       830       840       850
--CAGGGTCTTATCTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCT
  || |    |  |   |    | |    | ||||||   || | |  ||||| |||   |||  |||  |
GGCA-GAAGGTGGCAGAGCAGGAGCGAACAGCTCAGCAGCTGCGGG--CAGAGAAGGCCAGCT--ATG--CA
  1320      1330      1340      1350      1360        1370          1380

     860       870        X
GGAGCAGGTCGTCTCGTTCCAGTCGAC
| ||||| |   |  | |  ||  | |
G-AGCAGCTGAGCATGCTGAAGAAGGCGCATGGCCTG
       1390      1400      1410


15. US-08-162-407-1 (1-879)
    HSNUMAU6G    H.sapiens NuMA gene (Clone U6).

 LOCUS       HSNUMAU6G     4762 bp    RNA             PRI       15-APR-1993
 DEFINITION  H.sapiens NuMA gene (Clone U6).
 ACCESSION   Z14227
 KEYWORDS    alternative splicing; NuMA gene.
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 4762)
   AUTHORS   Tang,T.K.
   TITLE     Direct Submission
   JOURNAL   Submitted (05-AUG-1992) to the EMBL/GenBank/DDBJ databases. Tang T.
             K., Institute of Biomedical Sciences, Laboratory of Cell Biology,
             Section 2, Academy Road, Taipei, Taiwan, Republic of China, 115
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 4762)
   AUTHORS   Tang,T.K., Tang,C.J., Chen,Y.L. and Wu,C.W.
   TITLE     Nuclear proteins of the bovine esophageal epithelium. II. The NuMA
             gene gives rise to multiple mRNAs and gene products reactive with
             monoclonal antibody W1
   JOURNAL   J. Cell. Sci 104, 249-260 (1993)
   STANDARD  full automatic
 COMMENT     NCBI gi: 296120
 FEATURES             Location/Qualifiers
      source          1..4762
                      /organism="Homo sapiens"
                      /cell_line="U251"
                      /clone_lib="U251 cDNA library"
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                      /clone="Clone U6"
      mRNA            <1..3465
                      /gene="NuMA"
                      /note="alternative splice product"
                      /evidence=experimental
 BASE COUNT     1231 a   1180 c   1579 g    772 t
 ORIGIN

Initial Score     =   153  Optimized Score  =   403  Significance =  9.20
Residue Identity  =   51%  Matches          =   491  Mismatches   =   334
Gaps              =   128  Conservative Substitutions          =     0

             X        10            20           30        40        50
             GTC-GACTGGAACG-AG--ACGA-CCTGCTCTG---TCACAGGCATGAGGGGTCCCCGGCAG
             | | | |||||||| ||   |||  |||  | |   || | ||| |||| ||  |   ||
   GGAGCAGGCTGACAGCCTGGAACGCAGCCTCGAGGCTGAGCGGGCCTCCCGGGC-TGAGCGGGACAGTGCTC
       1600  X   1610      1620      1630      1640       1650      1660

       60        70        80        90       100       110       120
   AGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGT-CCT
    |  |||  ||| || |||||  | |||   ||      ||| |  |||   |   | |   | |||| |||
   TGGAGACTCTGCAGG-GCCAG-TTAGAGGAGAA----GGCCCAGGAGCT-AGGGCACAG--TCAGAGTGCCT
      1670       1680       1690          1700       1710        1720

      130         140         150         160       170       180        190
   T-GCCTGCGGGGGACACCTGACT--GTT-ACTTCAGC-CACAGTCCCATCTCCTCCAACTTCAAAG-TGAAG
   | |||| |||   | ||  || |  | |  |||| || |  ||   ||   ||    ||  ||| | |||||
   TAGCCT-CGGCCCA-ACGGGAGTTGGCTGCCTTCCGCACCAAGGTACAAGACC----ACAGCAAGGCTGAAG
   1730        1740      1750      1760      1770          1780      1790

         200           210           220       230       240       250
   TTTAGAGAGTTGAC----TGACC----ACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCA--
    | || |    | |    || ||     || ||   | | | |   ||  |   | ||| || |||  ||
   ATGAGTGGAAGGCCCAGGTGGCCCGGGGCCGGCAAGAGGCTGA--GAGGAAAAATAGCC-TC-ATCAGCAGC
       1800      1810      1820      1830        1840       1850       1860

         260       270       280       290       300       310
   --GGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAA----CTGAA
     ||| ||| ||   | ||   || ||    |||   |||| |   || |  ||  |||||||     ||||
   TTGGAGGAGGAGGTGTCCA--TCC-TGAATCGCCAGGTCCTGGAGAAG-GAGGGGGAGAGCAAGGAGTTGAA
         1870        1880       1890      1900       1910      1920

   320           330       340       350        360       370       380
   --GACTG----TGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGA-CGTCAACACCGAGATACATTTTGTCA
     | |||    |||| | |||  ||| |     |   ||||||||  | |  | ||  | | ||    |  |
   GCGGCTGGTGATGGCCGAGTCAGAGAAGAGCCAGAAGCTGGAGGAGAGGCTGCGCC-TGCTGCAGGCAGAGA
 1930      1940      1950      1960      1970      1980       1990

      390         400       410           420       430       440       450
   CCTCATGTACC--TTCCAGCCCCTACCAGAATG----TCTGCGATTCGTCCAGACCAACATCTCCCACCTCC
   |  |  | | |  | ||||   || | |||| |    |||||  | ||    ||    ||       |||||
   CAGCCAGCAACAGTGCCAG-AGCTGC-AGAACGCAGCTCTGCTCTGCGGGAGGAGGTGCA----GAGCCTCC
2000      2010       2020       2030      2040      2050          2060

          460       470        480       490       500        510       520
   TGAAGGACACCTGCACACAGCTGCTTGC-TCTGAAGCCCTGTATCGGGAAGGCCTG-CCAGAATTTCTCTCG
    | ||||  |    | ||||| | | || || ||   ||||   ||| | |  ||| ||  |    ||
   GGGAGGAGGCTGAGAAACAGCGGGTGGCTTCAGAGAACCTG---CGGCAGGAGCTGACCTCACAGGCTGAGC
    2070      2080      2090      2100         2110      2120      2130
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           530       540          550            560       570       580
    GTGCCTGGAGGTGCAGTGCC---AGCCGGACTCCT-CCA----CCCTGCTGCCCCCAAGGAGTCCCATAGCC
    ||||  ||||| || | |||   |   | |  | |  ||       | ||  ||  || |||   ||  |||
    GTGC--GGAGGAGCTGGGCCAAGAATTGAAGGCGTGGCAGGAGAAGTTCT-TCCAGAAAGAG---CA-GGCC
        2140      2150      2160      2170      2180       2190

       590       600         610       620       630       640          650
    CTAGAAGCCACGGAGCTC--CCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTG-CTGCT--GCCTC
    ||     || |  |||||   || | ||    | |||||  ||| ||     ||||||| | |||  ||  |
    CTCTCCACCCTGCAGCTCGAGCACA-CCAGCACACAGGC-CCTGGTGAGTGAGCTGCTGCCAGCTAAGCACC
 2200      2210      2220       2230       2240      2250      2260

          660       670         680       690       700           710
    TCACACTGGTGCTGCTGGC--AGCCGCCTGGGGCCTTCGCTGGCAAAGGGCA--AGAAGGAG--GGGGGAGC
    ||   | |  ||||| |||  ||| | | |  |||       || |  |  |  ||  ||||  | |  |||
    TCTGCCAGCAGCTGCAGGCCGAGCAGGCCGCTGCCGAGAAACGCCACCGTGAGGAGCTGGAGCAGAGCAAGC
 2270      2280      2290      2300      2310      2320      2330      2340

    720          730        740         750       760       770        780
    TCCACCCTGGGG---TGC-CCCTCCCCTCC--CATCCCTAGGATTCGAGCCTTGTGCATC-GTTGACTCAGC
        | ||||||   |||   |    || |  |   || ||     ||| |||| | | | | |  ||| ||
    AGGCCGCTGGGGGACTGCGGGCAGAGCTGCTGCGGGCCCAG--CGGGAG-CTTGGGGAGCTGATTCCTCTGC
         2350      2360      2370      2380         2390      2400      2410

           790       800       810       820       830       840       850
    --CAGGGTCTTATCTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCT
      || |    |  |   |    | |    | ||||||   || | |  ||||| |||   |||  |||  |
    GGCA-GAAGGTGGCAGAGCAGGAGCGAACAGCTCAGCAGCTGCGGG--CAGAGAAGGCCAGCT--ATG--CA
           2420      2430      2440      2450        2460      2470

         860       870        X
    GGAGCAGGTCGTCTCGTTCCAGTCGAC
    | ||||| |   |  | |  ||  | |
    G-AGCAGCTGAGCATGCTGAAGAAGGCGCATGGCCTG
      2480      2490      2500      2510
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sqlinv.res made by  on Wed 5 Apr 95 21:32:49-PDT.


Query sequence being compared:US-08-162-407-1'  (1-879)
Number of sequences searched:                   313646
Number of scores above cutoff:                    4947

       Results of the initial comparison of US-08-162-407-1' (1-879) with:
   Data bank : EMBL-NEW 1, all entries
   Data bank : GenBank 86, all entries
   Data bank : GenBank-NEW 1, all entries
   Data bank : UEMBL 41_86, all entries

100000-
      -
N     -
U50000-
M     -       ***
```

```
B     -     *   * *
E     -          *
R     -    *
      -            *
O     -   *         *
F10000-              *
      -  *            *
S     -
E 5000- *              **
Q     -*
U     -                  *
E     -                   *
N     -                    *
C     -
E     -                     *
S 1000-                      *
      -                       **
      -
   500-
      -                         *
      -
      -                          *
      -                           *
      -                               *
      -                            **
   100-
      -                              *
      -                                *
    50-
      -
      -                                 **
      *                                   **
      -                                       *
      -                                          *
      -
    10-                                     *  *
      -
      -                                      *
     5-                                         *  *
      -
      -                                                      *
      -
      -
      -
      -                                              **      *        *
     0----------------------------------------------------------------------
      |   |  ||   | | |   ||   |  ||   | | |   ||  |   |      |      |
SCORE 0   | 22|   |44 |   66   | 88|   109 |  131  | 153    175    197
STDEV    -1   0   1   2   3    4   5   6   7   8   9

                             PARAMETERS

Similarity matrix      Unitary     K-tuple                      4
Mismatch penalty             1     Joining penalty             30
Gap penalty               1.00     Window size                 32
Gap size penalty          0.33
Cutoff score                 2
Randomization group          0
```

```
Initial scores to save      45     Alignments to save        15
Optimized scores to save     0     Display context           10.

                              SEARCH STATISTICS

Scores:                     Mean         Median      Standard Deviation
                             30            30          12.72

Times:                      CPU                      Total Elapsed
                      01:48:40.01                    01:48:46.00

Number of residues:              288682119
Number of sequences searched:       313646
Number of scores above cutoff:        4947

Cut-off raised to 23.
Cut-off raised to 27.
Cut-off raised to 30.
Cut-off raised to 33.
Cut-off raised to 36.
Cut-off raised to 39.
Cut-off raised to 41.
Cut-off raised to 44.
Cut-off raised to 47.
Cut-off raised to 50.
Cut-off raised to 53.
Cut-off raised to 56.
Cut-off raised to 59.
Cut-off raised to 62.
Cut-off raised to 65.
Cut-off raised to 67.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                     Init. Opt.
Sequence Name     Description                 Length Score Score  Sig. Frame
-----------------------------------------------------------------------------
                       **** 13 standard deviations above mean ****
   1. GCRINVA     G.crassicaudatus involucrin g  1155  197   406  13.13   0
                       **** 11 standard deviations above mean ****
   2. ATRINVSA    Owl monkey involucrin (small    894  172   347  11.16   0
   3. HUMINV2     Human involucrin gene, exon 2  2108  172   414  11.16   0
   4. HUMINV2     Human involucrin gene, exon 2  2108  172   414  11.16   0
                       **** 10 standard deviations above mean ****
   5. CEZK638     Caenorhabditis elegans cosmid  1762  167   403  10.77   0
                       ****  9 standard deviations above mean ****
   6. DMU13397    Drosophila melanogaster Orego  2091  145   406   9.04   0
                       ****  8 standard deviations above mean ****
   7. CRUPA1V     Chinese hamster pro-alpha-1 (  6114  144   408   8.96   0
   8. GORINVOLUB  Gorilla gorilla involucrin ge  1818  141   407   8.73   0
   9. HUMCA1V     Human mRNA for collagen alpha  5676  139   397   8.57   0
  10. HUMPA1V     Human pro-alpha-1 (V) collage  7138  139   399   8.57   0
  11. HUMPA1V     Human pro-alpha-1 (V) collage  7138  139   399   8.57   0
  12. HS4ULIR3    epstein-barr virus simple rep  1150  134   370   8.18   0
```

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  13. CHPINVOL     Chimpanzee (P.paniscus) invol   1683   134   407   8.18   0
  14. U02454       Cloning vector pCMVEBNA, comp   5452   134   385   8.18   0
  15. U02428       Cloning vector pDR2, complete  10737   134   385   8.18   0
  16. U02455       Cloning vector rpDR2, complet  10850   134   385   8.18   0
  17. EBV          Epstein-Barr virus (EBV) geno 172281   134   385   8.18   0
  18. HS4B958RAJ   Epstein-Barr virus, artifactu 184113   134   385   8.18   0
  19. HS4B958RAJ   Epstein-Barr virus, artifactu 184113   134   385   8.18   0
  20. EBV          Epstein-Barr virus (EBV) geno 172281   134   385   8.18   0
  21. EBV          Epstein-Barr virus (EBV) geno 172281   134   385   8.18   0
  22. HUMARC1      Human androgen receptor gene,   1753   133   399   8.10   0
  23. SRCEL1G      S.reticuli cell gene for myce   2760   133   391   8.10   0
  24. HUMANDREC    Human androgen receptor (AR)    3569   133   399   8.10   0
  25. I09510       Sequence 1 from patent WO 890   3569   133   399   8.10   0
  26. HSANDREC     Human androgen receptor (AR)    3569   133   399   8.10   0
  27. I08490       Sequence 3 from patent WO 870   2000   132   390   8.02   0
  28. MMSCSLN8B    M.musculus rearranged T-cell    4560   132   377   8.02   0
                    ****  7 standard deviations above mean ****
  29. HSKER65A     Human DNA for 65 kD keratin t   1192   131   295   7.94   0
  30. DRO3AKLP     Drosophila melanogaster (chro   4394   130   394   7.86   0
  31. USTNFR20S3   Mus musculus tumor necrosis f   1481   129   200   7.78   0
  32. GIBINVOL     Hylobates lar involucrin gene   1569   129   405   7.78   0
  33. MUSAGRIN3    Mus musculus agrin gene, exon   1952   127   387   7.63   0
  34. ORAINVOL     Orang-utan involucrin gene, c   2508   127   408   7.63   0
  35. HUMIGCB1     Human Ig germline J-mu-delta    3182   127   376   7.63   0
  36. HUMIGCB1     Human Ig germline J-mu-delta    3182   127   376   7.63   0
  37. HSIGCB1      Human Ig germline J-mu-delta    3182   127   376   7.63   0
  38. CGPD2        Cricetulus griseus nucleotide  13664   127   386   7.63   0
  39. HUMIGLZC     Human immunoglobulin light ch    482   126   216   7.55   0
  40. HUMIGLZB     Human immunoglobulin light ch    482   126   217   7.55   0
  41. XAADHLB      Xanthobacter autotrophicus ha   1015   126   373   7.55   0
  42. PFACSNURI    Plasmodium knowlesi circumspo   1485   126   371   7.55   0
  43. HSCOL4A2     Human mRNA for alpha-2 chain    3416   126   385   7.55   0
  44. M78027       EST01614 Homo sapiens cDNA cl    416   125   187   7.47   0
  45. HUMIGLZD     Human immunoglobulin light ch    482   125   216   7.47   0


1. US-08-162-407-1' (1-879)
   GCRINVA      G.crassicaudatus involucrin gene, complete cds.

LOCUS       GCRINVA      1155 bp ds-DNA              PRI       15-SEP-1990
DEFINITION  G.crassicaudatus involucrin gene, complete cds.
ACCESSION   J05437
KEYWORDS    involucrin.
SOURCE      G.crassicaudatus fibroblast DNA.
  ORGANISM  Galago crassicaudatus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Primates; Strepsirhini; Galagidae.
REFERENCE   1  (bases 1 to 1155)
  AUTHORS   Phillips,M., Djian,P. and Green,H.
  TITLE     The involucrin gene of the Galago: Existence of a correction
            process acting on its segment of repeats
  JOURNAL   J. Biol. Chem. 265, 7804-7807 (1990)
  STANDARD  full automatic
COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
            by P.Dijian, 26-MAR-1990.

            NCBI gi: 176996
FEATURES             Location/Qualifiers
     source          1..1155
                     /organism="Galago crassicaudatus"
     CDS             1..1155
                     /note="involucrin;  NCBI gi: 176997"
                     /codon_start=1
                     /translation="MSQQHTLPVTLPPALRQELLGTLSPPAAAQQEQRKQPTPLPTAC
                     QKVGSELPGEVPSKHEEKGTDPVKGVLEQECGQQEPELHLGKQQDVHLMKRQDPQEPE
                     LHLGKQPEPEGPEPHLGKEQQHQESQDPELHLGKQQQQESQEQELYPGKQQEPQDPEL
                     HLGKQQQQESQEQGLCLIKQREPQESQEQRLHLGKEQESQEQRLHLGEEQASQEQRLH
                     LGEEQASQEQRLHLGEEQASPEQRLQLLPQGPQEQELHLGKQQQQQESQQHQEQHEEH
                     QKAEDLGQQHRQEKAQREQQLEEQLDEGKKLLDQQLDQEAVKRHEQLQRDEQFGMKKE
                     QLLEPPGQQKGQLEKPVFVPVPGQVQDIQPAQTAKGEALLLPEQPQEPEV"
 BASE COUNT      339 a    299 c    379 g    138 t
 ORIGIN

Initial Score    =    197  Optimized Score =    406  Significance = 13.13
Residue Identity =    51%  Matches         =    492  Mismatches   =   334
Gaps             =    121  Conservative Substitutions        =     0

              X       10         20        30            40         50
              GTCGACTGGAACG-AGACGACCTGCTCCAGACCAT----TCAGCAAT-CCTGCTCTGGGCTC
              | | |||  |  |   ||  | ||  |||||   |    || |   | ||||    || | |
    AAAGGAAGCAGCCAACTCCACTGCCCACTGCGTG--CCAGAAGGTGGGCTCCGAGCTCCCTGGAGAGGTCCC
    100       110       120       130         140       150       160

       60        70        80         90       100       110             120
    C-CAAGGGCTGAGATTACAGGTGTA-ACCGAGATAAGACCCTGGCTGAGTCAACGAT----GCACAAG--GC
    | ||| |  ||||   | |||   | | |  |  ||     ||  |||| |||  ||    |||  ||  ||
    CTCAAAGCATGAGGAGAAAGGCACAGATCCTGTAAAAGGGGTGCTTGAG-CAAGAATGTGGGCAGCAGGAGC
    170       180       190       200       210        220       230

               130       140        150         160       170       180
    TCGA----ATCCTAGGGATGGGAG-GGGAGGGGCACCCCAGG--GTGGAGCTCCCCCCTCCTTCTTGCCCTT
     |||      ||| ||||  | ||  ||| | ||| |  | |  | ||     ||| |     |  |  ||
    CCGAGCTGCACCT-GGGAAAGCAGCAGGATGTGCATCTGATGAAGCGGCAGGACCCACAAGAGCCCGAGCTA
   240       250        260       270       280       290       300

      190        200           210       220       230       240       250
    TGCCAGCGAAGGC-CCCAG-GC---GGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCA
      || | |||  |  |||| ||    |  ||| | | |||   || |  ||| |||||||||| ||||||
    CACCTGGGAAAACAACCAGAGCCAGAGGGGCCGGAACCACATCTGGGCAAGG-AGCAGCAGCATCAGGAGTC
  310       320       330       340       350       360        370        380

         260       270       280       290       300       310       320
    ACAGCTGCCTGGGCCGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGG
    |||    || | ||   |  |||||||   | |  ||    ||  |    ||| ||   ||    |||| ||
    ACAAGACCCGGAGC--TGCATCTGGGAAAGCAGCAGC----AG--C---AGGAGTCACAGG----AGCA-GG
           390         400       410                420       430

       330       340        350       360        370        380       390
    TGGAGGAGTCCGGCTGGCA-CTGCACCTCCAGGCACCGAGAG-AAATTCTG-GCAGGCCTTCCCGATACAGG
        | |  | ||    || | | | | ||||| ||| ||||      ||| ||| ||    | |   ||||
    AACTGTATCCTGGAAAACAGCAGGAGCCCCAGG-ACCCAGAGCTGCACCTGGGCAAGC--AGCAGCAGCAGG
     440       450       460        470       480       490         500

          400       410       420       430       440       450       460
    -GCTTCA-GAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAG
     |  ||| ||||| | | |||||| | |   |    |||  || |    | |   ||||  | ||   ||||
    AGTCTCAGGAGCAGGGA-CTGTGT-CTG--ATAAAACAGCGGGAGCCTCAGG--AGTCT-CAGGA---GCAG
      510       520         530         540       550          560

         470       480        490        500       510         520
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    ACA-TTCTGGTAGGGGCTG-GAAGGTACATGAGGTG-ACAAAATGTATCTCGGTGTTGA--CGTCCTC-CAG
    | | | |   | |||   | | |||    | ||| | | | | || | || || |  ||   | | || |||
    AGACTGCACCTGGGGAAAGAGCAGGAGTCTCAGGAGCAGAGACTGCACCTGGGGGAAGAGCAGGCGTCTCAG
    570       580       590       600       610       620       630

  530          540        550       560       570        580       590
    AAGC---GTTTGCATCT-TAGACCCTGCCACAGTCTTCAGTTGCTCTATCCAGC-GCTGGGCTAGGAAGAGG
     |||   |  |||| ||   |     ||    ||| ||||  ||   |  | ||  |||||  | ||  |||
    GAGCAGAGACTGCACCTGGGGGAAGAGCAGGCGTC-TCAGGAGC-AGAGACTGCACCTGGGGGAAGAGCAGG
  640       650       660       670        680        690       700

        600         610        620           630       640       650
    ---CTCC--ACAAGGCCTTGCAG-TGCTTC----TCGTCCTGAAGATTGACGGCCACAGTGACTGGGTAATC
       ||||  |  ||    ||||| |||| |      | ||  | ||  |  ||  || |   ||||| || |
    CGTCTCCGGAGCAGAGACTGCAGCTGCTGCCACAGGGACCACAGGA--GCAGG-AACTGCACCTGGGAAAAC
  710       720       730       740       750         760        770

   660         670       680          690       700          710       720
    TTTA--AGCAGGTGGTCAGTCAAC-TCTCTA--AACTTCACTTTGAA-GTTGGA--GGAGATGGGACTGTGG
       |  |||||  ||    |||||  | | |  |||  ||    |||  |  ||  | |||  |  ||| ||
    AGCAGCAGCAGCAGGAGTCTCAACAGCACCAGGAACAGCATGAGGAACATCAGAAAGCAGA-AGACCTGGGG
   780       790       800       810       820       830        840

         730       740       750       760       770       780       790
    CTGAAGTAACAGTCAGGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTT
    | | ||  | || |||| |      |||   ||||   ||||||| | |  ||||||     ||| |||
    CAGCAG-CATAGGCAGGAG---AAAGCA-CAAAGGGAACAGCAGCTGGAGGAGCAGC----TGGATGAA---
  850        860          870        880       890       900

       800        810        820        830       840         850        860
    GGGCTCCAG-GCTGGCGCCAGC-ACTGTCATC-TCTGCCGGGGACCCCTCATG--CCTGTG-ACAGAGCAGG
    |||    ||  || |  ||||| ||||  |||    | | | ||     ||||  |   || | ||||  |
    GGGAAGAAGCTCTTGGACCAGCAACTG-GATCAAGAGGCAGTGAAGAGACATGAACAACTGCAGAGAGATGA
  910       920       930        940       950       960       970       980

             870        X
    TCGTCTCG--TTCCAGTCGAC
     |   |||   |  ||  |
    ACAATTCGGAATGAAGAAGGAGCAGTTGTTG
           990    1000      1010


2. US-08-162-407-1' (1-879)
   ATRINVSA     Owl monkey involucrin (small allele) gene, partial

 LOCUS       ATRINVSA       894 bp ds-DNA               PRI       15-SEP-1990
 DEFINITION  Owl monkey involucrin (small allele) gene, partial cds.
 ACCESSION   M25314
 KEYWORDS    involucrin.
 SOURCE      Owl monkey keratinocyte DNA.
   ORGANISM  Aotus trivirgatus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Platyrrhini; Cebidae; Aotinae.
 REFERENCE   1  (bases 1 to 894)
   AUTHORS   Tseng,H. and Green,H.
   TITLE     The involucrin gene of the owl monkey: Origin of the early region
   JOURNAL   Mol. Biol. Evol. 6, 460-468 (1989)
   STANDARD  full automatic
 COMMENT     Draft entry and computer-readable sequence for [Mol. Biol. Evol.
             (1989) In press] kindly provided
             by H.Tseng, 03-JUN-1989.
             The involucrin gene is made up of about 30 base pair type A or B
             repeats of about 30 base pairs.

             NCBI gi: 176559
 FEATURES             Location/Qualifiers
      source          1..894
                      /organism="Aotus trivirgatus"
      CDS             <1..>894
                      /note="involucrin (small allele);  NCBI gi: 176560"
                      /codon_start=1
                      /translation="EFPEQQEGQLKRLEQQEGHLELPEQQEGQLKHLEQQEGQLKHLE
                      QEEKQSELPEQQRGQLKYLEQQEGQLKHLEQQEKQSELPEQQRGQLKYLEQQEGQLKH
                      LEEQKGQLKHLEHQEGQLELPEQVGQPKHLEQLEKQLEHPEQQEGQLKQLEEQEGQVK
                      HLEQQEEQLKHLEQQEGQPKHLEQLEKQLEHLEQQEGQLKHLEQREEQLELPEQQVGQ
                      SKHLEQEEKQLEHPEQQEGQLKHLGKQEAQLELPEQVGQPKHLEQQEKQLEHPEQQEG
                      QLKPQEQQEGQLKGLEQQERQL"
 BASE COUNT      266 a    209 c    350 g     69 t
 ORIGIN

Initial Score    =    172  Optimized Score  =    347  Significance = 11.16
Residue Identity =    52%  Matches          =    419  Mismatches   =   274
Gaps             =    103  Conservative Substitutions              =     0

           130       140       150       160       170       180       190
    TCGAATCCTAGGGATGGGAGGGGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCCCTTTGCCAGC
              | | |   |   |||  |||    |||| | ||||     | |||    ||     || ||
              GAGTTCCCA---GAGCAGCA--GGAGGG-GCAGCT-GAAACGCCT-GGAGC----AGCAAGA
              X          10          20          30         40            50

         200       210       220       230       240       250       260
    GAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCCTGG
    |  ||| || ||  ||| |||| |||| |||   ||| |||||| | |||| | |||||| |||  |
    G-GGGCACCTGG-AGCTCCCAG-AGCAGCAG---GAGGGGCAGCTGAAGCACCTGGAGCAGCAGGAGGGGCA
             60         70            80        90       100       110

       270           280        290        300       310       320
    GCCGAGGCTCTGGGA----GCTCCGTGGC-TTCT-AGGGCTATGGGACTCCTTGGGGGCAGCAG-GGT----
    || || || |  |||    |    |  ||  ||| ||  |   | |   |   ||||||||| |  ||
    GCTGAAGCACCTGGAACAGGAGGAGAAGCAGTCTGAGCTCCCAGAGCAGCAGAGGGGGCAGCTGAAGTACCT
     120       130       140       150       160       170       180

      330       340        350       360       370       380       390
    GGAGGAGTCCGGCTGGCA-CTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGGGCT
    |||| ||   |   |||| ||| | | || || || |   || |  | | | |  || || ||  |||
    GGAGCAGCAGGAGGGGCAGCTGAAGCACCTGGAACAGCAGGAGAAGCAGTCTGAGCTCCCAGA-GCAG----
   190       200       210       220       230       240       250

     400       410        420       430       440        450       460
    TCAGAGCAAGCAGCTG-TGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTG-GTCTGGACGAATCGCAGACA
     |||||   |||||||  || |  | |  |  ||||||| || || ||  |   ||||| ||   ||||| |
    -CAGAGGGGGCAGCTGAAGTACCTG-GAGCAGCAGGAGG-GGCAGCTGAAGCACCTGGAAGA---GCAGAAA
       260       270        280       290        300       310          320

      470         480       490       500       510       520          530
    -TTCTG--GTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTGACGTCCTCCAG---AAG
       | |  | ||   |||| ||   || |||| | ||   || | |||   |   | ||    |||   |||
    GGGCAGCTGAAGCATCTGG-AGCACCAGGAGG-GGCA-GCTGGAGCTCCCAGAGCAGGTGGGGCAGCCAAAG
          330       340        350         360       370       380       390
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            540        550       560       570       580         590
    CGTTTG---CATCT-TAGACCCTGCCACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAG--GAAGAGGCT
    |   ||   || ||  |||  |  | | || |  | |  ||   | | || |  |||| ||  ||||  |||
    CACCTGGAACAGCTGGAGAAGCAACTAGAG-CACCCGGAGC---AGC-AG-GAGGGGC-AGCTGAAGCAGCT
           400       410       420        430            440        450

      600       610        620       630       640       650       660
    ---CCACAAGGCCTTGCA-GTGCTTCTCGTCCTGAAGATTGACGGCCACAGTGACTGGGTAATCTTTA--AG
         |  |||    ||| |||   | | |   | ||   ||  |   ||||   ||    ||||  |  ||
    GGAGGAGCAGGAGGGGCAGGTGAAGCACCTGGAGCAGCAGGA--GGAGCAGT---TGAAGCATCTGGAGCAG
      460       470       480       490         500          510       520

        670         680       690       700          710       720       730
    CAGG-TGGTCAGTCAA--CTCTCTAAACTTCACTTTGAAG---TTGGAGGAGATGGGACTGTGGCTGAAGTA
    ||||  || ||| |||  | |    |||  |     ||||    | ||| |  |||    |  || | ||
    CAGGAGGGACAGCCAAAGCACCTGGAACAGC-TGGAGAAGCAACTAGAGCACCTGG---AGCAGCAGGAGGG
         530       540       550        560       570          580       590

            740       750        760       770       780         790
    ACAG-TCAGGTGTCCCCCGCAG-GCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGG--AATTTGGGC
     ||| | | |  ||    |||| || ||||  |||| | |||  |   |||| |||| |||  | |    ||
    GCAGCTAAAGCATCTGGAGCAGCGCGAGGA-ACAGCTGGAGCTCCCAGAGCAGCAGGTAGGGCAGTCAAAGC
           600       610       620        630       640       650       660

   800         810         820       830       840       850        860
    TCCAG--GCTGGCG--CCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAG-AGCAGGTCGTC
     || |  || || |    |||| |   | | |  || | |   |  || |   | | |||  | ||  | |
    ACCTGGAGCAGGAGGAGAAGCAGTTGGAACAC--CCAGAG---CAGCAAG--AGGGGCAGCTGAAGCACCTG
          670       680       690            700         710       720

      870        X
    TCGTTCCAGTCGAC
      |   |||  | |
    GGGAAGCAGGAGGCACAGCTGGAG
     730       740       750


3. US-08-162-407-1' (1-879)
   HUMINV2     Human involucrin gene, exon 2.

 LOCUS       HUMINV2   2108 bp ds-DNA               PRI       06-JAN-1995
 DEFINITION  Human involucrin gene, exon 2.
 ACCESSION   M13903
 KEYWORDS    involucrin; keratinocyte protein.
 SEGMENT     2 of 2
 SOURCE      Human keratinocyte, cDNA to mRNA; and DNA, clone lambda-1-3.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2108)
   AUTHORS   Eckert,R.L. and Green,H.
   TITLE     Structure and evolution of the human involucrin gene
   JOURNAL   Cell 46, 583-589 (1986)
   STANDARD  full automatic
 COMMENT     NCBI gi: 186519
 FEATURES             Location/Qualifiers
      source          1..2108
                      /organism="Homo sapiens"
                      /sequenced_mol="DNA"
      intron          <1..10
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                      /map="1q21-q22"
                      /note="G00-119-355"
                      /number=1
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                      /gene="IVL"
                      /map="1q21-q22"
                      /note="NCBI gi: 386834"
                      /codon_start=1
                      /gdb_xref="G00-119-355"
                      /product="involucrin"
                      /translation="MSQQHTLPVTLSPALSQELLKTVPPPVNTHQEQMKQPTPLPPPC
                      QKVPVELPVEVPSKQEEKHMTAVKGLPEQECEQQQKEPQEQELQQQHWEQHEEYQKAE
                      NPEQQLKQEKTQRDQQLNKQLEEEKKLLDQQLDQELVKRDEQLGMKKEQLLELPEQQE
                      GHLKHLEQQEGQLKHPEQQEGQLELPEQQEGQLELPEQQEGQLELPEQQEGQLELPEQ
                      QEGQLELPQQQEGQLELSEQQEGQLELSEQQEGQLELSEQQEGQLKHLEHQEGQLEVP
                      EEQMGQLKYLEQQEGQLKHLDQQEKQPELPEQQMGQLKHLEQQEGQPKHLEQQEGQLE
                      QLEEQEGQLKHLEQQEGQLEHLEHQEGQLGLPEQQVLQLKQLEKQQGQPKHLEEEEGQ
                      LKHLVQQEGQLKHLVQQEGQLEQQERQVEHLEQQVGQLKHLEEQEGQLKHLEQQQGQL
                      EVPEQQVGQPKNLEQEEKQLELPEQQEGQVKHLEKQEAQLELPEQQVGQPKHLEQQEK
                      HLEHPEQQDGQLKHLEQQEGQLKDLEQQKGQLEQPVFAPAPGQVQDIQPALPTKGEVL
                      LPVEHQQQKQEVQWPPKHK"
 BASE COUNT      602 a    526 c      711 g    269 t
 ORIGIN      About 1188 bp after segment 1.

Initial Score    =    172  Optimized Score   =   414  Significance = 11.16
Residue Identity =    53%  Matches           =   517  Mismatches   =   297
Gaps             =    156  Conservative Substitutions              =     0

              X       10        20         30          40              50
              GTCGACTGGAACGAGACGACCTGCTCCA-GACCA--TTCAGCAATC----CTGC--TCTGGG
              | |  ||||| |     || | ||   | |  ||  |  |||  ||    | ||     |||
    CAGCAGGAGGGGCAGCTGGAGCTCTCTGAGCAGCAGGAGGGGCAGCTGGAGCTCTCTGAGCAGCAGGAGGGG
           720       730       740       750       760       770       780

          60        70         80         90       100       110       120
    C-TCCCAAGGGCTGAGATTA-CAGGTGTAACCGAGAT-AAGACCCTGGCTGAGTCAACGATGCACAAGGCTC
    |  |   ||  ||  ||  | |||| |  ||  || | |||  |||||   |  | | || |  ||  |||
    CAGCTGGAGCTCTCTGAGCAGCAGGAGGGAC--AGCTGAAGCACCTGGAGCA--CCAGGAGGGGCA--GCTG
         790       800       810         820       830         840

          130               140            150         160       170
    GA-ATCCTAG-GGA-----TGGG--AGGGGAGG-----GGCACCCCAG--GGTGGAGCTCCCCCCTCCTTCT
    ||  ||| || |||     ||||  ||  || |     || ||  |||  || | ||||     | |||
    GAGGTCCCAGAGGAGCAGATGGGGCAGCTGAAGTACCTGGAACAGCAGGAGGGGCAGCT-GAAGCACCTGGA
   850       860       870       880       890       900        910

   180       190       200       210       220       230       240       250
    TGCCCTTTGCCAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAG
    | |     ||  | ||||   ||||   ||| |||| |||| |||  || | |||||| | |||| | ||||
    T-C----AGCAGGAGAAGCAGCCAG--AGCTCCCAG-AGCAGCAG-ATG-G-GGCAGCTGAAGCACCTGGAG
  920            930         940        950         960        970       980

           260       270        280           290        300        310
    CAACAGCTGCCTGGGCCGAGGC-TCTGGGAGCTCC----GTGGCTTCTAGGGC-TATGG-GACTCCTTGGGG
    || |||  |     ||| | || ||| |||||  |    | |||  || | ||   ||| |   |    |||
    CAGCAGGAGGGGCAGCCTAAGCATCT-GGAGCAGCAGGAGGGGCAACTGGAGCAGCTGGAGGAGCAGGAGGG
           990      1000       1010      1020      1030      1040      1050

      320            330       340        350         360       370
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    GCAGCAG-----GGTGGAGGAGTCCGGCTGGCA-CTGCACCTCCAG--GCACCGAGAGAAATTCTGGCAGGC
    ||||| |       ||||| ||   |   |||| ||| | | || |  ||||| || |||   | |   ||
    GCAGCTGAAGCACCTGGAGCAGCAGGAGGGGCAGCTGGAGCACCTGGAGCACC-AG-GAAGGGCAGCTGGGG
         1060      1070      1080      1090      1100        1110      1120

  380         390        400       410       420       430       440
    CTTCCCGA--TACAGG-GCTTCAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTG-G
    || || ||    |||| ||| |||   ||||||||  | | ||        ||| ||| || ||     |
    CTCCCAGAGCAGCAGGTGCTGCAGCTGAAGCAGCT-AGAGAAG--------CAGCAGG-GGCAGCCAAAGCA
         1130      1140      1150       1160              1170       1180

    450       460         470       480       490        500       510
    TCTGGACGAATCGCA--GACATTCTGGTAGGGGCTGGAAGGTACATGAGGTG-ACAAAATGTATCTCGGTGT
     ||||| ||   | |  | ||  || | ||   ||||  |   || |||| | |    | | |||| ||||
    CCTGGAGGAGGAGGAGGGGCA-GCT-GAAGCACCTGG-TGCAGCAGGAGGGGCAGCTGAAGCATCT-GGTG-
       1190      1200        1210       1220      1230      1240       1250

     520       530       540         550         560       570        580
    TGACGTCCTCCAGAAGCGTTTGCATCT-TAG-ACCCTGCCA--CAGTCTTCAGTTGCTCTATCCAGC-GCTG
           |  ||| || |   ||| ||  || | |  |  |  |||  |  ||   ||  |  |||| | ||
    -------CAGCAGGAGGG---GCAGCTGGAGCAGCAGGAGAGGCAG-GTGGAGCACCTGGA-GCAGCAGGTG
                 1260         1270      1280       1290      1300       1310

        590       600       610       620       630           640
    GGCTAGGAAGAGGCTCCACAAGGCCTTGCAGTGCTTCTCGTCCTGAAG-AT-TG--ACGGCCACAGTG--AC
    ||  | |  || || ||   |||    |||| |     |   |||||| || ||   | ||  ||| |  |
    GGGCA-GCTGAAGCACCTAGAGG---AGCAG-GAGGGAC-AGCTGAAGCATCTGGAGCAGCAGCAGGGGCAG
           1320      1330          1340       1350      1360      1370

  650       660       670       680       690       700       710       720
    TGGGTAATCTTTAAGCAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTG
    | ||   ||    |||||  |||  | || | |    |||  |    || ||  |||||||| |  ||||
    TTGGAGGTCCCAGAGCAGCAGGTGGGGCAGC-CAAAGAAC--C----TGGAGCAGGAGGAGAAGCAACTGGA
    1380      1390      1400       1410            1420      1430      1440

                730         740         750          760       770       780
    GCT----GA--AGTAACA--GTCAGGTG--TCCCCCGCAG--GCAAG-GACTCAGCAGCAGCAACAGCAGCA
    |||    ||  || || |  | ||||||   | || | ||  ||| | | | |||| | |||  |   ||||
    GCTCCCAGAGCAGCAAGAGGGCCAGGTGAAGCACCTGGAGAAGCAGGAGGCACAGCTGGAGCTCCCAGAGCA
         1450      1460      1470      1480      1490      1500      1510

           790                  800        810          820       830
    ACAGGGAGGA----------ATTTGG-GCTCCAGG-CTGGCGCC---AGCACTGTCATCTCTGCCGG--GGA
     |||| ||||          |  |||  |  ||||    || ||   |||||   ||   | || ||  |||
    GCAGGTAGGACAGCCAAAGCACCTGGAACAGCAGGAAAAGCACCTAGAGCAC--CCAGAGCAGCAGGACGGA
       1520      1530      1540      1550      1560        1570      1580

      840       850       860       870        X
    CCCCTCATGCCTGTGACAGAGCAGGTCGTCTCGTTCCAGTCGAC
    |  || |  | | ||    ||||||  |    | |  ||  |||
    CAACTAAAACATCTGGAGCAGCAGGAGGGGCAGCTGAAG--GACCTGGAGCAGC
       1590      1600      1610      1620      X 1630

4. US-08-162-407-1’ (1-879)
   HUMINV2      Human involucrin gene, exon 2.

 LOCUS       HUMINV2      2108 bp ds-DNA             PRI       30-MAR-1994
 DEFINITION  Human involucrin gene, exon 2.
 ACCESSION   M13903
```

```
KEYWORDS    involucrin; keratinocyte protein.
SEGMENT     2 of 2
SOURCE      Human keratinocyte, cDNA to mRNA; and DNA, clone lambda-1-3.
  ORGANISM  Homo sapiens
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE   1  (bases 1 to 2108)
  AUTHORS   Eckert,R.L. and Green,H.
  TITLE     Structure and evolution of the human involucrin gene
  JOURNAL   Cell 46, 583-589 (1986)
  STANDARD  full automatic
COMMENT     NCBI gi: 186519
FEATURES             Location/Qualifiers
     source          1..2108
                     /organism="Homo sapiens"
                     /sequenced_mol="DNA"
     intron          <1..10
                     /gene="IVL"
                     /map="1q21-q22"
                     /number=1
     CDS             30..1787
                     /gene="IVL"
                     /map="1q21-q22"
                     /note="NCBI gi: 386834"
                     /codon_start=1
                     /product="involucrin"
                     /translation="MSQQHTLPVTLSPALSQELLKTVPPPVNTHQEQMKQPTPLPPPC
                     QKVPVELPVEVPSKQEEKHMTAVKGLPEQECEQQQKEPQEQELQQQHWEQHEEYQKAE
                     NPEQQLKQEKTQRDQQLNKQLEEEKKLLDQQLDQELVKRDEQLGMKKEQLLELPEQQE
                     GHLKHLEQQEGQLKHPEQQEGQLELPEQQEGQLELPEQQEGQLELPEQQEGQLELPEQ
                     QEGQLELPQQQEGQLELSEQQEGQLELSEQQEGQLELSEQQEGQLKHLEHQEGQLEVP
                     EEQMGQLKYLEQQEGQLKHLDQQEKQPELPEQQMGQLKHLEQQEGQPKHLEQQEGQLE
                     QLEEQEGQLKHLEQQEGQLEHLEHQEGQLGLPEQQVLQLKQLEKQQGQPKHLEEEEGQ
                     LKHLVQQEGQLKHLVQQEGQLEQQERQVEHLEQQVGQLKHLEEQEGQLKHLEQQQGQL
                     EVPEQQVGQPKNLEQEEKQLELPEQQEGQVKHLEKQEAQLELPEQQVGQPKHLEQQEK
                     HLEHPEQQDGQLKHLEQQEGQLKDLEQQKGQLEQPVFAPAPGQVQDIQPALPTKGEVL
                     LPVEHQQQKQEVQWPPKHK"
BASE COUNT      602 a    526 c    711 g    269 t
ORIGIN      About 1188 bp after segment 1.

Initial Score    =    172  Optimized Score  =    414  Significance = 11.16
Residue Identity =    53%  Matches          =    517  Mismatches   =   297
Gaps             =    156  Conservative Substitutions              =     0

          X       10        20         30          40              50
          GTCGACTGGAACGAGACGACCTGCTCCA-GACCA--TTCAGCAATC----CTGC--TCTGGG
          | |  ||||| |     || | ||   | |  ||  |  |||  ||    | ||     |||
CAGCAGGAGGGCAGCTGGAGCTCTCTGAGCAGCAGGAGGGCAGCTGGAGCTCTCTGAGCAGCAGGAGGGG
       720       730       740       750       760       770       780

      60        70         80         90        100       110       120
C-TCCCAAGGGCTGAGATTA-CAGGTGTAACCGAGAT-AAGACCCTGGCTGAGTCAACGATGCACAAGGCTC
|  |   ||  ||  ||  | |||| |  ||  || | |||  |||||   |  | | || |  ||  |||
CAGCTGGAGCTCTCTGAGCAGCAGGAGGGAC--AGCTGAAGCACCTGGAGCA--CCAGGAGGGGCA--GCTG
     790       800       810         820       830         840

      130                 140            150         160       170
GA-ATCCTAG-GGA-----TGGG--AGGGGAGG-----GGCACCCCAG--GGTGGAGCTCCCCCCTCCTTCT
||  ||| || |||     ||||  ||  || |     || ||  |||  || | ||||     | |||
GAGGTCCCAGAGGAGCAGATGGGGCAGCTGAAGTACCTGGAACAGCAGGAGGGGCAGCT-GAAGCACCTGGA
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 850       860       870       880       890       900        910

 180       190       200       210       220       230       240       250
  TGCCCTTTGCCAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAG
  | |     ||  | ||||   ||||   ||| |||| |||| |||  || | |||||| | |||| | ||||
  T-C----AGCAGGAGAAGCAGCCAG--AGCTCCCAG-AGCAGCAG-ATG-G-GGCAGCTGAAGCACCTGGAG
920            930         940        950         960        970         980

         260       270        280           290        300        310
  CAACAGCTGCCTGGGCCGAGGC-TCTGGGAGCTCC----GTGGCTTCTAGGGC-TATGG-GACTCCTTGGGG
  || |||  |     ||| | || ||| |||||  |    | |||  || | ||   ||| |   |    |||
  CAGCAGGAGGGGCAGCCTAAGCATCT-GGAGCAGCAGGAGGGGCAACTGGAGCAGCTGGAGGAGCAGGAGGG
         990     1000       1010      1020      1030      1040      1050

    320            330       340        350         360       370
  GCAGCAG-----GGTGGAGGAGTCCGGCTGGCA-CTGCACCTCCAG--GCACCGAGAGAAATTCTGGCAGGC
  ||||| |       ||||| ||   |   |||| ||| | | || |  ||||| || |||   | |   ||
  GCAGCTGAAGCACCTGGAGCAGCAGGAGGGGCAGCTGGAGCACCTGGAGCACC-AG-GAAGGGCAGCTGGGG
       1060      1070      1080      1090      1100        1110      1120

380         390        400       410       420       430       440
  CTTCCCGA--TACAGG-GCTTCAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTG-G
  || || ||    |||| ||| |||   ||||||||  | | ||        ||| ||| || ||     |
  CTCCCAGAGCAGCAGGTGCTGCAGCTGAAGCAGCT-AGAGAAG--------CAGCAGG-GGCAGCCAAAGCA
       1130      1140      1150       1160              1170       1180

  450       460         470       480       490        500       510
  TCTGGACGAATCGCA--GACATTCTGGTAGGGGCTGGAAGGTACATGAGGTG-ACAAAATGTATCTCGGTGT
   ||||| ||   | |  | ||  || | ||   ||||  |   || |||| | |    | | |||| ||||
  CCTGGAGGAGGAGGAGGGGCA-GCT-GAAGCACCTGG-TGCAGCAGGAGGGGCAGCTGAAGCATCT-GGTG-
     1190      1200        1210       1220      1230      1240       1250

   520       530       540         550         560       570        580
  TGACGTCCTCCAGAAGCGTTTGCATCT-TAG-ACCCTGCCA--CAGTCTTCAGTTGCTCTATCCAGC-GCTG
         |  ||| || |   ||| ||  || | |  |  |  |||  |  ||   ||  |  |||| | ||
  -------CAGCAGGAGGG---GCAGCTGGAGCAGCAGGAGAGGCAG-GTGGAGCACCTGGA-GCAGCAGGTG
               1260         1270      1280       1290      1300       1310

      590       600       610       620       630           640
  GGCTAGGAAGAGGCTCCACAAGGCCTTGCAGTGCTTCTCGTCCTGAAG-AT-TG--ACGGCCACAGTG--AC
  ||  | |  || || ||   |||    |||| |     |   |||||| || ||   | ||  ||| |  |
  GGGCA-GCTGAAGCACCTAGAGG---AGCAG-GAGGGAC-AGCTGAAGCATCTGGAGCAGCAGCAGGGGCAG
         1320      1330          1340       1350      1360      1370

650       660       670       680       690       700       710       720
  TGGGTAATCTTTAAGCAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTG
  | ||   ||    |||||  |||  | || | |    |||  |    || ||  |||||||| |  ||||
  TTGGAGGTCCCAGAGCAGCAGGTGGGGCAGC-CAAAGAAC--C----TGGAGCAGGAGGAGAAGCAACTGGA
  1380      1390      1400       1410            1420      1430      1440

              730         740         750          760       770       780
  GCT----GA--AGTAACA--GTCAGGTG--TCCCCCGCAG--GCAAG-GACTCAGCAGCAGCAACAGCAGCA
  |||    ||  || || |  | ||||||   | || | ||  ||| | | | |||| | |||  |   ||||
  GCTCCCAGAGCAGCAAGAGGGCCAGGTGAAGCACCTGGAGAAGCAGGAGGCACAGCTGGAGCTCCCAGAGCA
       1450      1460      1470      1480      1490      1500      1510

         790                  800        810          820       830
  ACAGGGAGGA----------ATTTGG-GCTCCAGG-CTGGCGCC---AGCACTGTCATCTCTGCCGG--GGA
   |||| ||||          |  |||  |  ||||    || ||   |||||   ||   | || ||  |||
  GCAGGTAGGACAGCCAAAGCACCTGGAACAGCAGGAAAAGCACCTAGAGCAC--CCAGAGCAGCAGGACGGA
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       1520      1530      1540      1550      1560        1570      1580

      840       850       860       870        X
    CCCCTCATGCCTGTGACAGAGCAGGTCGTCTCGTTCCAGTCGAC
    |  || |  | | ||    ||||||  |    | |  ||  |||
    CAACTAAAACATCTGGAGCAGCAGGAGGGGCAGCTGAAG--GACCTGGAGCAGC
       1590      1600      1610      1620      X 1630


5. US-08-162-407-1' (1-879)
   CEZK638      Caenorhabditis elegans cosmid ZK638.

 LOCUS       CEZK638      1762 bp    DNA              INV       14-OCT-1994
 DEFINITION  Caenorhabditis elegans cosmid ZK638.
 ACCESSION   Z12018
 KEYWORDS    .
 SOURCE      nematode.
   ORGANISM  Caenorhabditis elegans
             Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditia;
             Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.
 REFERENCE   1  (bases 1 to 1762)
   AUTHORS   Metzstein,M. and Hawkins,T.
   TITLE     Direct Submission
   JOURNAL   Submitted (05-MAY-1992) jes@mrc-lmba.cambridge.ac.uk or
             rw@nematode.wustl.edu
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1762)
   AUTHORS   Sulston,J., Du,Z., Thomas,K., Wilson,R., Hillier,L., Staden,R.,
             Halloran,N., Green,P., Thierry-Mieg,J., Qiu,L., Dear,S.,
             Coulson,A., Craxton,M., Durbin,R., Berks,M., Metzstein,M.,
             Hawkins,T., Ainscough,R. and Waterston,R.
   TITLE     The C. elegans genome sequencing project: a beginning [see
             comments]
   JOURNAL   Nature 356, 37-41 (1992)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 1762)
   AUTHORS   Roberts,L.
   TITLE     The Worm Project
   JOURNAL   Science 248, 1310-1313 (1990)
   STANDARD  full automatic
 COMMENT     NOTES:
             This is a cosmid fragment sequenced to bridge the gap between
             cosmids ZK643 and R08D7.
             Bases 1 to 86 of this entry correspond to bases 39449 to 39534 of
             cosmid ZK643 (EMBL:CEZK643, accession number Z11126). Bases 1758 to
             1762 of this entry correspond to bases 1 to 5 of cosmid R08D7
             (EMBL:CER08D7).

             NCBI gi: 6966
 FEATURES             Location/Qualifiers
      source          1..1762
                      /organism="Caenorhabditis elegans"
 BASE COUNT      487 a    403 c    459 g    413 t
 ORIGIN

Initial Score    =   167  Optimized Score  =    403  Significance = 10.77
Residue Identity =   51%  Matches          =    493  Mismatches   =   328
Gaps             =   129  Conservative Substitutions             =     0

               X        10          20        30        40              50
```

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           GTCGACTG--GAACGAGAC-GACCTGCTCCAGACCATTCAGCA--ATC--CTGC-TCTG--G
           |||  | |  | | || ||  | | |     |||   ||| ||  |||  || | ||||  |
 ACTCGTCTTCGTCATCAGGCGGAGGATACTCATCGGGAGGTGACAGCTCATCATCATCATCTTCATCTGGAG
        200       210       220       230       240       250       260

          60        70        80         90        100         110
 GCT---CCCAAGGGCTGAGATTACAGGTGTAACCGAGAT-AAGACCCT-GGCTG--AGTCAACGATGCACAA
 | |   |   ||||  | |||| ||   ||   |||| | |  | ||| | |||   |  |   || |  |
 GATATTCGGGAGGG-AGTGATT-CA-TCGT---CGAGCTCATCATCCTCGTCTGGTGGATATTCATCCGGAG
      270        280            290       300       310       320

 120       130            140       150         160       170       180
 GGCTCGAATCCTAG-GGAT----GGGAGGGGAGGGGCACCCCAG--GGTGGAGCTCCCCCCTCCTTCTTGCC
 |   || || || | | ||     ||||| || |  | |  | |  || |||  | ||   | |||| |  |
 GAGGCG-ATGCTGGAGCATCATCTGGAGGAGA-GTCCTCTTCTGCAGGAGGATATTCCGGAT-CTTCAT--C
330        340       350        360       370       380        390

      190         200       210        220       230       240       250
 CTTTGCCAGCGAAG--GCCCCAGGCGGCTGC-CAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGC
     |   | ||||   |  | || || | | | |  | | |   || |||| ||||| ||||  ||| |||
 AAGCGGAGGAGAAGCATCATCCGGAGGATACTCTGGTGGATC---GTCAGAGCCAGCACCAGCTCCAGAAGC
   400       410       420       430          440       450       460

       260            270       280       290       300       310
 AACAGCTGC-----CTGGGCCGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCA
 | || ||||     |||||  ||  ||| ||  | ||||  ||  |    |  | |   ||||   |  |||
 AGCACCTGCTTCATCTGGG-GGATACTCAGGAGGATCCGAAGCAGCACCAG--AAGCTGCTCC--AGCAGCA
    470       480        490       500       510         520         530

320         330         340       350         360        370       380
 GCA--GGGTGGAGGAGTCCGG--CTGGCACTGCACCTCCAG--GCACCGAGAG-AAATTCTGGCAGGCCTTC
  ||   ||||||  | || ||  |||   |||||||   ||  || ||   ||     || ||  |   |||
 CCATCAGGTGGA-TATTCAGGATCTGAGGCTGCACCAGAAGCTGCTCCAGCAGCCCCATCAGGTGGATATTC
       540        550       560       570       580       590       600

     390       400       410       420       430       440        450
 CCGATACAGGGCTTCAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGG-TCTGGAC
   ||| |   |   |||  | || |||||  | |||  |  |  ||  |||| ||| ||   || |||| |
 AGGATCC---GAAGCAGCACCAGAAGCTG-CTCCAGCAG--CACCATCAGGT-GGATATTCAGGTTCTGAA-
         610       620        630         640        650       660

    460       470       480         490        500       510       520
 GAATCGCAGACATTCTGGTAGGGGCT--GGAAGGTACATGAGGT-GACAAAATGTATCTCGGTGTTGACGTC
      || | ||  | || ||  |||   |  |   |||  ||| || |   || |||| |  |  |
 -----GCTG-CA--CCGGAAGCCGCTCCAGCGGCCCCATCCGGTGGATACTCTGGATCT-GAAGCAG-----
       670          680       690       700       710        720

     530          540       550       560          570        580
 CTCCAGAAGC-GTT--TGCATCTTAGACCCTGCCACAGTC---TTCAGTTGCTCTATCCAG-CGCTGGGCTA
 | |||||||| | |   ||| ||    |   |  | | ||    ||||  ||    |||||  || |  | |
 CACCAGAAGCAGCTCCAGCAGCTCCATCTGGGGGATATTCCGGATCAGAGGC-AGCTCCAGAAGCCGCACCA
    730       740       750       760       770        780       790

590       600        610       620        630         640        650
 GGAAGAGGCTCCA-CAAGGCCTTGCAGTGCTTCT-CGTCCTGAAGA-TTGACG-GCCACAGTGA-CTGGGTA
 | |    || ||| |  ||   | |   |  |||   |||| |  |  || ||  ||| ||  | ||  ||
 GCA----GCCCCATCTGGGGGATACTCAGGATCTGAATCCTCAGCACCTGCCGCTCCAGAGCCAGCTCCGTC
       800       810       820       830       840       850       860

   660       670       680       690       700        710       720
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    ATCTTTAAGCAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGG-AGATGGGACTGTG--GCT
     |||  | ||   |    ||  |       |  ||  | |  |  | |||||| ||     ||| ||  | |
    TTCTGGAGGCTATTCTGGAG-GAGGAGGTGACGCTGGA-TCAGCTGCTGGAGGCAGCAACTACTCTGGAGGT
        870       880       890       900       910       920       930

       730         740        750        760       770       780       790
    GAAGTAACAG-TC-AGGTGTCCC-CCGC-AGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAAT
    |  | ||| | || || || ||| || | ||    |||  ||||   | |     ||| | ||||  |  |
    GGTGAAACCGCTCCAGCTGCCCCACCACCAGCTCCGGAACCAGCTCAAACCTACTCAGGAGCAGGTGGAGAG
        940       950       960       970       980       990      1000

         800       810       820       830       840       850       860
    TTGGGCTCCAGGCTGGCGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAGCAGGTCG-
    | || | ||  ||  || |||||||   |||||  |  | |||  |    ||   |||   |||| ||| |
    TCGGCCGCC--GC-CGCACCAGCAC---CATCT-GGAGGAGGATAC--AGTGGAAGTGGAGGAGCCGGTGGA
     1010         1020         1030       1040        1050      1060

              870          X
    TCTC------GTTCCAGT--CGAC
     | |      |  |||  |   |||
    GCACCAAATGGAGCCAATTATGACGAAGCACAAG
  1070      1080      1090 X    1100
```

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6. US-08-162-407-1’ (1-879)
   DMU13397     Drosophila melanogaster Oregon R DTIS11 protein mR

 LOCUS       DMU13397     2091 bp    mRNA            INV       30-AUG-1994
 DEFINITION  Drosophila melanogaster Oregon R DTIS11 protein mRNA, complete cds.
 ACCESSION   U13397
 KEYWORDS    .
 SOURCE      fruit fly.
   ORGANISM  Drosophila melanogaster
             Eukaryotae; Hyperchondria; Eukaryote crown group; Metazoa/Eumycota
             group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia;
             Arthropoda; Tracheata; Insecta; Pterygota; Neoptera; Holometabola;
             Diptera; Brachycera; Cyclorrhapha; Drosophilidae; Drosophila;
             Sophophora; melanogaster group; melanogaster subgroup.
 REFERENCE   1  (bases 1 to 2091)
   AUTHORS   Ma,Q., Wadleigh,D., Chi,T. and Herschman,H.
   TITLE     The Drosophila TIS11 homologue is a developmentally controlled gene
   JOURNAL   Oncogene (1994) In press
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 2091)
   AUTHORS   Ma,Q.
   TITLE     Direct Submission
   JOURNAL   Submitted (12-AUG-1994) Qiufu Ma, Molecular Biology, Bristol-Myers
             Squibb Pharmaceutical Research Institute, Road 206/Province line
             Road, Princeton, NJ 08543, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 532795
 FEATURES             Location/Qualifiers
      source          1..2091
                      /clone_lib="Drosophila eye disc lambda gt10 cDNA library"
                      /chromosome="X"
                      /strain="Oregon R"
                      /organism="Drosophila melanogaster"
                      /map="12B"
                      /dev_stage="instar, larval"
      CDS             301..1614
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                      /note="NCBI gi: 532796"
                      /codon_start=1
                      /product="DTIS11 protein"
                      /translation="MSADILQKSREQDDSHYFERGDISKYVTMNDHLGDFDCNEVRKE
                      IRMLLAHGANLDQQHQQQPHRHHGGLTRTISQPAQLIQQQQQQHQQQQQQQQPPVASL
                      VTITENLGNMNLHRKLERTQSEPLPPQQPMNTSRYKTELCRPFEEAGECKYGEKCQFA
                      HGSHELRNVHRHPKYKTEYCRTFHSVGFCPYGPRCHFVHNADEARAQQAAQAAKSSTQ
                      SQSQSQQSSSQNFSPKSNQSSNQSSNSSSSSSSSGGGGGGGNSINNNNGSQFYLPLSP
                      PLSMSTGSDRESPTGSLSLSPTNSLTSFPFHDALQHGYLASNGAKSNSSASSTSSASG
                      MGLGMSMGIGQGMIIGQGLGMGHHGPATPPESPNVPISPVHTPPPYDVVVSGSGAGNN
                      SVGSKQLLQKSVSTPMQQEDTPRLPVFNRLSSGVEAYQQQSNLGL"
      misc_feature    724..897
                      /note="encodes cysteine/histidine repeats"
 BASE COUNT      658 a   580 c   472 g   381 t
 ORIGIN

Initial Score    =    145  Optimized Score  =  406    Significance =  9.04
Residue Identity =    52%  Matches          =  504    Mismatches   =   315
Gaps             =    139  Conservative Substitutions              =     0

              X        10           20             30          40
              GTCGACTG-GAACGA-GA--CGACCTGC-TCCAG----ACCATTCAGC--AATCC--TGCTC
               || |  | | | || ||  ||  || | || ||     | ||  | |  ||| |    |
    TTCTGCAGAAATCAAGAGAGCAGGATGATTCGCACTACTTCGAGCGTGGCGATATATCCAAATACGTAACGA
        320   X   330       340       350       360       370       380

   50          60            70             80        90        100
    TG--GGCTCCCAAGGGCTGA----GATTAC----AGGTG-TAACCGAGATAA-GACCCTGGCTGAGTCAACG
    ||   | || |  ||| |||    |||| |    |||||   |  || |||| ||  || |||  | | |||
    TGAACGATCACTTGGG-TGATTTCGATTGCAACGAGGTGCGCAAGGAAATAAGGATGCT-GCT-CGCCCACG
      390       400        410       420       430       440         450

  110       120       130       140       150        160       170       180
    ATGCACAAGGCTCGAATCCTAGGGATGGGAGGGGAGGGGCA-CCCCAGGGTGGAGCTCCCCCCTCCTTCTTG
      || |||  || | |||    | |   |   | ||   || | |||   ||| | |     |||   |
    GCGC-CAA--CTTGGATCAGCAGCACCAG-CAGCAGCCACATCGCCACCATGGCGGT-----CTCACACGCA
        460         470       480        490       500            510

           190       200       210       220       230       240       250
    CCCTTTGCCAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCA
    || |||  ||||   || ||||| |   | ||||||||| |||    |    || |||||||||||| ||||
    CCATTTCACAGC--CGG-CCCAG-CTCAT-CCAGCAGCAGCAGCAGCAACACCAACAGCAGCAGCAGCAGCA
    520         530         540        550       560       570       580

         260       270        280        290       300       310       320
    ACAGCTGCCTGGGCCGAGGCTCTGG-GAGC-TCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAG
     ||||  ||||   | ||  ||||| || | ||   |    |  |||| |   ||  |||   |  | | |
    GCAGCCACCTGTTGCCAG--TCTGGTGACCATCACCGAGAACCTGGGCAACATGA-ACCT---GCACCGAAA
       590       600         610       620       630        640          650

          330          340       350       360         370         380
    GGTGGAG-GAGTCC---GGCTGGCACTGCACCTCCAGGCACCGA-GA-GAAATTCTG--GCAGGCCTTCCCG
    | ||||| ||  ||    |  | ||||||  |  |||   |||| ||  | || | |   || | |    |
    GCTGGAGCGAACCCAATCGGAGCCACTGCCGCCACAGCAGCCGATGAACACATCCAGATACAAGACCGAGCT
           660       670       680       690       700       710       720

     390       400       410       420       430       440         450
    ATACAGGGCTTCAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTC--TGGACGA
     | | |  | |  ||| | || |  |  ||||   || |  |  || |||  |   ||| | |  ||   ||
    GTGCCGTCCGTTCGAGGAGGCCGGAGAATGCA--AGTACGGCGAGAAGTGCCA---GTTCGCCCATG---GA
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       730       740       750         760       770          780

   460       470       480       490         500       510       520
  ATCGCAGACATTCTGGTAGGGGCTGGAAGGTACAT--GAGGTGACAAAATGTATCTCGGTGTTGACGTCCTC
  | |   ||  ||  |  | |   || |  || |||   | || |||| | | |   |  ||  | |  | ||
  AGCCATGA-GTTGCGAAACG---TGCACCGT-CATCCCAAGT-ACAAGACGGAATAC--TGCCG-CACCTTC
   790        800          810        820        830         840

   530       540       550         560        570       580       590
  CAGAAGCGTTTGCATCTTAGACCCTGC-CACAG-TCT-TCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAG
  ||  |||||  || |||  | |||| |  || |  || ||| ||  | |   ||  || || | |||
  CA-CAGCGTGGGCTTCT--GTCCCTACGGACCGCGCTGTCACTT--TGTTCACAATGC-GGACGAGGCCCGC
850        860         870       880       890         900        910

    600       610       620       630         640       650        660
  GCTCCACAAGGCCTTGCAGTGCTTCTCGTCCTGAA--GATTGACGGCCACAGTGACTG-GGTAATCTTTAAG
  || |||  ||||    |||     |  |||||  |   | |  | | | ||||  | |  ||  || |   |
  GC-CCAACAGGCGGCCCAGGCAGCCAAGTCCTCCACCCAGTCGCAGTCGCAGTCGCAGCAGTCGTCGT--CG
     920       930       940       950       960       970       980

     670            680       690       700       710       720       730
  CAGGTGGTC-AGTCAA----CTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGACTGTGGCTGAAGTAA
  |||    ||  | | |    |   |  | |  ||  |  |||| | |  || | | |  |  || | || |
  CAGAACTTCTCGCCGAAGAGCAACCAGAGCAGCA-ATCAAAGTAGCAACAG-TAGCA--GCAGCAGCAGCAG
     990      1000      1010       1020      1030         1040      1050

        740       750       760       770       780       790
  CAGTCAGGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATT-----TG-GG
  |||   || |  |  ||  |||  ||   || ||||| ||||| || |||| |     ||||     ||  |
  CAG--CGGCG-GCGGCGGTGGC--GGCGGCAACAGCATCAACAACAACAACGGTAGCCAATTCTATCTGCCG
        1060       1070        1080      1090      1100      1110

      800         810       820       830               840          850
  CT----CCA-GGCTG-GCGCCAGCACTGTCATCTCTGCCGGGGA---CCC-C----TCA-TG--CCTGTGAC
  ||    |||  |||| ||   ||||| |  |||    ||||| |   ||| |    ||| ||  |||  | |
  CTAAGCCCACCGCTGAGCATGAGCACAG-GATC-GGACCGGGAATCGCCCACCGGATCACTGTCCCTCAGCC
1120     1130      1140       1150       1160      1170      1180

       860           870         X
  AGAGCAGGTCGT---CTCG-TTCCAG-TCGAC
    | ||  ||||   |  | |||| | || ||
  CCACCAACTCGTTGACCAGCTTCCCGTTCCACGATGCCCTGC
1190     1200      1210      1220      1230


7. US-08-162-407-1' (1-879)
   CRUPA1V      Chinese hamster pro-alpha-1 (V) collagen mRNA, com

LOCUS       CRUPA1V      6114 bp ss-mRNA             ROD       14-JAN-1992
DEFINITION  Chinese hamster pro-alpha-1 (V) collagen mRNA, complete cds.
ACCESSION   M76730
KEYWORDS    alpha-1 type V collagen.
SOURCE      Cricetulus longicaudatus male adult cDNA to mRNA.
  ORGANISM  Cricetulus longicaudatus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Cricetidae; Cricetinae; Cricetini.
REFERENCE   1  (bases 1 to 6114)
  AUTHORS   Greenspan,D.S., Cheng,W. and Hoffman,G.G.
  TITLE     The pro-alpha-1(V) collagen chain: Complete primary structure,
            distribution of expression, and comparison with the pro-alpha-1(XI)
```

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            collagen chain
  JOURNAL   J. Biol. Chem. 266, 24727-24733 (1991)
  STANDARD  full automatic
COMMENT     NCBI gi: 191150
FEATURES             Location/Qualifiers
     source          1..6114
                     /organism="Cricetulus longicaudatus"
                     /dev_stage="adult"
                     /sequenced_mol="cDNA to mRNA"
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                     /gene="pro-alpha-1 (V) collagen"
                     /note="NCBI gi: 191151"
                     /codon_start=1
                     /product="pro-alpha-1 type V collagen"
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                     MLDFHNLPSGVTKTTGFCATRRSSRGPDVAYRVSKDAQLSMPRKQLYPDSDFAEDFSI
                     LTTVKAKKGSQAFLVSVYNEQGIQQVGMELGRSPVFLYEDHTGKPGPEEYPLFPGINL
                     SDGKWHRIAISVYRKNVTLILDCKKKVVKFLNRSDHPIIDVNGIIMFGSRILDDEIFE
                     GDIQQLLFVSDHRAAYDYCEHYSPDCDTAVPDTPQSQDPNPDEYYPEGDGETYYYEYP
                     YYEDPEDLGKEPAPTQKPVEAARETTEVPEEQTQPPPEAPTVPETSDPAGKEDDPGFG
                     DYDYVPTDDYYTPAPYEDLGYGEGVENPDQPTNPDSGAEVPTSTIITSNTSNPAPSPG
                     EDKDDLGGEFTEETIKNLEENYYDPYFDPDSDSNVSPSEIGPGMPANQDTIYEGIGGP
                     RGEKGQKGEPAIIEPGMLIEGPPGPEGPAGLPGPPGTTGPTGQVGDPGERGPPGRPGL
                     PGADGLPGPPGTMLMLPFRFGGGGDAGSKGPMVSAQESQAQAILQQARLALRGPAGPM
                     GLTGRPGPMGPPGSGGLKGEPGDMGPQGPRGVQGPPGPTGKPGRRGRAGSDGARGMPG
                     QTGPKGDRGFDGLAGLPGEKGHRGDPGPSGPPGLPGDDGERGDDGEVGPRGLPGEPGP
                     RGLLGPKGPPGPPGPPGVTGMDGQPGPKGNVGPQGEPGPPGQQGNPGAQGLPGPQGAI
                     GPPGEKGPLGKPGLPGMPGADGPPGHPGKEGPPGEKGGQGPPGPQGPIGYPGPRGVKG
                     ADGIRGLKGTKGEKGEDGFPGFKGDMGIKGDRGEIGPPGPRGEDGPEGPKGRGGPNGD
                     PGPLGPTGEKGKLGVPGLPGYPGRQGPKGSIGFPGFPGANGEKGGRGTPGKPGPRGQR
                     GPTGPRGERGPRGITGKPGPKGNSGGDGPAGPPGERGPNGPQGPTGFPGPKGPPGPPG
                     KDGLPGHPGQRGETGFQGKTGPPGPPGVVGPQGPTGETGPMGERGHPGPPGPPGEQGL
                     PGVAGKEGTKGDPGPAGLPGKDGPPGLRGFPGDRGLPGPVGALGLKGSEGPPGPPGPA
                     GSPGERGPAGAAGPIGIPGRPGPQGPPGPAGEKGVPGEKGPQGPAGRDGLQGPVGLPG
                     PAGPVGPPGEDGDKGEIGEPGQKGSKGDKGEQGPPGPTGPQGPIGQPGPSGADGEPGP
                     RGQQGLFGQKGDEGSRGFPGPPGPVGLQGLPGPPGEKGETGDVGQMGPPGPPGPRGPS
                     GAPGADGPQGPPGGIGNPGAVGEKGEPGEAGEPGLPGEGGPLGPKGERGEKGEVGPSG
                     AAGPPGPKGPPGDDGPKGSPGPVGFPGDPGPPGEPGPAGQDGPPGDKGDDGEPGQTGS
                     PGPTGEPGPSGPPGKRGPPGPAGPEGRQGEKGAKGEAGLEGPPGKTGPIGPQGAPGKP
                     GPDGLRGIPGPVGEQGLPGSPGPDGPPGPMGPPGLPGLKGDSGPKGEKGHPGLIGLIG
                     PPGEQGEKGDRGLPGPQGSSGPKGEQGITGPSGPLGPPGPPGLPGPPGPKGAKGSSGP
                     TGPKGEAGHPGLPGPPGPPGEVIQPLPIQASRTRRNIDASQLLDDGAGESYLDYADGM
                     EEIFGSLNSLKLEIEQMKRPLGTQQNPARTCKDLQLCHPDFPDGEYWVDPNQGCSRDS
                     FKVYCNFTAGGSTCVFPDKKSEGARITSWPKENPGSWFSEFKRGKLLSYVDAEGNPVG
                     VVQMTFLRLLSASAHQNITYNCYQSVAWQDAATGSYDKAIRFLGSNDEEMSYDNNPYI
                     RALVDGCATKKGYQKTVLEIDTPKVEQVPIVDIMFNDFGEASQKFGFEVGPACFLG"
BASE COUNT     1372 a   1768 c   1883 g   1091 t
ORIGIN

Initial Score    =   144  Optimized Score  =   408  Significance =  8.96
Residue Identity =   52%  Matches          =   508  Mismatches   =   301
Gaps             =   157  Conservative Substitutions       =     0

              X       10        20        30         40           50
              GTCGACTGGAACGAGACGACCTGCTCCAGACCATTCA-GCAATCCTGCT---CTGGG-CTCC
              | | | ||| | ||| ||       || | || | || ||   |||| |   |||| ||  |
    GGAGAAACCGGCCCAATGGGA-GAG-CGTGGCCACCCTGGCCCTCCAGGCCCCCCTGGTGAACAGGGCCTTC
       3060   X  3070        3080      3090      3100      3110      3120
    60        70        80        90         100        110       120
   CAAGGGCTGAGATTACAGGTGTAACCGAGATAAGACCCTGG--CTG-AGTCAACGATGCACAAGGCTCGAAT
   || | | ||     | ||  |  ||  ||    ||||| ||  ||| || |  |  || | |||| | |
   CAGGAGTTGCTGGAAAAGAAGGGACTAAG-GGGGACCCAGGCCCTGCAGGCCTCCCTGGA-AAGGATGGCCC
      3130      3140      3150       3160      3170      3180       3190

    130          140       150       160         170            180
   CCTAGGGATG---GGAGGGGAGGGGCACCCCAGGGTGGAGCTCCC--CCCT-----CCTTCTTGCCCT--TT
    | |||  ||   |||      ||| |||     | |||  ||||  ||||        |||||  ||
   TCCAGGATTGCGTGGATTCCCTGGGGACC-----GAGGACTTCCCGGCCCTGTGGGAGCTCTTGGGCTAAAA
      3200      3210      3220           3230      3240      3250      3260

    190       200       210       220       230       240       250
   GCCAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCT
   | |||||||||||||  | |||  ||  |||  || | | |     ||| || || || |||| || | |
   GGCAGCGAAGGCCCCCCG-GGC--CCTCCAGGTCCTGCGGGTTCTCCAGGAG-AG-AG-AGGACCAGCTGGG
         3270       3280        3290      3300       3310        3320

  260         270       280        290       300        310       320
   GC--CTGGGCCGAGGCTCTGGGAGCTCC-GTGGCTTCTAGGGCTATGGGA-CTCCTTGGGGGCAGCAGG-GT
   ||  ||||||| |   ||  |||  ||| | |    || ||||   |||| ||||   ||| |||| || |
   GCTGCTGGGCCCA---TC--GGAATTCCAGGGAGACCTGGGCCTCAGGGACCTCC--AGGGCCAGCTGGAGA
   3330         3340        3350      3360      3370        3380      3390

      330       340          350       360       370       380       390
   G-GAGGAGTCCGGCTGGC---ACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATAC---
   |  ||| || |  |||||   |  |  || | |||| |    ||     |  |  ||||| |  | | |
   GAAAGGGGTTC--CTGGCGAGAAAGGTCCACAAGGCCC----AGCTGGCCGAGATGGCCTCCAAGGTCCTGT
        3400        3410      3420          3430      3440      3450

          400       410       420        430       440       450        460
   AGGGCTTCAGAGCAAGCAGCTGTGTGCAGGT-GTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGA-ATCG
    |||||||   |    |||| | |  | | | ||||| | |||    | |||||  | |  ||  || ||||
   GGGGCTTCCTGG--TCCAGCCG-GCCCCGTTGGTCCTCCTGGA----GAAGATGGAGATAAGGGAGAGATCG
  3460        3470       3480      3490          3500      3510      3520

          470       480        490       500       510           520
   CAGACATTCTGGTAGGGGCTGGAAGGTA-CATGAGGTGACAAAATGTATCTCGGT----GTTGAC------G
     ||      |  | |||| | |||| | || | || ||||||    | |  |||     | |||      |
   GGGA------GCCA-GGGCAGAAAGGAAGCAAG-GGGGACAAAGGCGAGCAGGGTCCTCCTGGACCTACGGG
             3530       3540       3550      3560      3570      3580

         530         540       550       560       570          580
   TCCTCCAGAAGCGTTTG--CATCTTAGACCCTGCCACAGTCTTCAGTTGCTCTATCCAG---CGCTGGGCTA
   ||||| ||   |  |||  || |   | |||| |   ||    ||| || |  | ||||   | |  ||  |
   TCCTCAAGGCCCCATTGGACAGCCAGGTCCCT-CGGGAG----CAGATGGT-GAGCCAGGTCCTCGTGGACA
   3590      3600      3610       3620          3630       3640      3650

  590       600       610       620       630            640       650
   GGAAGAGGCTCCACAAGGCCTTGCAGTGCTTCTCGTCCTGAAGA--TT---GACGGCCACAGTGACTGGGTA
   | ||| | ||   |  |||   | |  |   |     || ||||  ||    | | |||| | | |   ||
   GCAAG-GCCTGTTC-GGGC--AGAAAGGAGACGAAGGCTCAAGAGGTTTCCCAGGACCACCGGGGC-CAGTG
        3660         3670      3680      3690      3700      3710

     660       670       680       690       700       710       720
   ATCTTTAAGCAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTGGCTGAA
      ||  ||  | | | |||  | ||| |   |    |   |||      ||||||||    || | | ||
   GGATTACAG-GGTTTGCCAG-GACCTC-CAGGAGAGAAGGGTGA---GACAGGAGATG----TGGGCCAGAT
3720       3730       3740       3750      3760         3770          3780
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730       740         750         760       770            780
GTAACAGTCAGGTGTCCCCC--GCAGGCAAGGA--CTCAGCAGCAGCAACAGC-----AGCAACAG------
|  ||  || || |||||||  ||   | ||||  ||| | |||  ||   ||      || ||||
GGGAC-CTCCGG-GTCCCCCAGGCCCCCGAGGACCCTCTGGAGCTCCAGGTGCTGATGGGCCACAGGGTCCT
      3790       3800      3810      3820      3830      3840      3850

      790       800          810       820             830         840
---GGAGGAATTTGGGCTCCAG--GCTG-GCGCCAGCACTGTCATCTCT------GCCGGGGACCC--CTCA
   ||||||||| |    || |  || | | |  |  |  |  | | ||      || || || ||   ||
CCCGGAGGAATTGGCAACCCTGGTGCAGTGGGAGAAAAGGGGGAGC-CTGGTGAAGCTGGAGAGCCTGGTC-
     3860      3870      3880      3890       3900      3910      3920

     850       860       870           X
TGCCTGTGACAGAGCAGGTCGTCTCGTTCC---AGTCGAC
| || | || | || |||||  || |  ||   ||  ||
TTCCAG-GAGA-AGGAGGTCCCCTGGGACCTAAAGGAGAAAGAGGGGAGA
      3930       3940      3950      3960


8. US-08-162-407-1’ (1-879)
   GORINVOLUB   Gorilla gorilla involucrin gene medium allele, com

LOCUS       GORINVOLUB   1818 bp ds-DNA             PRI       08-SEP-1994
DEFINITION  Gorilla gorilla involucrin gene medium allele, complete cds.
ACCESSION   M23604 J04499
KEYWORDS    epidermal protein; involucrin.
SOURCE      Gorilla gorilla (individual_isolate Gorilla K) (library: vagina)
            DNA.
  ORGANISM  Gorilla gorilla
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Primates; Haplorhini; Catarrhini; Pongidae.
REFERENCE   1  (bases 1 to 1818)
  AUTHORS   Teumer,J. and Green,H.
  TITLE     Divergent evolution of part of the involucrin gene in the
            hominoids: Unique intragenic duplications in the gorilla and human
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 1283-1286 (1989)
  STANDARD  full automatic
COMMENT     Draft entry and computer readable copy of sequence [1] kindly
            provided by J.K. Teumer (03-31-89).

            NCBI gi: 340978
FEATURES             Location/Qualifiers
     source          1..1818
                     /organism="Gorilla gorilla"
                     /isolate="Gorilla K"
                     /cell_type="keratinocyte"
                     /sequenced_mol="DNA"
                     /clone="pIGorH6.1"
                     /tissue_lib="vagina"
     CDS             1..1818
                     /note="NCBI gi: 536828"
                     /codon_start=1
                     /product="involucrin"
                     /translation="MSLQHTLPVTLSPALSQELLKTVPPPVNTQQEQMKLPTPLPPPC
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                     NPEQQLKQEKAQRDQQLNKQLEEEKKLLDQQLDQELVKRDEQLGMKKEQLLELPEQRE
                     GQLKHLEQQKGQLELPEQQEGQLELPEQQEGQLKHLEQQKGQLELPEQQEGQLELPEQ
                     QEGQLELPEQQEGQLKHLEQQEGQLELPEQQEGQLELPEQQEGQLKHLEQQEGQLKHL
                     ENQEGQLEVPEEQVGQLKYLEQQEGQLKHLDQQEKQPELPEQQVGQLKHLEQQEGQPK
                     HLEQQEGQLEHLEEQEGQLKHLEQQEGQLEHLEHQEGQLGLPEQQVRQLKQLEKEEGQ
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                         PKHLEEEEGQLKHLVQQEGHVEHLVQQEGQLEHLVQQEGQLEQQEGQVEHLEQQVGQL
                         KHLEEQEGQLKHLEQQQGQLGVPEQQVGQPNNLEQEEKQLELPEQQEGQLKHLKKQEA
                         QLELPEQQVGQPKHLEQQEKQLEHPEQQDGQLKHLEQQEGQLKDLEQQKGQLEQPVFA
                         PAPGQVQDIQPALPTKGELLLPIEHQQQKQEVQWPPKHK"
 BASE COUNT      531 a    454 c    657 g    176 t
 ORIGIN

Initial Score    =    141  Optimized Score =    407  Significance =  8.73
Residue Identity =    52%  Matches         =    499  Mismatches   =   329
Gaps             =    120  Conservative Substitutions          =     0

            X       10          20           30        40          50
            GTCGACTGGA-ACGAGACG-ACCT---GCTCCAGACCATTCAGCAATCCTGCT--CTGGGCT
            |  |   ||| |   || | ||||   ||  ||||     ||||  |   |||  | | ||
  TCCCAGAGCAGCAGGAGGGACAGCTGAAGCACCTGGAGCAGCAGAAGGGGCAGC--TGGAGCTCCCAGAGCA
      560   X   570       580       590       600         610       620

       60            70        80        90         100             110
  CC--CAAGGGC----TGAGATTACAGGTGTAACCGAGATAAGACCCTG--GCT----GAGTCA--ACGATGC
   |   | ||||     ||| |  || | | | | | ||   |   |||  |||    ||| ||  | || |
  GCAGGAGGGGCAGCTGGAGCTCCCA-GAGCAGCAG-GAGGGGCAGCTGGAGCTCCCAGAG-CAGCAGGAGGG
      630       640        650        660       670       680        690

      120         130         140        150       160       170       180
  ACAAGGCTCGAA--TCCTAGGGATG--GGAGGGG-AGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTG
  |||  ||| |||   ||||| |  |   |||||| ||  | | | |   | | |||         |  || |
  ACA--GCT-GAAGCACCTAGAGCAGCAGGAGGGGCAGCTGGAGCTCCCAGAGCAGC-AGGAGGGGCAGCTGG
          700       710       720       730       740        750       760

         190       200         210         220       230       240
  CCCTTTGCCAGCGAAGGCCCCAGG--CGGCTG--CCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGG
    |  | |||| | | ||   |||  | ||||   || | | | |||   ||| |||||| | |||| | ||
  AGC--TCCCAGAGCA-GCAGGAGGGACAGCTGAAGCACCTGGAGCAGCAGGAGGGGCAGCTGAAGCATCTGG
           770        780       790       800       810       820

 250       260        270         280        290        300       310
  AGCAACAGCTGCCTGGGC-CGAGG-CTCTG-GGAGC-TCCGTGGCTTCT-AGGGCTATGGGACTCCTTG-GG
  || | |||  |     ||  |||| | | | |||||    | |||  || | |    ||| ||  |  | ||
  AGAACCAGGAGGGGCAGCTGGAGGTCCCAGAGGAGCAGGTGGGGCAGCTGAAGTACCTGGAACAGCAGGAGG
830       840       850       860       870       880       890       900

     320         330       340       350       360       370       380
  GGCAGC--AGGGTGGAGGAGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCC
  ||||||  | |     ||| ||  || ||    ||| | |   || || |||| |   | ||  || |   |
  GGCAGCTGAAGCACCTGGA-TC-AGCAGGAGAAGCAGC-CGGAGCTCCCAGAGCA--GCAGGTGGGGC-AGC
        910       920         930        940       950         960

     390           400       410       420        430       440        450
  CGATACA---GG-GCTTCAGAGCAAGCAGCTGTGTGCAGGT-GTCCTTCAGGAGGTGGGAGATGTTG-GTCT
   ||  ||   || ||  |||     |||||  |  |||  | |  |  ||||||| || |  ||  |   ||
  TGAAGCACCTGGAGCAGCAGGAGGGGCAGC-CTAAGCATCTGGAGCAGCAGGAGG-GGCAACTGGAGCACCT
  970       980       990       1000      1010      1020       1030

         460         470       480       490       500       510       520
  GGACGAATCGCA--GACATTCTGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTGAC
  ||| ||   | |  | ||  || | ||   |||| ||   || |||| | ||   || | | |  ||  ||
  GGAGGAGCAGGAGGGGCA-GCT-GAAGCACCTGG-AGCAGCAGGAGG-GGCA-GCTGGAGCAC-CTG--GA-
 1040      1050        1060       1070      1080        1090         1100

         530       540       550       560       570          580
```

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  GTCCTCCAGAAGCGTTTGCATCTTAGACCCTGCCACAGTCTTCAGTTGCTCTA--TCCAGC-GCTGGGCTAG
  |  | |||| |  |   ||| ||  |   || ||| || |  ||| |||   |  |  ||| ||| |   ||
  G--CACCAGGAAGG---GCAGCT--GGGGCTCCCAGAG-CAGCAGGTGCGGCAGCTGAAGCAGCTAGAGAAG
          1110           1120      1130       1140      1150      1160

590        600        610        620       630          640        650
  GAAGAGGCTC-CACAAGGC-CTTGCA-GTGCTTCTCGTCCTGAAGATTGAC--GG-CCA-CAGTGACTGGGT
  || ||||  |   ||| || |||| | | |      |  | |  ||   ||  ||  || ||| ||  |||
  GAGGAGGGGCAGCCAAAGCACCTGGAGGAGGAGGAGGGGCAGTTGAAGCACCTGGTGCAGCAG-GA-GGGGC
    1170      1180      1190      1200      1210      1220        1230

     660       670        680       690         700       710       720
  AATCTTTAAGCAGGTGGT-CAGTCAACTCTCTAAACTTCA-CTT-TGAAGTTGGAGGAGATGGGACTGTGGC
  |  | |  ||||  |||| ||| ||        | ||  | | | ||  |  | |||||  |   |||  ||
  A--CGTGGAGCACCTGGTGCAG-CAGGAGGGGCAGCTGGAGCATCTGGTGCAGCAGGAGGGGCAGCTGGAGC
      1240      1250       1260      1270      1280      1290      1300

      730       740         750          760          770       780
  TGAAGTAACAGTCAGGTG--TCCCCCGCAG--GCAAG-GACTCAGC---AGCAGCAACAGCAGCAACAGGGA
   | ||  |  | ||||||   | || | ||  ||| | |   ||||   |||| | | || ||||  ||||
  AGCAG-GAGGGGCAGGTGGAGCACCTGGAGCAGCAGGTGGGGCAGCTGAAGCACCTAGAGGAGCAGGAGGG-
      1310      1320      1330      1340      1350      1360      1370

  790       800       810       820       830         840       850
  GGAATTTGGGCTCCAGGCTGGCGCCAGCACTGTCATCTCTGCCGGGGACCC--CTCATGCCTGTGACAGAGC
  | || |   ||  | ||   ||  |||||  | ||  |     |||| |||    || ||  |||    |||
  GCAACTGAAGCATCTGG--AGCAGCAGCAGGGGCAGTT----GGGGGTCCCAGAGCA-GCAGGTGGGGCAGC
     1380      1390        1400          1410      1420       1430

  860       870        X
  AGGTCGTCTCGTTCCAGTCGAC
      |  |  |   |||  |
  CAAACAACCTGGAGCAGGAGGAGAAGCAGCTG
1440      1450      1460      1470


9. US-08-162-407-1’ (1-879)
   HUMCA1V      Human mRNA for collagen alpha 1(V) chain, complete

 LOCUS       HUMCA1V      5676 bp ss-mRNA           PRI       29-AUG-1991
 DEFINITION  Human mRNA for collagen alpha 1(V) chain, complete cds.
 ACCESSION   D90279
 KEYWORDS    alpha 1(V) chain; collagen.
 SOURCE      Human placenta, cDNA to mRNA.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 5676)
   AUTHORS   Takahara,K., Sato,Y., Okazawa,K., Okamoto,N., Noda,A., Yaoi,Y. and
             Kato,I.
   TITLE     Complete primary structure of human collagen alpha1(V) chain
   JOURNAL   J. Biol. Chem. 266, 13124-13129 (1991)
   STANDARD  full automatic
 COMMENT     These data kindly submitted in computer readable form by: Kazuhiko
             Takahara
             Takara Shuzo Co., Ltd.
             Biotechnology Research Laboratories
             3-4-1 Seta, Otsu
             Shiga 520-21
             Japan
```

```
              Phone: 81-775-43-7200
              Fax:     81-775-43-2494.

              NCBI gi: 219509
 FEATURES                Location/Qualifiers
      source             1..5676
                         /organism="Homo sapiens"
      sig_peptide        127..237
                         /note="signal peptide of collagen alpha 1(V) chain"
                         /codon_start=1
      CDS                127..5643
                         /note="collagen alpha 1;  (V) chain precursor;  NCBI gi:
                         219510"
                         /codon_start=1
                         /translation="MDVHTRWKARSALRPGAPLLPPLLLLLWAPPPSRAAQPADLLK
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                         SDGKWHRIALSVHKKNVTLILDCKKKTTKFLDRSDHPMIDINGIIVFGTRILDEEVFE
                         GDIQQLLFVSDHRAAYDYCEHYSPDCDTAVPDTPQSQDPNPDEYYTEGDGEGETYYYE
                         YPYYEDPEDLGKEPTPSKKPVEAAKETTEVPEELTPTPTEAAPMPETSEGAGKEEDVG
                         IGDYDYVPSEDYYTPSPYDDLTYGEGEENPDQPTDPGAGAEIPTSTADTSNSSNPAPP
                         PGEGADDLEGEFTEETIRNLDENYYDPYYDPTSSPSEIGPGMPANQDTIYEGIGGPRG
                         EKGQKGEPAIIEPGMLIEGPPGPEGPAGLPGPPGTMGPTGQVGDPGERGPPGRPGLPG
                         ADGLPGPPGTMLMLPFRFGGGDAGSKGPMVSAQESQAQAILQQARLALRGPAGPMGL
                         TGRPGPVGPPGSGGLKGEPGDVGPQGPRGVQGPPGPAGKPGRRGRAGSDGARGMPGQT
                         GPKGDRGFDGLAGLPGEKGHRGDPGPSGPPGPPGDDGERGDDGEVGPRGLPGKPGPRG
                         LLGPKGPPGPPGPPGVTGMDGQPGPKGNVGPQGEPGPPGQQGNPGAQGLPGPQGAIGP
                         PGEKGPLGKPGLPGMPGADGPPGHPGKEGPPGEKGGQGPPGPQGPIGYPGPRGVKGAD
                         GIRGLKGTKGEKGEDGFPGFKGDMGIKGDRGEIGPPGPRGEDGPEGPKGRGGPNGDPG
                         PLGPPGEKGKLGVPGLPGYPGRQGPKGSIGFPGFPGANGEKGGRGTPGKPGPRGQRGP
                         TGPRGERGPRGITGKPGPKGNSGGDGPAGPPGERGPNGPQGPTGFPGPKGPPGPPGKD
                         GLPGHPGQRGETGFQGKTGPPGPPGVVGPQGPTGETGPMGERGHPGPPGPPGEQGLPG
                         LAGKEGTKGDPGPAGLPGKDGPPGLRGFPGDRGLPGPVGALGLKGNEGPPGPPGPAGS
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                         GPVGPPGEDGDKGEIGEPGQKGSKGDKGEQGPPGPTGPQGPIGQPGPSGADGEPGPRG
                         QQGLFGQKGDEGPRGFPGPPGPVGLQGLPGPPGEKGETGDVGQMGPPGPPGPRGPSGA
                         PGADGPQGPPGGIGNPGAVGEKGEPGEAGEPGPSGRSGPPGPKGERGEKGESGPSGAA
                         GPPGPKGPPGDDGPKGSPGPVGFPGDPGPPGEPGPAGQDGPPGDKGDDGEPGQTGSPG
                         PTGEPGPSGPPGKRGPPGPAGPEGRQGEKGAKGEAGLEGPPGKTGPIGPQGAPGKPGP
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                         GEQGEKGDRGLPGPQGSSGPKGEQGITGPSGPIGPPGPPGLPGPPGPKGAKGSSGPTG
                         PRGEAGHPGPPGPPGPPGEVIQPLPIQASRTRRNIDASQLLDDGNGENYVDYADGMEE
                         IFGSLNSLKLEIEQMKRPLGTQQNPARTCKDLQLCHPDFPDGEYWVDPNQGCSRDSFK
                         VYCNFTAGGSTCVFPDKKSEGARITSWPKENPGSWFSEFKRGKLLSYVDAEGNPVGVV
                         QMTFLRLLSASAHQNVTYHCYQSVAWQDAATGSYDKALRFLGSNDEEMSYDNNPYIRA
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      mat_peptide        238..5640
                         /note="mature peptide of collagen alpha 1(V) chain"
                         /codon_start=1
 BASE COUNT     1181 a   1803 c   1872 g    820 t
 ORIGIN

Initial Score    =    139  Optimized Score =    397  Significance =  8.57
Residue Identity =    50%  Matches         =    472  Mismatches   =   348
Gaps             =    109  Conservative Substitutions          =     0

          X          10         20        30        40          50
          GTCGACTG---GAACGAGACGA-CCTGCTCCAGACCATTCAGCAATC-CTGCTC-TGGGCTC
          | | | ||   || || | | | ||||  ||   || |  | |   |  ||  |  |||||
GGAGAAACGGGCCCAATGGGTGAGCGTGGCCACCCTGGGCC---CCCTGGACCCCCCGGTGAACAGGGGCTT
```

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       3150 X    3160      3170      3180         3190      3200      3210

    60          70        80        90         100        110       120
  CCAAGGGC--TGAGATTACAGGTGTAACCGAGATAAGACCCTGG--CTG-AGTCAACGATGCACAAGGCTCG
  ||  ||||  ||     | ||  |  | |||     ||||| ||  ||| || |  |  ||   || | | |
  CC--GGGCCTTGCTGGAAAAGAAGGGA-CGAAGGGTGACCCAGGCCCTGCAGGCCTCCCTG-GGAAAGATGG
          3220      3230       3240      3250      3260       3270

      130       140          150       160       170         180       190
  AATCCTAGGGATGGGAGG---GGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCC--TTCTTGCCCTTTGCCA
      | |||  |  | ||       ||| | || |||     ||| ||   |||  |    || ||| | |
  CCCTCCAGGATTACGTGGTTTCCCTGGGGA-CCGAGG-----GCTTCCTGGTCCAGTGGGAGCTCTTGGACT
3280      3290      3300       3310           3320      3330      3340

         200       210       220       230       240       250       260
  GCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCCT
  |  |||||       |||  || |   ||||||     | || | |  |||  |   |||   ||||||
  G-AAAGGCAATGAAGGGCCCCCTGGCCCACCAGGCCCTGCGGGATCTCCAGGGGAGAGAGGTCCAGCTGGAG
     3350      3360      3370      3380      3390      3400      3410

       270       280        290       300       310         320       330
  GGGCCGAGGCTCTGGGAGCTCC-GTGGCTTCTAGGGCTATGGGACTCCTTGGG--GGCAGCAGGGTGGAGGA
    || | | |  | |||  ||| | |    || || |   ||||| ||  |||  ||||| || |    ||
  CCGCTGGGCCCATCGGAATTCCAGGGAGACCTGGGCCCCAGGGACCCCCAGGGCCGGCAGGAGAGAAAGGGG
   3420      3430      3440      3450      3460      3470      3480

         340       350       360            370       380       390
  GTCC-GGCTGGCACTGCACCTCCAGGCACCG-----AGAGAAATTCTGGCAGGCCTTCCCGATACAGGGCTT
   ||| |||  | |  || || | |||| | |      ||||   |||  ||||    ||   |   |||||
  CTCCTGGCGAGAAAGGC-CCACAAGGCCCAGCTGGCCGAGACGGTCT-CCAGG--GGCC---TGTGGGGCTC
 3490      3500       3510      3520      3530         3540         3550

  400         410       420       430       440       450       460
  CAGAG-CAAGC-AGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAGACAT
  | | | | |||  ||  ||||  |||  || |   || |  ||||||   ||    || | ||||  ||
  CCGGGTCCAGCTGGCCCTGTG--GGTCCCCCTGGAGAAGACGGAGATAAGGG---AGA-G-ATCGGGGA---
      3560      3570        3580      3590      3600           3610

  470       480        490       500       510        520       530
  TCTGGTAGGGGCTGGAAGGTA-CATGAGGTGACAAAATGTATCTCGGT-GTTGACGTCCTCCAGAAGC----
      |  ||||| | |||| | || | || ||||||    | |  |||  |    | ||| |||   |
  ----GCCGGGGCAGAAAGGAAGCAAG-GGGGACAAAGGAGAACAGGGTCCTCCTGGGCCTACAGGTCCTCAA
        3620      3630       3640      3650      3660      3670      3680

      540       550       560         570          580       590       600
  GTTTGCATCTTAGACCCTGCCACAGTCTTCAGTTG--CTCTATCCAG---CGCTGGGCTAGGAAGAGGCTCC
  |    ||||  | | || | | |  |||  || ||    | | || |   | | |||| | | || | ||
  GGCCCCATCGGACAGCCAGGC-CCCTCTGGAGCTGACGGCGAGCCGGGGCCTCGGGGCCA-GCAGGGCCTTT
       3690      3700       3710      3720      3730      3740       3750

         610       620        630        640       650       660
  ACAAGGCCTTGCAGTGCTTCTCGT-CCTGAAGATTGAC-GGCCACAGTGACTGGGTAATCTTTAAGCAGG--
   |  |||      ||| |    || || || | ||  | || | |  ||   ||  | |      |||||
  TC-GGGCAGAAAGGTGATGAAGGTCCCAGAGGCTTTCCTGGACCCCCTG---GGCCAGTGGGGCTGCAGGGT
        3760      3770      3780      3790         3800      3810

 670       680       690       700       710        720       730
  TGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGAC-TGTGGCTGAAGTAACAGTCAGG
  | | |||   || ||| |  |        ||||   || || | | ||| || | | || |   |   | ||
  TTGCCAG--GAC-CTCCAGGC------GAGAAGGGTGA-GACAGGAGACGTGGGCCAGATGGGCCCCCCGGG
 3820         3830            3840       3850      3860      3870      3880

  740       750       760       770       780       790       800
    TGTCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTTGGGCTCCAGGCTGG---
    |  |||  ||   | ||||| |  | | |||  |||  ||   | ||   |    |  | ||||| |||
    TCCCCCTGGCCCCCGAGGAC-CCTCCGGAGCTCCAGGTGC-TGATGGCCCACAAGGTCCCCCAGG-TGGAAT
         3890      3900       3910      3920       3930      3940       3950

   810       820       830       840       850       860           870
    CGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAGCAGGT-CGTCT---CGTTCCAGTC
     |  | | |||    |  ||   | ||     |  ||||| |  | |||||||  | ||   | |||| |
    AGGAAACCCTG-GTGCAGTGGGAGAGA-AGGGCGAGCCTG-GCGA-AGCAGGTGAGCCTGGCCCTTCCGGGA
          3960       3970       3980       3990       4000      4010

      X
    GAC
    ||
    GAAGCGGCCCCC
  4020      4030


10. US-08-162-407-1' (1-879)
    HUMPA1V      Human pro-alpha-1 (V) collagen mRNA, complete cds.

 LOCUS       HUMPA1V      7138 bp ss-mRNA            PRI       07-JAN-1995
 DEFINITION  Human pro-alpha-1 (V) collagen mRNA, complete cds.
 ACCESSION   M76729
 KEYWORDS    alpha-1 type V collagen.
 SOURCE      Homo sapiens cDNA to mRNA.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 7138)
   AUTHORS   Greenspan,D.S., Cheng,W. and Hoffman,G.G.
   TITLE     The pro-alpha 1(V) collagen chain. Complete primary structure,
             distribution of expression, and comparison with the pro-alpha 1(XI)
             collagen chain
   JOURNAL   J. Biol. Chem. 266, 24727-24733 (1991)
   STANDARD  full automatic
 COMMENT     NCBI gi: 189519
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                      /sequenced_mol="cDNA to mRNA"
      CDS             230..5746
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                      /map="9q34.2-q34.3"
                      /note="NCBI gi: 189520"
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                      GDIQQLLFVSDHRAAYDYCEHYSPDCDTAVPDTPQSQDPNPDEYYTEGDGEGETYYYE
                      YPYYEDPEDLGKEPTPSKKPVEAAKETTEVPEELTPTPTEAAPMPETSEGAGKEEDVG
                      IGDYDYVPSEDYYTPSPYDDLTYGEGEENPDQPTDPGAGAEIPTSTADTSNSSNPRPP
                      PGEGADDLEGEFTEETIRNLDENYYDPYYDPTSSPSEIGPGMPANQDTIYEGIGGPRG
                      EKGQKGEPAIIEPGMLIEGPPGPEGPAGLPGPPGTMGPTGQVGDPGERGPPGRPGLPG
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                      GPKGDRGFDGLAGLPGEKGHRGDPGPSGPPGPPGDDGERGDDGEVGPRGLPGEPGPRG
                      LLGPKGPPGPPGPPGVTGMDGQPGPKGNVGPQGEPGPPGQQGNPGAQGLPGPQGAIGP
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                      PTGEPGPSGPPGKRGPPGPAGPEGRQGEKGAKGEAGLEGPPGKTGPIGPQGAPGKPGP
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                      GEQGEKGDRGLPGPQGSSGPKGEQGITGPSGPIGPPGPPGLPGPPGPKGAKGSSGPTG
                      PKGEAGHPGPPGPPGPPGEVIQPLPIQASRTRRNIDASQLLDDGNGENYVDYADGMEE
                      IFGSLNSLKLEIEQMKRPLGTQQNPARTCKDLQLCHPDFPDGEYWVDPNQGCSRDSFK
                      VYCNFTAGGSTCVFPDKKSEGARITSWPKENPGSWFSEFKRGKLLSYVDAEGNPVGVV
                      QMTFLRLLSASAHQNVTYHCYQSVAWQDAATGSYDKALRFLGSNDEEMSYDNNPYIRA
                      LVDGCATKKGYQKTVLEIDTPKVEQVPIADIMFNDFGEASQKFGFEVGPACFMG"
 BASE COUNT     1546 a   2238 c   2278 g   1076 t
 ORIGIN

Initial Score    =   139  Optimized Score  =   399  Significance =  8.57
Residue Identity =   50%  Matches          =   473  Mismatches   =   347
Gaps             =   108  Conservative Substitutions          =     0

             X          10          20        30        40          50
             GTCGACTG---GAACGAGACGA-CCTGCTCCAGACCATTCAGCAATC-CTGCTC-TGGGCTC
             | | | ||   || || | | | ||||  ||   || |  | |   |  ||  |  |||||
    GGAGAAACGGGCCCAATGGGTGAGCGTGGCCACCCTGGGCC---CCCTGGACCCCCGGTGAACAGGGGCTT
      3250    X 3260      3270      3280         3290      3300      3310

      60          70        80        90          100        110       120
    CCAAGGGC--TGAGATTACAGGTGTAACCGAGATAAGACCCTGG--CTG-AGTCAACGATGCACAAGGCTCG
    ||  ||||  ||     | ||  |  | |||     ||||| ||  ||| || |  |  ||   ||| |
    CC--GGGCCTTGCTGGAAAAGAAGGGA-CGAAGGGTGACCCAGGCCCTGCAGGCCTCCCTGGGAAAGACGGC
         3320      3330       3340      3350      3360      3370      3380

        130       140          150       160       170         180       190
    AATCCTAGGGATGGAGG---GGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCC--TTCTTGCCCTTTGCCA
      ||| |||  |  | ||       ||| | || |||     ||| ||   |||  |    || ||| | |
    CCTCC-AGGATTACGTGGTTTCCCTGGGGA-CCGAGG-----GCTTCCTGGTCCAGTGGGAGCTCTTGGACT
         3390      3400      3410            3420      3430      3440

           200       210       220       230       240       250       260
    GCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCCT
    |  |||||       |||  || |   ||||||     | || | |  |||  |   |||   ||||||
    G-AAAGGCAATGAAGGGCCCCCTGGCCCACCAGGCCCTGCGGGATCTCCAGGGGAGAGAGGTCCAGCTGGAG
    3450      3460      3470      3480      3490      3500      3510

         270       280        290       300       310         320       330
    GGGCCGAGGCTCTGGGAGCTCC-GTGGCTTCTAGGGCTATGGACTCCTTGGG--GGCAGCAGGGTGGAGGA
      || | | |  | |||  ||| | |    || || |   ||||| ||  |||  ||||| || |    ||
    CCGCTGGGCCCATCGGAATTCCAGGGAGACCTGGGCCCCAGGGACCCCCAGGGCCGGCAGGAGAGAAAGGGG
  3520      3530      3540      3550      3560      3570      3580      3590
```

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         340       350       360            370       380       390
  GTCC-GGCTGGCACTGCACCTCCAGGCACCG-----AGAGAAATTCTGGCAGGCCTTCCCGATACAGGGCTT
   ||| |||  | |  || || | |||| | |      ||||   |||  ||||    ||   |   |||||
  CTCCTGGCGAGAAAGGC-CCACAAGGCCCAGCTGGCCGAGACGGTCT-CCAGG--GGCC---TGTGGGGCTC
        3600       3610      3620      3630       3640           3650

  400         410       420       430       440       450       460
  CAGAG-CAAGC-AGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAGACAT
  | | | | |||  ||  ||||  |||  || |   || |  ||||||   ||    || | ||||  ||
  CCGGGTCCAGCTGGCCCTGTG--GGTCCCCCTGGAGAAGACGGAGATAAGGG---AGA-G-ATCGGGGA---
   3660      3670        3680      3690      3700           3710

  470       480        490       500       510        520       530
  TCTGGTAGGGGCTGGAAGGTA-CATGAGGTGACAAAATGTATCTCGGT-GTTGACGTCCTCCAGAAGC----
      |  ||||| | |||| | || | || ||||||    | |  |||  |    | ||| |||   |
  ----GCCGGGGCAGAAAGGAAGCAAG-GGGGACAAAGGAGAACAGGGTCCTCCTGGGCCTACAGGTCCTCAA
     3720      3730       3740      3750      3760      3770      3780

      540       550       560         570          580       590       600
  GTTTGCATCTTAGACCCTGCCACAGTCTTCAGTTG--CTCTATCCAG---CGCTGGGCTAGGAAGAGGCTCC
  |    ||||  | | || | | |  |||  || ||    | | || |   | | |||| | | || | ||
  GGCCCCATCGGACAGCCAGGC-CCCTCTGGAGCTGACGGCGAGCCGGGGCCTCGGGGCCA-GCAGGGCCTTT
    3790      3800       3810      3820      3830      3840       3850

         610       620        630        640       650       660
  ACAAGGCCTTGCAGTGCTTCTCGT-CCTGAAGATTGAC-GGCCACAGTGACTGGGTAATCTTTAAGCAGG--
   |  |||      ||| |    || || || | ||  | || | |  ||   ||  | |      |||||
  TC-GGGCAGAAAGGTGATGAAGGTCCCAGAGGCTTTCCTGGACCCCCTG---GGCCAGTGGGGCTGCAGGGT
     3860      3870      3880      3890      3900         3910      3920

 670       680       690       700       710        720       730
  TGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGAC-TGTGGCTGAAGTAACAGTCAGG
  | | |||   || ||| |  |        ||||   || || | | ||| || | | || |   |   | ||
  TTGCCAG--GAC-CTCCAGGC------GAGAAGGGTGA-GACAGGAGACGTGGGCCAGATGGGCCCCCCGGG
        3930       3940            3950       3960      3970      3980

740       750       760       770       780       790       800
  TGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTTGGGCTCCAGGCTGG---
  |  |||  ||   | ||||| |  | | |||  |||  ||   | ||   |    |  | ||||| |||
  TCCCCCTGGCCCCCGAGGAC-CCTCCGGAGCTCCAGGTGC-TGATGGCCCACAAGGTCCCCCAGG-TGGAAT
    3990      4000       4010      4020       4030      4040       4050

 810       820       830       840       850       860          870
  CGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAGCAGGT-CGTCT--CGTTCCAGTCG
   |  | | |||    |  ||   | ||     |  ||||| |  | |||||||  | ||  | |||| |  |
  AGGAAACCCTG-GTGCAGTGGGAGAGA-AGGGCGAGCCTG-GCGA-AGCAGGTGAGCCTGGCCTTCCGGGAG
     4060       4070       4080      4090        4100      4110      4120

   X
  AC
  |
  AAGGCGGCCCCC
   X   4130

11. US-08-162-407-1' (1-879)
    HUMPA1V      Human pro-alpha-1 (V) collagen mRNA, complete cds.

 LOCUS       HUMPA1V      7138 bp ss-mRNA           PRI       14-JAN-1992
 DEFINITION  Human pro-alpha-1 (V) collagen mRNA, complete cds.
```

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ACCESSION   M76729
KEYWORDS    alpha-1 type V collagen.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE   1  (bases 1 to 7138)
  AUTHORS   Greenspan,D.S., Cheng,W. and Hoffman,G.G.
  TITLE     The pro-alpha-1(V) collagen chain: Complete primary structure,
            distribution of expression, and comparison with the pro-alpha-1(XI)
            collagen chain
  JOURNAL   J. Biol. Chem. 266, 24727-24733 (1991)
  STANDARD  full automatic
COMMENT     NCBI gi: 189519
FEATURES             Location/Qualifiers
     source          1..7138
                     /organism="Homo sapiens"
                     /sequenced_mol="cDNA to mRNA"
     CDS             230..5746
                     /gene="COL5A1"
                     /map="Unassigned"
                     /note="NCBI gi: 189520"
                     /codon_start=1
                     /product="pro-alpha-1 type V collagen"
                     /translation="MDVHTRWKARSALRPGAPLLPPLLLLLLWAPPPSRAAQPADLLK
                     VLDFHNLPDGITKTTGFCATRRSSKGPDVAYRVTKDAHVSAPTKQLYPASAFPEDFSI
                     LTTVKAKKGSQAFLVSIYNEQGIQQIGLELGRSPVFLYEDHTGKPGPEDYPLFRGINL
                     SDGKWHRIALSVHKKNVTLILDCKKKTTKFLDRSDHPMIDINGIIVFGTRILDEEVFE
                     GDIQQLLFVSDHRAAYDYCEHYSPDCDTAVPDTPQSQDPNPDEYYTEGDGEGETYYYE
                     YPYYEDPEDLGKEPTPSKKPVEAAKETTEVPEELTPTPTEAAPMPETSEGAGKEEDVG
                     IGDYDYVPSEDYYTPSPYDDLTYGEGEENPDQPTDPGAGAEIPTSTADTSNSSNPRPP
                     PGEGADDLEGEFTEETIRNLDENYYDPYYDPTSSPSEIGPGMPANQDTIYEGIGGPRG
                     EKGQKGEPAIIEPGMLIEGPPGPEGPAGLPGPPGTMGPTGQVGDPGERGPPGRPGLPG
                     ADGLPGPPGTMLMLPFRFGGGDAGSKGPMVSAQESQAQAILQQARLALRGPAGPMGL
                     TGRPGPVGPPGSGGLKGEPGDVGPQGPRGVQGPPGPAGKPGRRGRAGSDGARGMPGQT
                     GPKGDRGFDGLAGLPGEKGHRGDPGPSGPPGPPGDDGERGDDGEVGPRGLPGEPGPRG
                     LLGPKGPPGPPGPPGVTGMDGQPGPKGNVGPQGEPGPPGQQGNPGAQGLPGPQGAIGP
                     PGEKGPLGKPGLPGMPGADGPPGHPGKEGPPGEKGGQGPPGPQGPIGYPGPRGVKGAD
                     GIRGLKGTKGEKGEDGFPGFKGDMGIKGDRGEIGPPGPRGEDGPEGPKGRGGPNGDPG
                     PLGPPGEKGKLGVPGLPGYPGRQGPKGSIGFPGFPGANGEKGGRGTPGKPGPRGQRGP
                     TGPRGERGPRGITGKPGPKGNSGGDGPAGPPGERGPNGPQGPTGFPGPKGPPGPPGKD
                     GLPGHPGQRGETGFQGKTGPPGPPGVVGPQGPTGETGPMGERGHPGPPGPPGEQGLPG
                     LAGKEGTKGDPGPAGLPGKDGPPGLRGFPGDRGLPGPVGALGLKGNEGPPGPPGPAGS
                     PGERGPAGAAGPIGIPGRPGPQGPPGPAGEKGAPGEKGPQGPAGRDGLQGPVGLPGPA
                     GPVGPPGEDGDKGEIGEPGQKGSKGDKGEQGPPGPTGPQGPIGQPGPSGADGEPGPRG
                     QQGLFGQKGDEGPRGFPGPPGPVGLQGLPGPPGEKGETGDVGQMGPPGPPGPRGPSGA
                     PGADGPQGPPGGIGNPGAVGEKGEPGEAGEPGLPGEGGPPGPKGERGEKGESGPSGAA
                     GPPGPKGPPGDDGPKGSPGPVGFPGDPGPPGEPGPAGQDGPPGDKGDDGEPGQTGSPG
                     PTGEPGPSGPPGKRGPPGPAGPEGRQGEKGAKGEAGLEGPPGKTGPIGPQGAPGKPGP
                     DGLRGIPGPVGEQGLPGSPGPDGPPGPMGPPGLPGLKGDSGPKGEKGHPGLIGLIGPP
                     GEQGEKGDRGLPGPQGSSGPKGEQGITGPSGPIGPPGPPGLPGPPGPKGAKGSSGPTG
                     PKGEAGHPGPPGPPGPPGEVIQPLPIQASRTRRNIDASQLLDDGNGENYVDYADGMEE
                     IFGSLNSLKLEIEQMKRPLGTQQNPARTCKDLQLCHPDFPDGEYWVDPNQGCSRDSFK
                     VYCNFTAGGSTCVFPDKKSEGARITSWPKENPGSWFSEFKRGKLLSYVDAEGNPVGVV
                     QMTFLRLLSASAHQNVTYHCYQSVAWQDAATGSYDKALRFLGSNDEEMSYDNNPYIRA
                     LVDGCATKKGYQKTVLEIDTPKVEQVPIADIMFNDFGEASQKFGFEVGPACFMG"
BASE COUNT     1546 a   2238 c   2278 g   1076 t
ORIGIN

Initial Score    =    139  Optimized Score  =    399  Significance =  8.57
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Residue Identity =     50%  Matches                =    473  Mismatches    =    347
Gaps             =    108  Conservative Substitutions               =      0

              X          10         20        30        40          50
              GTCGACTG---GAACGAGACGA-CCTGCTCCAGACCATTCAGCAATC-CTGCTC-TGGGCTC
              | | | ||   || || | | | ||||  ||   || |  | |   |  ||  |  |||||
    GGAGAAACGGGCCCAATGGGTGAGCGTGGCCACCCTGGGCC---CCCTGGACCCCCCGGTGAACAGGGGCTT
      3250    X 3260      3270      3280         3290      3300      3310

      60          70        80        90         100        110       120
    CCAAGGGC--TGAGATTACAGGTGTAACCGAGATAAGACCCTGG--CTG-AGTCAACGATGCACAAGGCTCG
    ||  ||||  ||     | ||  |  | |||     ||||| ||  ||| || |  |  ||   ||| |
    CC--GGGCCTTGCTGGAAAAGAAGGGA-CGAAGGGTGACCCAGGCCCTGCAGGCCTCCCTGGGAAAGACGGC
         3320      3330       3340      3350      3360      3370      3380

        130       140          150       160       170         180       190
    AATCCTAGGGATGGGAGG---GGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCC--TTCTTGCCCTTTGCCA
      ||| |||  |  | ||       ||| | || |||     ||| ||   |||  |    || ||| | |
    CCTCC-AGGATTACGTGGTTTCCCTGGGGA-CCGAGG-----GCTTCCTGGTCCAGTGGGAGCTCTTGGACT
         3390      3400      3410            3420      3430      3440

           200       210       220       230       240       250       260
    GCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCCT
    |  |||||       |||  || |   ||||||     | || | |  |||  |   |||   ||||||
    G-AAAGGCAATGAAGGGCCCCCTGGCCCACCAGGCCCTGCGGGATCTCCAGGGGAGAGAGGTCCAGCTGGAG
    3450      3460      3470      3480      3490      3500      3510

         270       280        290       300       310         320       330
    GGGCCGAGGCTCTGGGAGCTCC-GTGGCTTCTAGGGCTATGGGACTCCTTGGG--GGCAGCAGGGTGGAGGA
      || | | |  | |||  ||| | |    || || |   ||||| ||  |||  ||||| || |    ||
    CCGCTGGGCCCATCGGAATTCCAGGGAGACCTGGGCCCCAGGGACCCCCAGGGCCGGCAGGAGAGAAAGGGG
  3520      3530      3540      3550      3560      3570      3580      3590

           340       350       360            370       380       390
    GTCC-GGCTGGCACTGCACCTCCAGGCACCG-----AGAGAAATTCTGGCAGGCCTTCCCGATACAGGGCTT
     ||| |||  | |  || || | |||| | |      ||||   |||  ||||    ||   |   |||||
    CTCCTGGCGAGAAAGGC-CCACAAGGCCCAGCTGGCCGAGACGGTCT-CCAGG--GGCC---TGTGGGGCTC
          3600       3610      3620      3630       3640           3650

    400         410       420       430       440       450       460
    CAGAG-CAAGC-AGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAGACAT
    | | | | |||  ||  ||||  |||  || |   || |  ||||||   ||    || | ||||  ||
    CCGGGTCCAGCTGGCCCTGTG--GGTCCCCCTGGAGAAGACGGAGATAAGGG---AGA-G-ATCGGGGA---
     3660      3670        3680      3690      3700           3710

    470       480        490       500       510        520       530
    TCTGGTAGGGGCTGGAAGGTA-CATGAGGTGACAAAATGTATCTCGGT-GTTGACGTCCTCCAGAAGC----
        |  ||||| | |||| | || | || ||||||    | |  |||  |    | ||| |||   |
    ----GCCGGGGCAGAAAGGAAGCAAG-GGGGACAAAGGAGAACAGGGTCCTCCTGGGCCTACAGGTCCTCAA
       3720      3730       3740      3750      3760      3770      3780

        540       550       560          570         580       590       600
    GTTTGCATCTTAGACCCTGCCACAGTCTTCAGTTG--CTCTATCCAG---CGCTGGGCTAGGAAGAGGCTCC
    |    ||||  | | || | | |  |||  || ||    | | || |   | | |||| | | || | ||
    GGCCCCATCGGACAGCCAGGC-CCCTCTGGAGCTGACGGCGAGCCGGGGCCTCGGGGCCA-GCAGGGCCTTT
      3790      3800       3810      3820      3830      3840      3850

           610       620        630        640       650       660
    ACAAGGCCTTGCAGTGCTTCTCGT-CCTGAAGATTGAC-GGCCACAGTGACTGGGTAATCTTTAAGCAGG--
     |  |||      ||| |    || || || | ||  | || | |  ||   ||  | |      |||||
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    TC-GGGCAGAAAGGTGATGAAGGTCCCAGAGGCTTTCCTGGACCCCCTG---GGCCAGTGGGGCTGCAGGGT
       3860      3870      3880      3890      3900         3910      3920

   670       680       690       700       710        720       730
    TGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGAC-TGTGGCTGAAGTAACAGTCAGG
    | | |||   || ||| |  |        ||||   || || | | ||| || | | || |   |   | ||
    TTGCCAG--GAC-CTCCAGGC------GAGAAGGGTGA-GACAGGAGACGTGGGCCAGATGGCCCCCCCGGG
          3930       3940            3950       3960      3970      3980

  740       750       760       770       780       790       800
    TGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTTGGGCTCCAGGCTGG---
    |  |||  ||   | ||||| |  | | |||  |||  ||   | ||   |    |  | ||||| |||
    TCCCCCTGGCCCCCGAGGAC-CCTCCGGAGCTCCAGGTGC-TGATGGCCCACAAGGTCCCCCAGG-TGGAAT
      3990      4000       4010      4020       4030      4040       4050

   810       820       830       840       850       860          870
    CGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAGCAGGT-CGTCT--CGTTCCAGTCG
     |  | | |||    |  ||   | ||     |  ||||| |  | |||||||  | ||  | |||| |  |
    AGGAAACCCTG-GTGCAGTGGGAGAGA-AGGGCGAGCCTG-GCGA-AGCAGGTGAGCCTGGCCTTCCGGGAG
       4060       4070       4080      4090        4100      4110      4120

     X
    AC
    |
    AAGGCGGCCCCC
     X   4130
```

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12. US-08-162-407-1’ (1-879)
    HS4ULIR3     epstein-barr virus simple repeat array (ir3).

 LOCUS       HS4ULIR3     1150 bp ds-DNA             VRL       15-JUN-1990
 DEFINITION  epstein-barr virus simple repeat array (ir3).
 ACCESSION   J02079
 KEYWORDS    repeat region.
 SOURCE      ebv (epstein barr virus) from human.
   ORGANISM  Epstein-Barr virus
             Viridae; ds-DNA enveloped viruses; Herpesviridae;
             Gammaherpesvirinae.
 REFERENCE   1  (bases 1 to 1150)
   AUTHORS   Heller,M., van Santen,V.L. and Keiff,E.
   TITLE     simple repeat sequence in epstein-barr virus dna is transcribed in
             latent and productive infections
   JOURNAL   J. Virol. 44, 311-320 (1982)
   STANDARD  full automatic
 COMMENT     NCBI gi: 330445
 FEATURES             Location/Qualifiers
      source          1..1150
                      /organism="Epstein-Barr virus"
 BASE COUNT      302 a    169 c    633 g     46 t
 ORIGIN

Initial Score    =    134  Optimized Score =    370  Significance =  8.18
Residue Identity =    49%  Matches         =    443  Mismatches   =   355
Gaps             =    102  Conservative Substitutions              =     0

              X       10         20         30         40        50        60
              GTCGACTGGAACGAG-ACGACCTGCTCCA-GACCATTCAGCAATCCTGCTCTGGGCTCCCAA
                 ||  || | ||| | ||   |   || || ||   || |          ||||    |
    GGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCA-GGAGGAGGGGCAGGAGGGGC-AGGAG
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        300  X    310       320       330        340      .350        360

           70        80           90         100        110        120
   GGGCTGAGATTACAGGTGTA-ACCGAG--ATAAGACCCTG-GCTGAGTCA-ACGATGCACAAGGCTC-GAAT
   |||| |      |||| | |    |||    | || |  | |  | | ||   |  |||  |||  | | |
   GGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAG
        370       380       390       400       410       420       430

    130        140        150       160       170       180         190
   CCTAGGGATGGG-AGG-GGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCC--CTTTGCCAGCGA
   |    ||| ||| ||| | ||| | |      || || ||     |         | |      | ||| ||
   CAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAG-GA
      440       450       460       470       480       490       500

          200       210       220       230          240       250
   AGGCC----CCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCA---GCAGCAGCAGGAGCAACAGCTG
    || |     |||| ||  |   |||| | |||   ||| ||||| |   |||| |||||||| |   || |
   GGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
     510       520         530       540       550       560       570

 260        270       280       290       300       310       320       330
   CCTGGGC-CGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTGGAGG
      ||||  ||||  |  |||||   | ||     ||||  |  |||  |    ||||||| |||| | |||
   GAGGGGCAGGAGGGGC-AGGAGC-AGGAGG-----AGGGGCA--GGA-GCAGGAGGGGCAGGAGGG-GCAGG
     580       590         600            610          620       630

          340       350       360       370       380       390        400
   AGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGG-GCTTCAGA
   ||   ||| ||  | | |    |||| | |  ||| |      | |||       |   |||| ||   ||
   AG--GGGCAGGAGCAGGAGGGGCAGG-AGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG
      640       650       660        670       680       690       700

         410         420       430         440        450          460
   GCAAGCAGCTG--TGTGCAGGTGTCCTTCAGGAGGTG--GGAG-ATGTTGGTCTGGACG---AATCGCA-GA
   |  || ||| |   | ||||| |     ||||||| |  |||| | |  || | ||| |   |   ||| ||
   GGCAGGAGCAGGAGGGGCAGGAG-----CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGA
     710       720            730       740       750       760       770

      470       480            490        500       510       520
   CATTCTGGTAGGGGCTGGA-----AGGTACATGAGGTG-ACAAAATGTATCTCGGTGTTGACGTCC---TCC
       | || |||||| |||     |||  || |||| | |  |   | |    ||    || |  |     |
   GGGGCAGG-AGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGC
        780        790       800       810       820       830       840

   530       540        550         560       570       580       590
   AGAAGCGTTTGCATCTTAGAC-CCTGC--CACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAGG
   || ||     |||     | |    ||   |  | |   ||  ||   |  ||| |  |||| ||| || ||
   AGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGA-GCAG-GAGGGGC-AGG-AGGGG
       850       860       870       880       890         900         910

    600       610        620        630       640       650       660
   CTCCACAAGGCCTTGCA-GTGCTTCTCG-TCCTGAAGATTGACGGCCACAGTGACTGGGTAATCTTTAAGCA
   |   |  |||    ||| | |   |  |  |  || ||  | | |   ||| ||  ||| |       ||||
   CAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAG-GA-GGGGCA-----GGAGCA
         920       930       940       950       960         970

    670        680       690       700         710        720          730
   GGTGGT-CAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAG--GAGATGGGACT-GTGGCTGAAGT--AAC
   || |||  || |     || |     ||  | || |  || |  |||  || | | | ||| |  ||  |
   GGAGGTGGAGGCCGGGGTCGAGGAGGCA-GTGGAGGCCGGGGTCGAGGAGGTAGTGGAGGCCGGGGTCGAGG
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   980       990      1000       1010      1020     1030      1040

       740       750       760       770       780       790      800
  AGTCAGGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTTGGGCTCCAGG
  ||  | |||    |||| ||   ||    || |   | || |||  ||   ||| |||| | | |    ||
  AGGTA-GTGGAGGCCGCCGG---GG-TAGAGGACGTGAAAGAGC--CA--GGGGGGGAAGTCGTGAAAGAGC
 1050       1060          1070      1080          1090     1100      1110

     810       820       830       840        X       860
  CTGGCGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAGCAGG
  | || |  ||    ||| |    | || |||     | |||  ||
  CAGG-GGGAG--AGGTCGT---GGACGTGGAGAAAGAGGCCCATG
           1120         1130      1140     1150


13. US-08-162-407-1’ (1-879)
    CHPINVOL      Chimpanzee (P.paniscus) involucrin, complete cds.

 LOCUS       CHPINVOL     1683 bp ds-DNA             PRI       15-MAR-1990
 DEFINITION  Chimpanzee (P.paniscus) involucrin, complete cds.
 ACCESSION   M26514
 KEYWORDS    epidermal protein; involucrin.
 SOURCE      P.paniscus (strain CHP) keratinocyte DNA.
   ORGANISM  Pan paniscus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Pongidae.
 REFERENCE   1  (bases 1 to 1683)
   AUTHORS   Djian,P. and Green,H.
   TITLE     Vectorial expansion of the involucrin gene and the relatedness of
             the hominoids
   JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 8447-8451 (1989)
   STANDARD  full automatic
 COMMENT     Draft entry and computer readable copy of sequence [1] kindly
             submitted by P.Djian, 26-JUL-1989.

             NCBI gi: 176809
 FEATURES             Location/Qualifiers
      source          1..1683
                      /organism="Pan paniscus"
      CDS             1..1683
                      /note="involucrin;  NCBI gi: 176810"
                      /codon_start=1
                      /translation="MSQQHTLPVTLSPALSQELLKTVPPPVNTQQEQMKQPTPLPPPC
                      QKMPVELPVEVPSKQEEKHMTAVKGLPEQECEQQQQEPQEQELQQQHWEQHEEYQKAE
                      NPEQQLKQEKAQRDPQLNKQLEEEKKLLDQQLDQELVKRDEQLGMKKEQLLELPEQQE
                      GHLKHLEQREGQLELPEQQEGQLKHLEQQKGQLELPEQQEGQLELPEQQEGQLKHLEQ
                      QEGQLKHLEHQEGQLEVPEEQVGQLKYLEQQEGQLKHLDQQEKQPELPEQQVGQLKHL
                      EQQEGQPKHLEQQKGQLEHLEEQEGQLKHLEQQEGQLEHLEHQEGQLGLPEQQVQQLK
                      QLEKEEGQPKHLEEEEGQLKHLVQQEGQLEHLVQQEGQLEHLVQQEGQLEQQEGQVEH
                      LEQQVEHLEQLGQLKHLEEQEGQLKHLEQQQGQLGVPEQVGQPKNLEQEEKQLELPEQ
                      QEGQLKHLEKQEAQLELPEQQVGQPKHLEQQEKQLEPPEQQDGQLKHLEQQEGQLKDL
                      EQQKGQLEQPVFAPAPGQVQDIQSALPTKGEVLLPLEHQQQKQEVQWPPKHK"
 BASE COUNT     496 a    419 c    597 g    171 t
 ORIGIN

Initial Score     =    134  Optimized Score  =    407  Significance =  8.18
Residue Identity  =    51%  Matches          =    493  Mismatches   =   341
Gaps              =    120  Conservative Substitutions          =     0

              X       10        20         30          40         50
```

```
            GTCGACTGGAACGAGACGACCTGCTCCA-GACCA--TTCAGCAATCCTGCTCTGGGCTCCCA
            | |  ||||| |     || | ||   | |  ||  |  |||   || |  | |
  CAGCAGAAGGGGCAGCTGGAGCTCCCAGAGCAGCAGGAGGGGCAGCTGGAGC-TCCCAGAGCAGCAGGAGGG
        570 X     580       590       600       610        620       630

 60        70        80                90       100       110       120
  AGGGCTGAGATTACAGGTGTAACCG-------AGAT-AAGACCCTGGCTGAGTCAACGATGCACAAGGCTCG
  |  |||||     || | | | | |       || | |||   ||||   |  | | || |  ||  ||| |
  ACAGCTGAAGCACCTGGAGCAGCAGGAGGGTCAGCTGAAGCATCTGGAGCA--CCAGGAGGGGCA--GCTGG
       640       650       660       670       680         690         700

       130        140       150          160         170         180
  A-ATCCTAG-GGATGGAGGGGAGGGGCACCCCAGG---GTGGAGCTCC--CCCCTCCTTCT--TGC-CCTT
  |  ||| || |||  | |  || |||||| |  | |    |||| |  |        |  ||   || |||
  AGGTCCCAGAGGA--GCA--GGTGGGGCAGCTGAAGTACCTGGAACAGCAGGAGGGGCAGCTGAAGCACCTG
         710           720       730       740       750       760

    190       200         210       220       230       240       250
  TGCCAGCGAAGGCCCCAGGCG--GCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACA
     ||||    |   ||| ||  ||| |||| |||| ||| ||  | |||||| | |||| | |||||| ||
  GATCAGCAGGAGAAGCAGCCGGAGCTCCCAG-AGCAGCAG-GT--GGGGCAGCTGAAGCACCTGGAGCAGCA
 770       780       790        800          810       820       830

    260       270        280           290        300        310       320
  GCTGCCTGGGCCGAGGC-TCTGGGAGCTCC----GTGGCTTCTAGGGC-TATGG-GACTCCTTGGGGGCAGC
  |  |     ||| | || ||| |||||  |    | |||  || | ||   ||| |   |    ||||||||
  GGAGGGGCAGCCTAAGCATCT-GGAGCAGCAGAAGGGGCAACTGGAGCACCTGGAGGAGCAGGAGGGGCAGC
   840       850        860       870       880       890       900

              330       340        350         360       370       380
  AG-----GGTGGAGGAGTCCGGCTGGCA-CTGCACCTCCAG--GCACCGAGAGAAATTCTGGCAGGCCTTCC
   |       ||||| ||   |   |||| ||| | | || |  ||||| || |||   | |   || || ||
  TGAAGCACCTGGAGCAGCAGGAGGGGCAGCTGGAGCACCTGGAGCACC-AG-GAAGGGCAGCTGGGGCTCCC
  910       920       930       940       950         960       970

       390        400       410         420           430       440
  CGA--TACAGG-GCTTCAGAGCAAGCAGCT-GTG-TGCAGG-TGTCCTTC---AGGAGGTGGGAGATGTTGG
   ||    |||| ||  |||   |||||||| | |  | |||  |  |  |   || |  | ||||  |  ||
  AGAGCAGCAGGTGCAGCAGCTGAAGCAGCTAGAGAAGGAGGAGGGGCAGCCAAAGCACCT-GGAGGAGGAGG
  980       990      1000      1010      1020      1030       1040

  450       460       470       480       490        500       510
  TCTGGACGAATCGCAGACATTCTGGTAGGGGCTGGAAGGTACATGAGGTG-ACAAAATGTATCTCGGTGTTG
     ||   | | | || ||  ||||| |  || || |||  ||   || | ||    || | |  |  |
  AGGGG--CAGTTGAAG-CA-CCTGGT-GCAGCAGG-AGGGGCAGCTGGAGCACCTGGTGCAGCAGGAGGGTC
1050        1060        1070        1080      1090      1100      1110

 520       530       540        550       560       570          580
  ACGTCCTCCAGAAGCGTTTGCATC-TTAGACCCTGCCACAGTCTTCAGTTGCTCTA--TCCAGC-GCTGGGC
  |    ||  || | |   |||| |   ||   | ||   || |  |||  |    |  |  |||  ||||
  A---GCTGGAGCATCTGGTGCAGCAGGAGGGGCAGCTGGAG-CAGCAGGAGGGGCAGGTGGAGCACCTGGAG
       1120      1130      1140      1150       1160      1170      1180

   590         600       610           620       630       640       650
  TAGGAAGAG--GCTCCACAAGGCCTT---GCAG-TGCTTCTCGTCCTGAAGATTGACGGCCACAGTGACTGG
   || | | |  || ||   ||   ||   |||| ||   | | |   | ||   || || ||     ||||
  CAGCAGGTGGAGCACCTGGAGCAGTTGGGGCAGCTGAAGCACCTAGAGGAGCAGGAGGGGCA-----ACTGA
      1190      1200      1210      1220      1230      1240

       660       670       680       690       700       710          720
```

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   GTAATCTTTAAGCAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAG--ATGGGA-CTGTG
      ||| |  |||||  |  |||   ||  | |     || |   | || ||| | ||  |  | | |||
   AGCATC-TGGAGCAGCAG--CAG-GGACAGT-TGGGGTCCCAGAGCAGGTGGGGCAGCCAAAGAACCTGGA
1250       1260         1270       1280      1290      1300      1310

         730       740       750            760       770       780
   GCTGAAGTAACAGTCAGGTGTCCCCCGCAG----GCAAG-GACTCAGCAGCAGCAACAGCAGCAACAGGGAG
   || | || |  || ||| ||   | | |||    ||||| |   |||| | |||| | | || | ||||  |
   GCAGGAGGAGAAG-CAGCTGGAGCTCCCAGAGCAGCAAGAGGGCCAGCTGAAGCACCTGGAGAAGCAGGAGG
   1320       1330      1340      1350      1360      1370      1380

  790          800        810       820       830       840       850
   GA-ATTTGG-GCT-CCAG-GCTGGCGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAG
    | |  ||| ||| |||| || |  |  || || | ||   |  | || |      || ||  |  |   ||
   CACAGCTGGAGCTCCCAGAGCAGCAGGTAGGACAGCCAAAGCACCTGGAG------CA-GCAGGAAAGCAG
  1390      1400      1410      1420      1430             1440      1450

     860       870            X
   C-AGGTCGTCTCGTTC--CA-GTCG-AC
   | ||  |  |  |  |  || | || ||
   CTAGAGCCCCCAGAGCAGCAGGACGGACAACTAAAACA
       1460      1470      1480      1490
```

```
14. US-08-162-407-1’ (1-879)
    U02454         Cloning vector pCMVEBNA, complete sequence.

 LOCUS        U02454         5452 bp    DNA   circular  SYN         08-NOV-1993
 DEFINITION   Cloning vector pCMVEBNA, complete sequence.
 ACCESSION    U02454
 KEYWORDS     .
 SOURCE       Cloning vector pCMVEBNA.
   ORGANISM   Cloning vector pCMVEBNA
              Artificial sequences; Cloning vector.
 REFERENCE    1  (bases 1 to 5452)
   AUTHORS    Kitts,P.A.
   TITLE      CLONTECH Vectors On Disc version 1.1
   JOURNAL    Unpublished
   STANDARD   full automatic
 REFERENCE    2  (bases 1 to 5452)
   AUTHORS    Swirski,R.A., Van Den Berg,D., Murphy,A.J., Lambert,C.M.,
              Friedberg,E.C. and Schimke,R.T.
   TITLE      Improvements in the Epstein-Barr-based shuttle vector system for
              direct cloning in human tissue culture cells
   JOURNAL    Methods: A Companion to Methods in Enzymology 4, 133-142 (1992)
   STANDARD   full automatic
 REFERENCE    3  (bases 1 to 5452)
   AUTHORS    Kitts,P.A.
   TITLE      Direct Submission
   JOURNAL    Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
              4030 Fabian Way, Palo Alto, CA 94303, USA
   STANDARD   full automatic
 COMMENT      This vector can be obtained from CLONTECH Laboratories, Inc., 4030
              Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415)
              424-8222 or (800) 662-2566, extension 1. International customers,
              please contact your local distributor.  For technical information,
              call (415) 424- 8222 or (800) 662-2566, extension 3.
              This sequence has been compiled from information in the sequence
              databases, published literature and other sources; this vector has
              not been completely sequenced. If you suspect there is an error in
```

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             this sequence, please contact CLONTECH's Technical Service
             Department at (415) 424-8222 or (800) 662-2566, extension 3 or
             E-mail CLONTECH@BIOTECHNET.COM.

             NCBI gi: 413820
 FEATURES             Location/Qualifiers
      source          1..5452
                      /organism="Cloning vector pCMVEBNA"
 BASE COUNT     1362 a   1246 c   1736 g   1108 t
 ORIGIN

Initial Score    =    134  Optimized Score   =    385  Significance = 8.18
Residue Identity =    48%  Matches           =    461  Mismatches   =  379
Gaps             =    108  Conservative Substitutions               =    0

              X       10         20         30        40        50        60
              GTCGACTGGAACGAG-ACGACCTGCTCCA-GACCATTCAGCAATCCTGCTCTGGGCTCCCAA
                 ||  || | ||| | ||   |   || || ||   || |          ||||    |
    GGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCA-GGAGGAGGGGCAGGAGGGGC-AGGAG
     1090      1100      1110      1120      1130       1140      1150

            70        80           90        100        110       120
    GGCTGAGATTACAGGTGTA-ACCGAG--ATAAGACCCTG-GCTGAGTCA-ACGATGCACAAGGCTC-GAAT
    |||| |      |||| | |    |||    | || |  | |  | | ||   |  |||  |||  | | |
    GGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAG
     1160      1170      1180      1190      1200      1210      1220

     130        140        150       160       170       180         190
    CCTAGGGATGGG-AGG-GGAGGGGCACCCCAGGTGGAGCTCCCCCCTCCTTCTTGCC--CTTTGCCAGCGA
    |    ||| ||| ||| | ||| | |      || || ||     |         | |      | ||| ||
    CAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAG-GA
   1230      1240      1250      1260      1270      1280      1290

           200       210       220       230          240       250
    AGGCC----CCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCA---GCAGCAGCAGGAGCAACAGCTG
     || |     |||| ||  |   |||| | |||   ||| ||||| |   |||| |||||||| |   || |
    GGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
  1300      1310        1320      1330      1340      1350      1360

  260        270       280       290       300       310       320       330
    CCTGGGC-CGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTGGAGG
       ||||  ||||  |  |||||   | ||     ||||  |  |||  |    ||||||| |||| | |||
    GAGGGGCAGGAGGGGC-AGGAGC-AGGAGG-----AGGGGCA--GGA-GCAGGAGGGGCAGGAGGG-GCAGG
  1370      1380       1390            1400         1410      1420

           340       350       360       370       380       390        400
    AGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGG-GCTTCAGA
    ||   ||| ||  | | |    |||| | |  ||| |      | |||       |   |||| ||    ||
    AG--GGGCAGGAGCAGGAGGGGCAGG-AGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG
 1430        1440      1450       1460      1470      1480      1490

          410         420       430         440        450          460
    GCAAGCAGCTG--TGTGCAGGTGTCCTTCAGGAGGTG--GGAG-ATGTTGGTCTGGACG---AATCGCA-GA
    |  || ||| |   | ||||| |     ||||||| |  |||| | |  || | ||| |   |   ||| ||
    GGCAGGAGCAGGAGGGGCAGGAG-----CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGA
  1500      1510      1520           1530      1540      1550      1560

       470       480            490        500       510       520
    CATTCTGGTAGGGGCTGGA-----AGGTACATGAGGTG-ACAAAATGTATCTCGGTGTTGACGTCC---TCC
        | || |||||| |||     |||  || |||| | |  |   | |    ||    || |  |     |
```

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    GGGGCAGG-AGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGC
     1570       1580      1590      1600      1610      1620      1630

    530       540        550         560       570       580       590
    AGAAGCGTTTGCATCTTAGAC-CCTGC--CACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAGG
    || ||     |||     | |    ||   |  | |   ||  ||   |  ||| |  |||| ||| || ||
    AGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGA-GCAG-GAGGGC-AGG-AGGGG
    1640      1650      1660      1670      1680        1690        1700

     600       610        620        630       640       650       660
    CTCCACAAGGCCTTGCA-GTGCTTCTCG-TCCTGAAGATTGACGGCCACAGTGACTGGGTAATCTTTAAGCA
    |   |  |||    ||| | |   |  |  |  || ||  | | |   ||| ||  ||| |       ||||
    CAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAG-GA-GGGGCA-----GGAGCA
      1710      1720      1730      1740      1750        1760

     670        680       690       700         710        720         730
    GGTGGT-CAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAG--GAGATGGGACT-GTGGCTGAAGT--AAC
    || |||  || |     || |     ||  | || |  || |  |||  || | | | ||| |  ||  |
    GGAGGTGGAGGCCGGGGTCGAGGAGGCA-GTGGAGGCCGGGGTCGAGGAGGTAGTGGAGGCCGGGGTCGAGG
 1770      1780      1790       1800      1810      1820      1830      1840

           740       750       760       770       780         790       800
    AGTCA--GGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAA--CAGGGAGGAATTTGGGCTC
    ||  |  || | || |||  |   |||||   | |  ||| |  |  | ||  |  | | ||    |||
    AGGTAGTGGAGGCCGCCGGGGTAGAGGAC-GTGAAAGAGCCAGGGGGGGAAGTCGTGAAAGAGCCAGGGGGA
          1850      1860       1870      1880      1890      1900      1910

                   810           820       830         840       850
    CAGG--------CTGGCGCCA----GCACTGTCATCTCTGCCG-GGGAC-CCCTCATGCCTGTGACAGAGCA
     |||         ||| |  |    || | |   || | |  |   | |  | |||| |  ||  |  | |
    GAGGTCGTGGACGTGGAGAAAAGAGGCCCAGGAGTCCCAGTAGTCAGTCATCATCATCCGGGTCTC-CACCG
         1920      1930      1940      1950      1960      1970       1980

   860       870         X
    GGTCGTCTCGTTCCA-GTCGAC
     |  | | |  |||| || ||
    CGCAGGCCCCCTCCAGGTAGAAGGCCATTTTT
        1990      2000   X  2010


15. US-08-162-407-1' (1-879)
    U02428          Cloning vector pDR2, complete sequence.

 LOCUS       U02428     10737 bp    DNA     circular  SYN       08-NOV-1993
 DEFINITION  Cloning vector pDR2, complete sequence.
 ACCESSION   U02428
 KEYWORDS    .
 SOURCE      Cloning vector pDR2.
   ORGANISM  Cloning vector pDR2
             Artificial sequences; Cloning vector.
 REFERENCE   1  (bases 1 to 10737)
   AUTHORS   Kitts,P.A.
   TITLE     CLONTECH Vectors On Disc version 1.1
   JOURNAL   Unpublished
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 10737)
   AUTHORS   Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
   TITLE     cDNA expression cloning in human cells using the plambdaDR2
             episomal vector system
   JOURNAL   Methods:A Companion to Methods in Enzymology 4, 111-131 (1992)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 10737)
   AUTHORS   Kitts,P.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
             4030 Fabian Way, Palo Alto, CA 94303, USA
   STANDARD  full automatic
 COMMENT     This vector can be obtained from CLONTECH Laboratories, Inc., 4030
             Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415)
             424-8222 or (800) 662-2566, extension 1. International customers,
             please contact your local distributor.  For technical information,
             call (415) 424- 8222 or (800) 662-2566, extension 3. This sequence
             was compiled by Andrew Murphy and revised at CLONTECH; this vector
             has not been completely sequenced. If you suspect there is an error
             in this sequence, please contact CLONTECH's Technical Service
             Department at (415) 424-8222 or (800) 662-2566, extension 3 or
             E-mail CLONTECH@BIOTECHNET.COM.

             NCBI gi: 413794
 FEATURES             Location/Qualifiers
      source          1..10737
                      /organism="Cloning vector pDR2"
 BASE COUNT     2686 a   2596 c   3033 g   2422 t
 ORIGIN

Initial Score    =    134  Optimized Score  =    385  Significance = 8.18
Residue Identity =    48%  Matches          =    461  Mismatches   =  379
Gaps             =    108  Conservative Substitutions              =    0

              X       10         20         30        40        50        60
              GTCGACTGGAACGAG-ACGACCTGCTCCA-GACCATTCAGCAATCCTGCTCTGGGCTCCCAA
                 ||  || | ||| | ||   |   || || ||   || |          ||||    |
    GGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCA-GGAGGAGGGGCAGGAGGGGC-AGGAG
  6620      6630      6640      6650      6660       6670      6680

            70        80           90        100        110       120
    GGGCTGAGATTACAGGTGTA-ACCGAG--ATAAGACCCTG-GCTGAGTCA-ACGATGCACAAGGCTC-GAAT
    |||| |      |||| | |    |||    | || |  | |  | | ||   |  |||  |||  | | |
    GGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAG
  6690      6700      6710      6720      6730      6740      6750      6760

     130        140        150       160       170       180         190
    CCTAGGGATGGG-AGG-GGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCC--CTTTGCCAGCGA
    |    ||| ||| ||| | ||| | |      || || ||     |         | |      | ||| ||
    CAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAG-GA
          6770      6780      6790      6800      6810      6820       6830

           200       210       220       230          240       250
    AGGCC----CCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCA---GCAGCAGCAGGAGCAACAGCTG
     || |     |||| ||  |   |||| | |||   ||| ||||| |   |||| |||||||| |   || |
    GGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
         6840      6850        6860      6870      6880      6890      6900

  260        270       280       290       300       310       320       330
    CCTGGGC-CGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTGGAGG
       ||||  ||||  |  |||||   | ||     ||||  |  |||  |    ||||||| |||| | |||
    GAGGGGCAGGAGGGGC-AGGAGC-AGGAGG-----AGGGGCA--GGA-GCAGGAGGGGCAGGAGGG-GCAGG
         6910       6920             6930         6940      6950       6960

           340       350       360       370       380       390       400
```

```
    AGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGG-GCTTCAGA
    ||   ||| ||  | | |    |||| | |  ||| |      | |||       |   |||| ||   ||
    AG--GGGCAGGAGCAGGAGGGGCAGG-AGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG
          6970      6980        6990      7000      7010      7020      7030

          410         420       430         440        450          460
    GCAAGCAGCTG--TGTGCAGGTGTCCTTCAGGAGGTG--GGAG-ATGTTGGTCTGGACG---AATCGCA-GA
    |  || ||| |   | ||||| |     ||||||| |  |||| | |  || | ||| |   |   ||| ||
    GGCAGGAGCAGGAGGGGCAGGAG-----CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGA
         7040      7050           7060      7070      7080      7090

       470       480            490       500       510       520
    CATTCTGGTAGGGGCTGGA-----AGGTACATGAGGTG-ACAAAATGTATCTCGGTGTTGACGTCC---TCC
        | || |||||| |||     |||  || |||| | |  |   | |    ||    || |  |     |
    GGGGCAGG-AGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGC
  7100       7110      7120      7130      7140      7150      7160

    530       540        550         560       570       580       590
    AGAAGCGTTTGCATCTTAGAC-CCTGC--CACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAGG
    || ||     |||     | |    ||   |  | |   ||  ||   |  ||| |  |||| ||| || ||
    AGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGA-GCAG-GAGGGGC-AGG-AGGGG
 7170      7180      7190      7200      7210       7220        7230

     600       610        620        630       640       650       660
    CTCCACAAGGCCTTGCA-GTGCTTCTCG-TCCTGAAGATTGACGGCCACAGTGACTGGGTAATCTTTAAGCA
    |   |  |||    ||| | |   |  |  || ||  | | |   ||| ||  ||| |       ||||
    CAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAG-GA-GGGGCA-----GGAGCA
   7240      7250      7260      7270      7280       7290            7300

     670        680       690       700         710        720         730
    GGTGGT-CAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAG--GAGATGGGACT-GTGGCTGAAGT--AAC
    || |||  || |     || |     ||  | || |  || |  |||  || | | | ||| |  ||  |
    GGAGGTGGAGGCCGGGGTCGAGGAGGCA-GTGGAGGCCGGGGTCGAGGAGGTAGTGGAGGCCGGGGTCGAGG
        7310      7320      7330       7340      7350      7360      7370

           740       750       760       770       780         790       800
    AGTCA--GGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAA--CAGGGAGGAATTTGGGCTC
    ||  |  || | || |||  |   |||||   | |  ||| |  |  | ||  |  | | ||    |||
    AGGTAGTGGAGGCCGCCGGGGTAGAGGAC-GTGAAAGAGCCAGGGGGGGAAGTCGTGAAAGAGCCAGGGGGA
       7380      7390      7400       7410      7420      7430      7440

                   810           820       830         840       850
    CAGG--------CTGGCGCCA----GCACTGTCATCTCTGCCG-GGGAC-CCCTCATGCCTGTGACAGAGCA
     |||         ||| |  |    || | |   || | |  |   | |  | |||| |  ||  |  | |
    GAGGTCGTGGACGTGGAGAAAAGAGGCCCAGGAGTCCCAGTAGTCAGTCATCATCATCCGGGTCTC-CACCG
      7450      7460      7470      7480      7490      7500      7510

   860       870         X
    GGTCGTCTCGTTCCA-GTCGAC
     |  | | |  |||| || ||
    CGCAGGCCCCCTCCAGGTAGAAGGCCATTTTT
     7520      7530      7540
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq1nsq.res made by  on Wed 5 Apr 95 17:37:49-PDT.
```

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Query sequence being compared:US-08-162-407-1 (1-879)
Number of sequences searched:                  57621
Number of scores above cutoff:                  4354

      Results of the initial comparison of US-08-162-407-1 (1-879) with:
   Data bank : N-GeneSeq 17, all entries

100000-
      -
N     -
U50000-
M     -
B     -
E     -
R     -
      -
O     -  *
F10000-
      - * *
S     -    *
E 5000-     *
Q     -
U     -
E     -         *  *
N     -      **       *
C     -        * ** *
E     -              *
S 1000-                *  *
      -                 *    *
      -                  *
   500-                    *
      -*                    *   *
      -                       *
      -                        * *
      -
      -                           * *
      -                                *
   100-                               *
      -                            * *
      -                                    *
    50-                                 **
      -
      -                                   * *** *
      -
      *
      -                                        *     *
      -                                                 *
    10-                                          ***  *
      -
      -                                             *
     5-                                                    *
      -
      -                                                *
      -                                                       ***
      -
      -
      -                                                  **  *      **
     0--------------------------------------------------------------------
```

```
          |       | |      | |      | |     |      |     | |     | |     ||      ||      |
SCORE 0    |16     | 33     | 49     |  65    |  82 |     98 |    114|     131|     147
STDEV      0       1        2        3        4     5        6      7        8

                                  PARAMETERS

Similarity matrix         Unitary      K-tuple                    4
Mismatch penalty                1      Joining penalty           30
Gap penalty                  1.00      Window size               32
Gap size penalty             0.33
Cutoff score                    2
Randomization group             0

Initial scores to save         45      Alignments to save        15
Optimized scores to save        0      Display context           10

                                  SEARCH STATISTICS

Scores:                    Mean         Median       Standard Deviation
                             18             13         14.85

Times:                      CPU                       Total Elapsed
                        00:03:47.03                   00:03:47.00

Number of residues:               24347505
Number of sequences searched:        57621
Number of scores above cutoff:        4354

Cut-off raised to 11.
Cut-off raised to 18.
Cut-off raised to 26.
Cut-off raised to 32.
Cut-off raised to 37.
Cut-off raised to 42.
Cut-off raised to 46.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                          Init. Opt.
Sequence Name     Description                     Length Score Score   Sig. Frame
---------------------------------------------------------------------------------
                    ****  8 standard deviations above mean ****
   1. Q13718        Phytoene synthase.              1198   147   398   8.69   0
   2. Q13359        Human mevalonate kinase gene.   1971   144   407   8.49   0
                    ****  7 standard deviations above mean ****
   3. N60307        Equine IFN-beta from pAH60.     2467   135   349   7.88   0
   4. Q43662        Acetobacter cdg3 operon.        4131   134   397   7.81   0
   5. Q29265        Human calcium channel 27980/7   2050   132   388   7.68   0
   6. N81083        Encodes human placental RNase   1698   131   407   7.61   0
   7. Q05150        Modified human adipsin gene w    835   129   270   7.47   0
   8. Q03566        Human adipsin/D cDNA hg 31-40    847   129   261   7.47   0
   9. Q05149        Human adipsin gene from the c   1093   128   261   7.41   0
  10. Q30966        Encodes vitamin K dependent c   2452   124   375   7.14   0
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```
11. Q25061       Clone 2918.4.                   1102    123    382    7.07    0
12. N70128       Novel DNA encoding a polypept   1363    123    387    7.07    0
13. Q10613       Rianodin receptor gene.        15672    122    402    7.00    0
                 ****  6 standard deviations above mean ****
14. Q37813       Sequence encoding the alpha 1   5904    120    396    6.87    0
15. Q13798       Zea mays 15 kD seed storage p   1747    119    376    6.80    0
16. Q23996       Mutant thermostable DNA polym   2043    117    344    6.67    0
17. Q23994       Mutant thermostable DNA polym   2274    117    392    6.67    0
18. Q23995       Mutant thermostable DNA polym   2364    117    392    6.67    0
19. Q24223       Modified Taq polymerase codin   2499    117    392    6.67    0
20. Q55406       A.chrysogenum beta-tubulin Ty   3445    116    409    6.60    0
21. Q55405       A.chrysogenum beta-tubulin I1   3445    116    409    6.60    0
22. Q48230       Acremonium chrysogenum beta-t   3445    116    409    6.60    0
23. N81258       Encodes recombinant human pre    881    115    330    6.53    0
24. Q53199       Human cyclin D3.                1963    115    416    6.53    0
25. N81254       cDNA sequence in plasmid pT3B   2444    115    388    6.53    0
26. Q11943       Nucleotide sequence of HIV-1    9192    115    363    6.53    0
27. N82456       Sequence of mouse 1gG gamma 2   1946    114    392    6.46    0
28. Q31875       Cyclin D3 gene.                 1962    114    417    6.46    0
29. N30041       Sequence encoding bovine leuk   1449    113    381    6.40    0
30. Q58988       Human HSA-PDI fusion.           1545    112    388    6.33    0
31. Q29619       HSA-PDI fusion protein.         1545    112    388    6.33    0
32. Q58987       Human PDI.                      2454    112    388    6.33    0
33. Q29618       PDI.                            2454    112    388    6.33    0
34. Q14630       Plasmid pTM3 insert encoding    3131    112    397    6.33    0
35. Q58776       Human glucagon receptor (pLJ6   1809    111    382    6.26    0
36. Q05055       Placenta-specific protein PP1   2400    111    380    6.26    0
37. Q05682       Islets of Langerhans cell clo   5051    111    389    6.26    0
38. Q28399       Human nestin gene.              4854    110    388    6.20    0
39. Q60714       Human brain Expressed Sequenc    397    109    156    6.13    0
40. Q47354       3' end of cDNA clone of myoto    936    109    321    6.13    0
41. Q45987       Prepro-HSA-G-CSF chimera enco   2382    109    388    6.13    0
42. N90366       Synthetic human 5-lipoxygenas   2499    109    383    6.13    0
43. Q06331       Human IL-2R beta chain.         4035    109    385    6.13    0
44. Q05872       Sequence encoding human inter   4035    109    385    6.13    0
45. Q04735       Gene fragment encoding human    1226    108    393    6.06    0
```

```
1. US-08-162-407-1 (1-879)
   Q13718       Phytoene synthase.

 ID   Q13718 standard; DNA; 1198 BP.
 AC   Q13718;
 DT   26-NOV-1991  (first entry)
 DE   Phytoene synthase.
 KW   GGPP; carotenoid; phytoene; zeaxanthin; lycopene; ss.
 OS   Erwinia herbicola EHO-10 (E. vulneris - ATCC 39368).
 FH   Key             Location/Qualifiers
 FT   CDS             16..939
 FT   /*tag=  a
 FT   /label= phytoene_synthase
 PN   WO9113078-A.
 PD   05-SEP-1991.
 PF   04-AUG-1991; U01458.
 PR   02-MAR-1990; WO-487613.
 PR   18-MAY-1990; US-525551.
 PR   03-AUG-1990; US-562674.
 PA   (STAD ) AMOCO CORP.
 PI   Ausich RL, Brinkhaus FL, Mukharji I, Proffitt JH, Yarger JG;
 PI   Yen HC;
```

```
DR   WPI; 91-281410/38.
DR   P-PSDB; R13983.
PT   Biosynthesis of carotenoid(s) in genetically engineered hosts -
PT   using DNA encoding enzymes from Erwinia herbicola
PS   Disclosure; Fig 4(1-3); 313pp; English.
CC   There are a total of six relevant genes in a 7900 bp region that
CC   cause E. coli cells to produce GGPP and the carotenoids phytoene
CC   through zeaxanthin diglucoside, which is the final prod. identified
CC   in the carotenoid pathway contd. in plasmid pARC376 (contg. a ca.
CC   13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol.,
CC   168:607 (1986).  The genes for geranylgeranyl pyrophosphate (GGPP)
CC   synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene
CC   cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase are
CC   represented in Q13716, Q13718, Q13719, Q13722, Q13724 and Q13726
CC   respectively.
CC   Recombinant expression plasmids can be used to produce large amts.
CC   of the enzymes and hence large amts. of the carotenoids which they
CC   synthesise.
SQ   Sequence   1198 BP;    214 A;    371 C;    417 G;    196 T;

Initial Score    =    147  Optimized Score   =    398  Significance =  8.69
Residue Identity =    50%  Matches           =    472  Mismatches   =   367
Gaps             =     93  Conservative Substitutions              =     0

    X        10        20          30           40            50
    GTCGA-CTGGAACGAGACGACCTGCTCTG--TCA-CAGG-CATG-AG----GGGTCCCCGGCAGAGAT
    |  || ||| || ||| | |||  | |||  | | || | || | ||     || |  ||||   ||
GATTGAGGATCTGCAATGAGCCAACCGCCGCTGCTTGACCACGCCACGCAGACCATGGCCAACGGC-TCGA-
    X   10        20        30        40        50        60        70

60        70        80        90        100       110        120
GACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTG-TTGCTGCTGTTGC-TGCTGCTGAGTCCTTGC
 | |||  || | ||     | |||     |||  ||| |    | || || || ||||| ||  ||    |
-AAAGTTTTGCCACCGCTGCGAAGC---TGTTCGACCCGGCCACCCGCCGTAGCGTGCTGATG-CTCTACAC
         80        90          100       110       120        130

130      140       150          160        170       180        190
CTGCGGGGGACACCTGACTGTTACTTCA--GCC-A-CAGTCCCATCTCCTCCAACTTCAAAG-TGAAGTTTA
|||  |  | || ||| |  | || |||  | | | ||| |||| |  || |  |  | | |  |  |   |
CTGGTGCCGCCA-CTG-CGATGACGTCATTGACGACCAGACCCA-CGGCTTCGCCAGCGAGGCCGCGGCGGA
140        150        160       170        180       190       200

    200       210         220       230       240       250       260
-GAG-AGTTGACTGACCACCTG--CTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAG
 ||| ||   ||  | | ||||  |     |   || | | | |||  | |||   |     || ||||| |
GGAGGAGGCCACCCAGCGCCTGGCCCGGCTGCGCACGCTGACCCTGGCGGCGT--TTGAAGGGGCCGAGATG
 210       220       230       240       250         260       270

    270       280       290       300       310       320         330
CACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTG--TGGCAGGGT
||      ||||||  |  |||| |||        ||||||      |  | |     | |  ||||  | |
CAGGATCCGGCCTT-CGCTGCCT-TTCAGGAGGTGGCGCTGACCCACGGTATTACGCCCCGCATGGC--GCT
 280       290         300       310       320       330       340

     340       350        360       370       380         390        400
CTAAGA-TGCAAACGCTTCTGGA-GGACGTCAACACCGAGATACATTTTGTCACC--TCATG-TACCTTCCA
| |  |   | |  ||||   || ||||||   | |  |||  |  | |||||||  | | | |||  | |
CGATCACCTCGACGGCTTTGCGATGGACGT-GGCTC--AGACCCGGTATGTCACCTTTGAGGATACGCTGC-
   350       360       370          380       390       400       410
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           410       420       430       440       450       460       470
    GCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCT
    ||  || | |  | ||  |||   |||   |      ||      |    ||| || |    |     |||
    GCTACTGCTATCACGT-GGCG-GGCGTGGTGGGTCTGATGATGGCCAGGGTGATGGGCGTGCGGGATGAGC-
         420        430        440       450       460       470       480

         480        490          500       510       520       530
    GCTTGCTCTGAAGC-CCTG-TATC--GGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTG-C
    |  ||||     || ||||  |||  |||  ||||| ||||        |  |  || |||  |  | || |
    GGGTGCTGGATCGCGCCTGCGATCTGGGGCTGGCCTTCCAGCTGACGAATATGGCCCGGGATAT-TATTGAC
          490       500       510       520       530       540        550

  540       550       560         570       580       590       600
    CAGCCGGACTCCTCCACCCTGCTGCC--CCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAG-
     |  ||| ||  |   | |||||  |  |||   ||||  |   ||    || |||  |  |  ||| |||
    GATGCGG-CTATTGACCGCTGCTATCTGCCCGCCGAGTGGC--TGC--AGGATGCCGGGCTGGCCCCGGAGA
          560       570       580       590           600       610

   610         620       630        640        650       660       670
    CCTCGGC--CCAGGCAGCTGTTGCTCC-TGCTGCTGCTGCTGC-CTCTCACACTGGTGCTGCTGGCAGCCG-
     ||  ||  |  || ||   | || ||  ||||  || |  ||     |  | || ||| || |  |||||
    ACTATGCCGCGCGGGAG-AATCGCCCCGCGCTGGCGCGGTGGCGGAGGCTTATTGATGCCGCAG--AGCCGT
  620       630        640       650       660       670       680

      680        690       700         710        720       730       740
    CCTGGGGC-CTTCGCTGGCAAAGGGCAAGA--AGGAGGGG-GGAGCTCCACCCTGGGGTGCCCCTCCCCTCC
     ||    | | || | |||   |||| | |  |   | || || ||||| |   || |  | || || | |
    ACTACATCTCCTCCCAGGC--CGGGCTACACGATCTGCGGCGGCGCTCCGCGTGGGCGATCGCCACCGCCCG
   690       700         710       720       730       740       750

         750           760         770       780       790       800
    CATC-CCTA---GGA-TTCGAGCCTT--GTGCATCGTTGACTCAGCCAGGGTCTTATCTCGGTTACACCTGT
    || |  |||   |||  ||| |  ||  |   |  |  |    || ||| | ||    |||    | || |
    CAGCGTCTACCGGGAGATCG-GTATTAAGGTAAAAGCGGCGGGAGGCAGCGCCTGGGATCG---CCGCCAGC
   760       770        780       790       800       810          820

   810       820       830       840       850       860       870         X
    AATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTCGTCTCGTTC-CAGTCGAC
    |  | ||||    | ||    |  ||     || ||   |  | || ||||||  | |||  |  || ||||
    ACAC-CAGCAAAGGTGAAAAAATTGCCATGCTGATGGCGGCACCGGGGCAGGTTAT-TCGGGCGAAGACGAC
     830        840       850       860       870       880        890     X

    GAGGGTGACG
     900


2. US-08-162-407-1 (1-879)
   Q13359       Human mevalonate kinase gene.

 ID   Q13359 standard; cDNA; 1971 BP.
 AC   Q13359;
 DT   12-NOV-1991  (first entry)
 DE   Human mevalonate kinase gene.
 KW   hMK; ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             92..1191
 FT   /*tag=  a
 PN   GB2241500-A.
 PD   04-SEP-1991.
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 PF   01-FEB-1991; 102244.
 PR   06-FEB-1990; US-475577.
 PA   (SQUI ) SQUIBB E R & SONS INC.
 PI   Tanaka RD, Ricci BS, Mosley ST.
 DR   WPI; 91-262010/36.
 DR   P-PSDB; R13720.
 PT   New nucleic acid encoding human mevalonate kinase - and derived
 PT   polypeptide(s) for studying cholesterol biosynthesis, identifying
 PT   cholesterol lowering agents or detecting mevalonate aciduria.
 PS   Claim 1; Fig 1; 44pp; English.
 CC   The DNA sequence was determined using the dideoxychain termination
 CC   method. The sequence or homologous DNA can be labelled for use in
 CC   detecting sequences encoding hMK, specifically for detecting the
 CC   genetic disorder mevalonic aciduria which is characterised by low
 CC   levels of hMK-coding sequences.
 SQ   Sequence   1971 BP;    384 A;    601 C;    597 G;    389 T;

Initial Score    =    144  Optimized Score    =    407  Significance =  8.49
Residue Identity =    52%  Matches            =    501  Mismatches   =   317
Gaps             =    129  Conservative Substitutions                 =     0

              X         10        20          30        40        50
              GTCGACTG--GAACGAGACGACCTGCTC-TGT-CACAGGCATGAGGGGTCCCCGGCAGAGAT
              || | |||  |   || ||   ||||||  || | |||  ||   ||  ||||  | ||  |
    CAGGGCCCTTGT-GGCTGGCGTCAGAAACAGGCTGCTCAAGTTCCCAGAGATCGTGGCCCCCCTCCTGACCT
  820       830        840       850       860       870       880       890

    60        70        80        90             100       110       120
    GACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTG------TTGCTGCTGTTGCTGCTGCTGAGTCC
     | |  | || |  |  |||||||    |   | | |  |      | |  |  |   | ||  | ||| |
    CA-ATAGATGCCATCTCCCTGGAGTGTGAGCGCGTGCTGGGAGAGATGGGGGAAGCCCCAGCCCCGGAG-CA
            900       910       920       930       940       950        960

       130         140       150       160       170        180       190
    TTGCCT-GCG-GGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCT-CCTCCAACTTCAAAGTGAAGTT
     | ||| | |  || | | || | ||  || | | |  |||  ||||||   | |  | ||   |||  |
    GTACCTCGTGCTGGAAGAGCTCATTG--ACATGAAC--CAGCACCATCTGAATGC--CCTCGGCGTG--GGC
           970       980         990        1000      1010        1020

        200       210       220       230       240        250         260
    TAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCA-ATCTTCAGGAC--GAGAA
     |  |  |     ||||| || ||   || | | ||||   | | || | ||| | |     |||  | | |
    CA-CGCCTCTCTGGACCAGCT-CTGCCAGGTGA-CCAGGGCCCGCGGACTTCACAGCAAGCTGACTGGCGCA
       1030      1040       1050       1060      1070      1080      1090

          270       280         290       300          310       320
    -GCACTGCAAGGCCTTGTGG-AGC-CTCTTCCTAGCCCAGCGCTGGA-TAG--AGCAACTGAAGAC--TGTG
     ||  ||   |||  ||||| | | | || |  |  |||| ||||||  ||  || || || || |   |
    GGCGGTG-GTGGC--TGTGGCATCACACTCCTCAAGCCAGGGCTGGAGCAGCCAG-AAGTGGAGGCCACGAA
       1100         1110      1120      1130      1140       1150      1160

     330       340       350           360       370       380       390
    GCAGGGTCTAAGATGCAAACGCTT---CTG-GAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTAC
    |||||  || |   ||    ||||   |||   |||   || || ||     |     ||| |  |||  ||
    GCAGGCCCTGACCAGCTGTGGCTTTGACTGCTTGGAAACCAGCATCGGTGCCCCCGGCGTCTC--CATCCAC
         1170      1180      1190      1200      1210      1220         1230

       400        410       420       430         440       450        460
    CTTCCAGCC-CCTACCAGAATGTCTGCGATTCGTCCAGACCAA--CATCTCCCACCTCCTGA-AGGACACCT
      || |||| ||| || | |   |  |||   ||||||  |||  | |      ||| |||| ||||  ||
  --TC-AGCCACCTCCCTGGACAGC--CGA---GTCCAG--CAAGCCCTGGATGGCCT-CTGAGGAGCCCA
          1240      1250           1260        1270       1280      1290

       470        480       490         500         510        520
  GCACACAGCTG-CTTGCTCTGAAGCCCTGTATCGGGA--AGGC--CTGCCAGAATTTC-TCTCGGTGCCTGG
    |||| || | |   | | || ||||  | || |||  |  |    | | | | |||  ||| ||| ||||
  CGACACTGCAGCCCCACCCAGATGCCC-CTTTCTGGATTATTCTGGGGGCTGCAGTTCGACTCTGTG-CTGG
      1300      1310       1320      1330      1340      1350       1360

 530       540       550       560       570       580        590
  AGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCC-CTAGAAGCCACGGAG
       ||| |   |||   |||||  || ||||||      || || |||  |||| || |  || | |
  ----CCAGCGAGCGCCCAGCTCCT-GACACTGCTG-----GAG-AGGCCC-CAGCCGCTTG--GCGATG--C
          1370      1380       1390            1400       1410

600       610       620       630       640           650          660
  CTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGC-TG--CTG-CCTCT-CA--CACTGGTG-C
  |  ||| || ||| ||     |||| || |  |||   |  || ||  ||| ||||| ||  | |||| | |
  CAGCCA-AG-CTCTGCAGTCCCAGCGGTGGGACCTAGGGAGGCATGGTCTGCCCTCTGCATCCTCTGGAGCC
1420        1430      1440      1450      1460      1470      1480

       670         680       690       700       710           720
  TGCTG-GCA-GCCGCCT-GGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGA---GCT-CCACCCTGGG
   || | ||| |  |||| || |  | | |||  | |   ||     |||| | ||   ||| |  ||||  |
  AGCCGAGCAGGAGGCCTAGGAGGGTCCTCTG--AGACTCCAGACCTGAGGCGAGAAGGGCTGCTTCCCT--G
1490      1500      1510        1520      1530      1540      1550

 730       740         750       760       770           780       790
  GTGCCCCTCCCCTCCCATC--CCTAGGATTCGAGCCTTGTGCATCGT--TGACT--CAGCCAGGGTCTTAT-
    || ||  |  |||||||  | |  |   |  ||||||  |   ||  |  ||  | ||| |||||  ||
  AAGCTCCCACAGTCCCATCTGCTTCAGGCCCCCGCCTTGGCCTGTGTTCTTCCTGGCCGCCTGGGTCCAATG
  1560      1570      1580      1590      1600      1610      1620

      800       810       820       830       840       850       860
  CTCGGTTACACCTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTC---
  ||| | |    |||    ||    ||   ||||    | ||    |  ||   |  || ||  | || |
  CTCAGGT---GCTGGGGCCTGGTTCC--CGGAGAAGTGTGCCTTCTCTCT-CCTTTTCAGGGACCGGCCCCC
1630         1640      1650        1660      1670       1680      1690

           870       X
  -GTCTC---GTTCCAGTCGAC
   |||||   |  |||| |  |
  TGTCTCTCAGGGCCAGGCCTCTCCCTCCTCC
    1700      1710    X 1720


3. US-08-162-407-1 (1-879)
   N60307        Equine IFN-beta from pAH60.

ID   N60307 standard; DNA; 2467 BP.
AC   N60307;
DT   10-JUN-1991  (first entry)
DE   Equine IFN-beta from pAH60.
KW   IFN-beta; equine; interferon; ss.
OS   Equus cabalus.
FH   Key             Location/Qualifiers
FT   CDS             677..1254
FT   /*tag=  a
FT   /product= IFN-beta
FT   sig_peptide     697..759
```

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FT   /*tag=  b
FT   mat_peptide     760..1254
FT   /*tag=  c
FT   polyA_signal    1446..1451
FT   /*tag=  d
FT   polyA_signal    1516..1521
FT   /*tag=  e
FT   polyA_signal    1705..1710
FT   /*tag=  f
FT   misc_RNA        2441..2467
FT   /*tag=  g
FT   /note= "pUC9 start"
PN   EP-186098-A.
PD   02-JUL-1986.
PF   17-DEC-1985; 116083.
PR   18-DEC-1984; DE-446122.
PA   (BOEH ) BOEHRINGER INGELHEIM.
PI   Himmler A, Hauptmann R, Hauel N, Adolf G, Swetley P.
DR   WPI; 86-170649/27.
DR   P-PSDB; P60398.
PT   New equine and canine interferon - and recombinant DNA molecules
PT   coding for them, and transformed cells.
PS   Disclosure; Fig 8; 149pp; German.
CC   Microorganisms transformed with the recombinant sequence produce IFN
CC   which is useful therapeutically in veterinary medicine.
CC   See also N60306-13 and N60938.
SQ   Sequence   2467 BP;    720 A;    563 C;    556 G;    628 T;

Initial Score    =    135  Optimized Score =    349  Significance =  7.88
Residue Identity =    49%  Matches         =    418  Mismatches   =   320
Gaps             =    103  Conservative Substitutions             =     0

             X       10               20        30         40        50
             GTCGACTGGAAC------GAGAC-GACCTGCTCTGTCACAGGCATG-AGGGGTCCCCGGCAG
             || | || || |       | || ||  |    ||  | || || | || ||  |  | |
   GAGAAGAAATGT-GGCTTGAGCCCCATATAAACGGAATTAAAATGGGAGAGACAGGCAGAGGCTCTGGACTC
1670      1680       1690      1700      1710      1720      1730      1740

       60          70        80        90         100       110       120
   AGATGACAGTGCTG--GCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTT-GCTGCTGCTGAGTC
   ||| ||| | ||||  ||  | |||  | | ||      ||| |||   |  | ||| |   ||| ||  ||
   AGAGGACGGGGCTGCTGCTTCTGCCCTGTGTCC----CGCTCTCTGGCCCCACAGTTAGAATCTGATGGCTC
         1750      1760      1770          1780      1790      1800

       130          140        150       160       170       180       190
   CTTGCCTGC---GGGGGACACCTGA-CTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAG
      |  |||   | || | |  | | || || | |  |||     | |||| ||| | |  ||   | || |
   TCAGGGTGCCCAGAGGAATATGTCAGCTCTTGCGTTTGCCTGGAGCTCATC-CCTACTA--TCTGCGAGATG
 1810      1820      1830      1840      1850       1860        1870

         200       210        220         230       240       250       260
   TTTAGAGAGTTGACTGACCACCTGCTTA-AAGAT--TACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAG
    |  |        |   || |   |  | | |||  ||     |  ||||| ||  ||| | | ||   |||
   CTCTGCCTCCCCCCACCCCTCAACCCCACAGGATTGTAAAATATTTCTGTGCCCTGCAAGCCTAAGCGGGAG
  1880      1890      1900      1910      1920      1930      1940

          270         280          290           300           310
   AAGCACTGCAAGGC-CTTGT-GGAGCCTCT---TCCTAGCCC----AGCG----CTGGATAGAGCAACTGAA
   |||   | | |||| ||| | |||  || |   |   || ||    |  |    ||   | |  |||| ||
   AAG---TCCCAGGCACTTCTGGGACACTGTAAGTGGCAGTCCCTTTATGGTACTCTTCTTGGGACAACCGA-
 1950         1960      1970      1980      1990      2000      2010

  320       330          340       350       360          370        380
    GACTGTGGCAGG-GTCTAA--GATGCAAACGCTTCTGGAGGACGTCAA---CACCGAGA-TACATTTTGTCA
      ||||  |||| ||||||  |  || | ||  ||| |    | || |   ||| || |  | |    |  |
    -GCTGT-ACAGGTGTCTAAGGGGAGCCAGCGTCTCT-GTCTCCTTCCAGGGCACAGACACAAGAGGAAGAAA
    2020       2030      2040      2050       2060      2070      2080

         390       400       410       420       430       440       450
    --CCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAA
       ||| |||   |||   ||||| |||    | |||   ||  ||    || |  | |||        |||
    GAACTC-TGT---TTCATACCCCTGCCA-TCGGCCTGGTTTTGCTC----CCTATTTTTCC-----AGAGAA
    2090          2100      2110       2120          2130           2140

       460       470       480       490       500       510       520
    GGACACCTGCACACAGCTGCTTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCT
    | |   |||| | | |||  || | |||  || |||  ||    ||||    || | | || | |   |||
    GCAAGTCTGCTC-CGGCT--TTTC-CTGCTGCTCTGCGTC-TCCAGGC----CACACTCTC-CCCAAAGCCA
      2150       2160         2170      2180           2190       2200

        530       540       550       560       570       580       590
    GG---AGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCAC
     |   | | ||||   |||| |      ||||  || | | ||     ||  ||   |  | | | || ||
    AGGCCAAG-GCAGGTGCAGCAGATTAGGTCCAGTCT-CAGGCCAGTGAGAAACCGGGAAGCATGGGAGACAA
    2210       2220      2230      2240       2250      2260      2270

      600       610       620       630       640       650       660
    GGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACTGGTG--CTG
    |||  | |  | |     |    |||| ||   | |||    |||  | |   ||   | | ||| |   |
    GGAAATTCAGGTGGGATAGAGAGGGCA-CTAACGTTCCCAGGGCT--TAC--ACTGGGAAATTGGAGATTTC
    2280      2290      2300       2310      2320          2330      2340

       670       680       690       700       710       720       730
    CTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGCCCCTC
    || | || | | | ||||    ||  ||| |  ||         |   | |||  ||||| ||  |  | |
    CTAGGAG-CTCTTTGGGCACCGGCCAGCATA--GCTGCTTTTCTGTCTGTGCTGAACCCTTGG--GAACGTG
       2350       2360      2370        2380      2390      2400        2410

    740       750         760       770          780       790       800
    CCCTCCCATCCCTAGGATT-CGA-GCCTTGTGCAT-CGTTGAC--TCAGCCAGGGTCTTATCTCGGTTA
    |  |   || |||    || | | |    | | || ||| |||   |||||| |  |||
    CATTATTATGCCTGTTCTTGCCATGAGCAGGGGATCCGTCGACCTGCAGCCAAG--CTT
          2420      2430      2440      2450      2460        X
```

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4. US-08-162-407-1 (1-879)
   Q43662        Acetobacter cdg3 operon.

 ID   Q43662 standard; DNA; 4131 BP.
 AC   Q43662;
 DT   13-OCT-1993  (first entry)
 DE   Acetobacter cdg3 operon.
 KW   Cyclic diguanylate; diguanylate phosphodiesterase;
 KW   diguanylate cyclase; cellulose production; ss.
 OS   Acetobacter xylinum.
 FH   Key              Location/Qualifiers
 FT   CDS              387..2606
 FT   /*tag=  a
 FT   /label= pdeA3
 FT   /note="a diguanylate phosphodiesterase gene;
```

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FT   the amino acid sequence R38155 cannot be
FT   deduced directly from this open reading
FT   frame due to a number of apparent
FT   (typographical ?) deletions in the printed
FT   sequence"
FT   misc_difference 741..742
FT   /*tag=  b
FT   /codon= seq: GT; aa: Val
FT   /note= "insertion of N between nucleotides 742 and
FT   743 will restore the reading frame"
FT   misc_difference 2522..2523
FT   /*tag=  c
FT   /codon= seq:GG; aa: Trp
FT   /note= "insertion of T between nucleotides 2521 and
FT   2522 will restore the reading frame"
FT   misc_difference 2560..2561
FT   /*tag=  d
FT   /codon= seq:CC; aa:Ala
FT   /note= "insertion of G between nucleotides 2559 and
FT   2560 will restore the reading frame"
FT   CDS              2657..4131
FT   /*tag= .e
FT   /label= dgc3
FT   /note= "a diguanylate cyclase gene;
FT   the ORF is described as continuing to
FT   nucleotide 4143 although the sequence is
FT   only shown up to nucleotide 4231. The amino
FT   acid sequence R38156 cannot be deduced
FT   directly from this open reading frame which
FT   is given as printed in the specification"
FT   misc_difference 3848..3850
FT   /*tag=  f
FT   /codon= seq:GGG; aa:Ala
FT   misc_difference 3962..3963
FT   /*tag=  i
FT   /codon= seq:CC; aa: Thr-Phe
PN   WO9311244-A.
PD   10-JUN-1993.
PF   14-OCT-1992; U08756.
PR   29-NOV-1991; US-800218.
PA   (WEYE ) WEYERHAEUSER CO.
PI   Ben-Bassat A,  Benziman M,  Calhoon RD,  Gelfand DH;
PI   Tal R,  Wong HC;
DR   WPI; 93-197062/24.
DR   P-PSDB; R38155, R38156.
PT   Polynucleotide sequence from Acetobacter cdg operon - encodes
PT   cyclic di:guanosine mono:phosphate degradation enzymes e.g.
PT   3-phosphodiesterase isozyme
PS   Claim 3; Page 70-72; 98pp; English.
CC   A gene bank of Acetobacter 1306-11 was constructed in the broad host
CC   range, mobilisable cosmid pKT230COS5. The average insert size was ca.
CC   30kb. The bank was screened with a 53bp PCR amplified probe whose
CC   sequence was expected to be an exact match for a diguanylate
CC   cyclase encoding gene. Three unique cosmid classes were identified
CC   corresponding to three different cdg operons. The cdg3 operon
CC   comprises at least 2 genes. Manipulating the expression levels of
CC   the different cdg3 genes is contemplated, particularly in cellulose
CC   producing bacteria.
SQ   Sequence   4131 BP;    864 A;    1275 C;    1197 G;    795 T;
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Initial Score     =    134  Optimized Score  =    397  Significance =  7.81
Residue Identity  =    52%  Matches          =    486  Mismatches   =   323
Gaps              =    124  Conservative Substitutions            =     0

              X       10          20        30          40        50
              GTCGACTGGAACGAGACG--ACCTGCTCTGTCA-CAGGC-ATGAGGGGTCCCCGGCAGAGAT
               |   || |||  | | |  |  |||| | ||| ||  | ||||     |  |||| |  ||
    TGGTATAATGATTATCTTGAATAATATGTAATATGCT-TATCATCATCCTATGATATTCCTGCGGCCGCCAT
       210    X  220       230       240        250       260       270

     60        70        80        90       100       110       120
    G-ACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCCTTGCC
    | || ||||   |||| |  ||  | |       | |||||    | | || ||  ||  | |  ||   ||
    GCACTGTGC--CCGCCCGGGTGATGGC------GCGCCCTGCATTTCCGGTCGC--CTTAT-ATACC---CC
      280         290       300             310       320          330

  130       140       150       160       170         180        190
    TGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCC--TCCAACTTCAAAGT-GAAGTTTAGAG
    ||| |  | | |||| | ||  || |  ||   ||||| | | |     ||| |||| ||  |||  ||
    TGCTGCAGCCGCCTGCCGGTGGCTGC--CCCTTGTCCCTTTTGCGAGGTAAC-TCAATGTCAAAGCCTAACC
        340       350         360       370       380        390       400

   200       210       220          230       240          250       260
    AGTTGACTGACCACCTGCTTAAAG-ATT--ACCCAGTCACTGTGG---CCGTCAATCTTCAGGACGAGAAGC
     |    ||||   |||| ||   | | |  | |  | ||  |  |   |||| | | || | ||| ||||
    TGAGCGCTGAAGTCCTGATTTCGGCACTGGAGCAGGCCATAGACGCAACCGTGATTATTGATGACAAGAACG
         410       420       430       440       450       460       470

       270         280       290       300       310       320       330
    ACTGCAAGGCCTT--GTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTC
    |   ||    |||   |   ||    ||  |  || | |  |  | || |||   |||| ||| || ||| |
    AAGTCATCTTCTTCAATCAGGCGGGATCGAA--CCTGTGGGGCCTCGA-CAA-GAAAGA-TGT-GCTGGG-C
       480       490       500         510       520          530

       340       350         360           370          380        390
    TAAGATGCAAACGCTTCTGGAG--GACG--TCAACA--CCGAG--ATAC-ATTTTGTC-ACCTCATGTACCT
     |  | |  |||| | |||| |   |||   || ||  ||| |    ||   |||||| | | ||    |
    AAGAACGTGAACG-TGCTGGTGCCCACGCTGCATCAGGCCGGGCACGACGCCTTTGTCGAGCGCA--GCCGG
  540       550        560       570       580       590       600

     400         410        420        430       440       450
    TCCAG--CCCCTACCAG-AATGTCTGCGATTCG-TCCAGACCAACATCTCCCACCTCCTGAAGG-----ACA
      |||  | | || | | | |||| ||   |||  | ||    |  || |||  |||  || ||     | |
    GGCAGCTCGCATAACCGCATTGTCGGCACCTCGCGCGAGGTGGAGTTCACCC-GCTC-GGATGGGGAATATA
   610       620       630       640      650       660         670

  460       470       480        490       500        510       520
    CCTGCACACAGCTGCTTGCTCT-GAAGCCCTGTATCGGGAAGGCCTGC-CAGAATTTCTCTCGGTGCCTGGA
     ||||    ||||| | ||| |  |||  |   | |  || | |  || ||   |||   | || |  || |
    TCTGCGGCGAGCTG-TCGCTGTCCAAGGTCGTGAAC--GATGACAAGCGCATCTTTTTCATGGGCGTATGAA
   680       690        700       710         720       730       740

  530       540         550       560       570       580       590
    GGTGCAGTGCCAGC--CGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCAC-GGA
    |    | || || |  || |  ||  || |  ||     ||   || |||   ||  | |   ||  | ||
    G----AATGTCACCAACGAAAGCCAGCAGC--GCAAGATCC--TGA-TCCTGCAGAACGACGTGCTGCAGGC
        750       760       770         780          790       800       810

   600        610          620       630       640       650        660
    GCTC-CCAGAGCC---TCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACAC-TGGTGCTG
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     ||| |||| | |     |  ||||| |  ||     ||| ||| ||| || |  |   |  | | ||||
    ACTCGCCAGCGACATGATGATCCAGG-ACGTGGCCGACCTTCTG-TGCCGCCGGGTGGAAAGCTTCGTGC--
           820       830        840       850        860       870

      670        680       690       700       710       720       730
    CTGGCA-GCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGCCCCT
    | |||| |  | | | |  | | ||||  |    || |||      ||| || | | |   |   || ||
    CCGGCACGGTGGCCGTGCTCAT-GCTG--ATTACGCCAGA-----CGGGCAGTTGCGC---GTTCTGTCCAG
   880       890       900          910            920          930

     740       750       760       770        780         790        800
    CCCCTCCCATCCCTAGGATTCGAGCCTTGTGCATCG-TTGACTCAGCCAG--GGTCTTATC-TCGGTTACAC
    |||| | |  ||| ||    ||   |  | || ||| | ||   |||| |   ||||  || || |  || |
    CCCCACACTGCCCAAG----CGCTAC-CGCGCCTCGCTCGA--GAGCCTGTATGTCTCGTCATCCG-AACTC
  940       950           960        970         980       990       1000

       810       820       830       840       850       860       870
    CTGTAATCTCAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGT-CGTCTCGTTC--CA
      | || ||  || | |  || |||| |||| |    | | ||||| |||  ||| | |  |||| ||  ||
    GAG-AAGCT--GCGCGT-CGATCCCA-AGCACGCCACCCGCATGGTGTGGACAGCTACCGCTCGCTCGGCA
        1010         1020       1030     1040      1050      1060       1070

          X
    -GTCGAC
      |||
    TCTCGCTTGGCCTGCAG
        1080


 5. US-08-162-407-1  (1-879)
    Q29265         Human calcium channel 27980/7.

  ID   Q29265 standard; DNA; 2050 BP.
  AC   Q29265;
  DT   03-MAR-1993  (first entry)
  DE   Human calcium channel 27980/7.
  KW   Plasmid pR9112-10.1.1.1; Ca-flux assay; ss.
  OS   Homo sapiens.
  FH   Key             Location/Qualifiers
  FT   misc_difference 1463
  FT   /*tag=  a
  FT   /note= "undefined"
  FT   misc_difference 1940
  FT   /*tag=  b
  FT   /note= "undefined"
  FT   misc_difference 1941
  FT   /*tag=  c
  FT   /note= "undefined"
  FT   misc_difference 1942
  FT   /*tag=  d
  FT   /note= "undefined"
  PN   EP-507170-A.
  PD   07-OCT-1992.
  PF   23-MAR-1992; 104970.
  PR   04-APR-1991; DE-110785.
  PA   (FARB ) BAYER AG.
  PI   Franz J, Rae P, Unterbeck A, Weingaertner B;
  DR   WPI; 92-333446/41.
  DR   P-PSDB; R27645.
  PT   Cloned human neuronal calcium channel sub-types - useful in
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PT   calcium flux assays to screen for neurone-specific calcium
PT   channel ligands
PS   Claim 2; Page 45-49; 101pp; German.
CC   Human neuroblastoma cell line, hippocampus, frontal and temporal
CC   cortex and visual cortex cDNA banks were screened with a probe
CC   containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
CC   pR9112-10.1.1.1 was sequenced and found to encode amino acids 991 to
CC   1650 containing part of the Domain III (s6), the whole fourth
CC   domain and a part of the C-terminal cytoplasmic region of the
CC   protein. This clone differs from pR9112-2.1.1.1 (see Q29267) and
CC   pR9112-4.1.1.1 (see Q29264) by a 57bp insert with splicing
CC   consensus sequences at both ends, thus offering the possibility of
CC   alternative splicing. The sequence can be inserted into a eukaryotic
CC   expression vector for use in transforming suitable host cells. Cell
CC   lines producing human neuronal calcium channel proteins can be used
CC   for screening for Ca channel ligands (agonists or antagonists).
CC   See also Q29259-Q29275.
SQ   Sequence   2050 BP;    464 A;    617 C;    532 G;    433 T;
SQ   4 Others;

Initial Score     =    132  Optimized Score  =    388  Significance =  7.68
Residue Identity  =    50%  Matches          =    473  Mismatches   =   338
Gaps              =    126  Conservative Substitutions             =     0

       X    10        20        30        40        50        60        70
    GTCGACTGGAACGAGACGACCTGCTCTGTCACAGGCATGAGGGGTCCCCGGCAGAGATGACAGTGCTGGCGC
       ||   |||| || | |  |   || | |||   ||    | ||   |||||  ||||  |  ||
       GA---GAAC-AG-CAAGTTTGACTTTGACA---AT----GTTC--TGGCAGCCATGATGGCCCTCTTCA
       X            10        20               30          40        50

          80         90       100       110         120       130       140
    CAGCCTGGAGC-CCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGC--TGAGTCCTTGCCTGCGGGGGACAC
    | | ||  | |  | ||      || |  ||||||| | | ||| |   || |||   |   |||  ||||
    CCGTCTCCACCTTCGAAGGGTGGCCAG-AGCTGCTG-TACCGCTCCATCGACTCC---CACACGGAAGACAA
       60        70        80         90        100          110       120

          150       160       170       180       190       200       210
    CTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTTGACTGACCACC
      | |.  | || || | || ||        ||||| ||||    | |  | || |   |    | | | ||
    GGGCCCCAT-CTACAACTACCGTGTGGAGATCTCCATCTTCTTCATCA--TCTACATCAT--CATCATCGCC
         130        140       150       160         170         180

        220       230       240               250             260       270
    TGCTTAAAGATTACCCAGTCACTGTGGC--CGTCA--ATC----TTCAGGA------CGAGAAGCACTGCAA
    | ||| | ||| | |   |   || |||  |||||   ||    |||||||       ||| || | | |||
    TTCTTCATGATGAACATCTTCGTG-GGCTTCGTCATCGTCACCTTTCAGGAGCAGGGGGAGCAGGAGTACAA
  190       200       210        220       230       240       250       260

              280       290        300        310       320       330
    GGCCT-TG---TGGAGCCTCTTCCTAGC-CCAGCGC-TGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAA
    |  || ||   |||| |     || |||  ||| || |||| | |    || ||| |   |||     |  |
    GAACTGTGAGCTGGA-CAAGAACC-AGCGACAGTGCGTGGA-ATACGCCCTCAAGGC-CCGGCCCCTGCGGA
           270        280        290        300       310        320

    340       350       360       370       380       390       400
    GATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACC
    | | ||     | |   || ||  || ||||   | | | | ||  || |  |  ||  |||| |  || |
    GGTACA-----TCCCCAAGAAC--CAGCACCAGTACAAAGTGTGGTACGTGGTCAAC--TCCACCTACTTCG
   330            340         350       360       370         380       390
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410          420        430       440         450        460       470
  AGAA--TG-TCTGCG-ATTCGTCCAGACCAACATCTCCCACCT--CC-TGAAGGACACCTGCACACAGCTGC
  || |  || | | ||   || ||| |  ||||| |  |  |||  || || || ||  | || || ||||||
  AGTACCTGATGTTCGTCCTCATCCTGCTCAACACCATCTGCCTGGCCATGCAGCACTACGGC-CAGAGCTGC
        400       410       420       430       440       450        460

     480         490         500       510       520       530        540
  TTGCTCTGAA--GCCCTG--TATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAG-TGCCA
   || ||  ||  ||| ||   |||   ||  | |||      ||| || |   | |    ||| || ||  |
  CTGTTCAAAATCGCCATGAACATCCTCAA--CATGC----TCTTCACTGGCCTCTTCACCGTGGAGATG--A
       470       480       490             500       510       520

          550       560       570       580       590       600       610
  GCCGGA--CTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCT
   || ||  ||| |    ||| |    |||||| |   | ||  |  | || | || |||  | |    | |
  TCCTGAAGCTCAT--TGCCTTC-AAACCCAAGCA---CTATTTCTGT-GATG-CATGGA-ATACATTTGAC-
   530         540        550          560        570         580

        620       630       640       650       660            670
  CGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACTGGT----GCTGCTG-GCAGCCGCCT
    |||  |   | ||| | |     || || |  |  |  ||||   |||     | ||||  ||  | |
  --GCCTTGATTGTTGTGGGTAGCATTGTTGAT-ATAGCAATCACCGAGGTAAACCCAGCTGAACATACCCAA
   590       600       610        620       630       640       650

 680       690       700       710          720       730       740
  GGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTC---CACCCTGGGGTGCCCCTCCCCTCCCATC
   |  |   | ||   || |   | |||       | | |||   |||| |     |||  | ||    |||
  TGCTCTCCCTCTATGAACGCAGAGGAAAACTCCCGCATCTCCATCACCTTCTTCCGCCTGTTCCGGGTCATG
  660       670       680       690       700       710       720

    750            760            770       780       790       800
  C--CTAG-GATTC----GAGCCTT-----GTGCATCGTTGACTCAGCCAGGGTCTTATCTCGGTTACACCTG
  |  || | ||  |    ||||| |     | |||||   ||| | ||   || | |   ||   |   | |
  CGTCTGGTGAAGCTGCTGAGCCGTGGGGAGGGCATC-CGGACGCTGCTGTGGACCTTCATCAAGT--CCTTC
730       740       750       760        770       780       790

  810       820          830       840       850        860       870
  TAATCTCAGCCCT-TG-GGAGC-CCAGAGCAGGATTGCTGAATGGTC-TGGAGCAGGTCGTCTCGTTCCAGT
   |  | | ||||| || ||  | || || |  || |||||  |  || |  |   |||  ||  | | |||
  CAGGCCCTGCCCTATGTGGCCCTCCTGATCGTGA-TGCTG-TTCTTCATCTACGCGGTGATCGGGATGCAGG
 800       810       820       830         840       850       860

     X
  CGAC
   |
  TGTTTGGGAAAATT
 870 X     880


6. US-08-162-407-1 (1-879)
   N81083        Encodes human placental RNase inhibitor

ID   N81083 standard; DNA; 1698 BP.
AC   N81083;
DT   30-OCT-1990  (first entry)
DE   Encodes human placental RNase inhibitor
KW   angiogenin inhibitory activity; neovascularisation disorders;
KW   human placental RNase inhibitor (PRI); rheumatoid arthritis;
KW   Kaposi's sarcoma; ss.
OS   synthetic.
```

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FH   Key             Location/Qualifiers
FT   CDS             122..1507
FT   /*tag=  a
FT   /product=human placental RNase inhibitor
PN   EP-291686-A.
PD   23-NOV-1988.
PF   12-APR-1988; 105781.
PR   14-APR-1987; US-038008.
PR   5-APR-1988; US-177942.
PA   (HARD) Harvard College.
PI   Shapiro R, Vallee BL;
DR   WPI; 88-331302/47.
DR   P-PSDB; P80646.
PT   Inhibitors of angiogenin, useful for inhibiting tumour growth -
PT   include human placental RNase inhibitor and active polypeptide
PT   segments
PS   Disclosure; p; English.
CC   cDNA sequence isolated from human placental library using probes
CC   N81071 to N81082. Tryptic digestion of the PRI protein encoded by
CC   this sequence produces peptide fragments possessing angiogenin
CC   inhibitory activity.
CC   Disorders associated with neovascularisation such as rheumatoid
CC   arthritis and Kaposi's sarcoma are treated by admin of these
CC   inhibitory peptides.
SQ   Sequence   1698 BP;   316 A;   535 C;   535 G;   312 T;

Initial Score     =    131  Optimized Score =    407  Significance =  7.61
Residue Identity  =    52%  Matches         =    493  Mismatches   =   328
Gaps              =    126  Conservative Substitutions             =     0

          X        10        20        30           40         50
          GTCGAC-TGGAACGAGACGACCTGCTCTGTCACAGGCATG---AGGGGTCC-CCGGCAGAGA
           | ||| |  |  | || || |||  | | | |  | |||    | | ||| ||  | |
CATCCAGAGCCTGGACATCCAGTGTGAGGAGCTGAGC-GACGCTAG-ATGGGCCGAGCTCCTCCCTCTGCTC
     140  X    150       160        170        180       190       200

 60         70        80        90       100       110       120
TGACAGTGC--TGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCCTTG
   ||||||   |  | ||| |||||   |     |||| | |  ||  | ||    |    | ||  ||
CAGCAGTGCCAAGTGGTCAGGCTGGACGACTGTGGCCTCACGGAAGC-ACGGTGCAAGGACATCAGCTCTGC
     210       220       230       240        250       260       270

130       140          150       160       170          180       190
CCTGCGGGGGACACCTG-ACTG--TTACTTCAGCCACAGTCCCATC-TCCT--CCAACTTCAAAGTGAAGT-
 || || |  |  |||| ||||    |  ||| ||   |   || |   ||   | |  ||   ||| | |
ACTTCGAGTCAACCCTGCACTGGCAGAGCTCAACCTGCGCAGCAACGAGCTGGGCGATGTCGGCGTGCATTG
    280       290       300       310       320       330       340

         200       210       220       230       240        250
----TTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCA-ATCTTCAG---GA
     |  || |    | |||| ||| ||  |||||   ||||   |||  |||  || | || | |   ||
CGTGCTCCAGGGCCTGCAGACCCCCTCCTGCAAGAT---CCAGAAGCTG-AGCCTCCAGAACTGCTGCCTGA
  350       360       370       380          390        400       410

 260        270       280        290       300       310       320
CGAGAAGC-ACTGCAAGGCCTTGTGGAGC-CTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTG
|| |   |  ||||  || | |||  ||| | || |  | ||| || |   |    |||   | || ||
CGGGGGCCGGCTGCGGGGTCCTGTCCAGCACACTACGCA-CCCTGCCC---ACCCTGCA---GGAG-CT---
    420       430       440       450        460             470
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  330       340       350       360       370       380          390
 GCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCA---CCTCATGTACC
 |||    || ||   ||| | ||  ||| ||| |    |    || | |  | ||  |    ||| || |||
 GCA---CCTCAGCGACAACCTCT--TGGGGGATGCGGGCCTGCAGCTGC--TCTGCGAAGGACTCCTGGACC
       480       490         500       510         520       530

   400       410       420       430       440         450       460
 TTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTC--CCACCTCCTGAAGGACACCTGCA
   ||||  ||  |  |||   ||||   | |   |   || | ||||  |  ||  |||  |  | ||||
 -CCCAGTGCCGCCTGGAAAAGCTGCAGCTGGAGTATTGCAGCCTCTCGGCTGCCAGCTG-CGAGCCCCTG-G
540       550       560       570       580       590        600

   470       480       490       500       510       520         530
 CACAGCTGCTTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGT--GCCTGGAGG--TG
 |    || | ||||| |  |||    | | |||    || | || |   ||| ||||  ||    | |
 C----CTCCGTGCTCAG-GGCC---AAGCCGGA----CTTCAAGGA--GCTCACGGTTAGCAACAACGACAT
    610       620           630           640         650       660

     540       550        560         570       580         590       600
 CAGTGCCAGCCGGACTCC-TCCACCCTGC--TGCCCCCAAGGAGTCCCATAGCC--CTAGAAGCCACGGAGC
 || ||   || ||  ||| |   |  |||   | ||  ||||| ||||   |||  || || ||     |||
 CAATG-AGGCTGGCGTCCGTGTGCTGTGCCAGGGCCTGAAGGACTCCCCCTGCCAGCTGGAGGCGCTCAAGC
  670        680       690       700       710       720       730

        610             620        630       640         650       660
 TCCCAGAGCCTCGG------CCCAGGCAGCTG-TTGCTCCTGCTGCTGC--TGCTGCCTCTCACACTGGTGC
 |   |||||  |||        ||| || |||   |  |||| ||| ||  ||  ||||| ||       ||
 T-GGAGAGCTGCGGTGTGACATCAGACAACTGCCGGGACCTG-TGCGGCATTGTGGCCTC-CAAGGCCTCGC
  740       750       760       770        780       790        800

     670        680       690       700        710       720       730
 TGCTGGCAGC-CGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGG-AGGGGGGAGCTCCACCCTGGGGTGCC
 ||| || |||  |||  ||||     |  ||   ||  | |  || | || ||||||   ||| ||| |||
 TGC-GGGAGCTGGCCCTGGGCAGCAACAAGC-TGGGTGATGTGGGCATGGCGGAGCTGTGCCCAGGGCTGCT
   810       820       830        840       850       860       870

     740       750       760       770              780         790
 CCTCCCCTCCCATCCCTAGGATTCGAGCCTTGTGCATC-----GT-TGAC-TCA--GCCAGGGTCTTATCTC
 || ||||  |  |||  ||| |  |  || |||| |||     || || | |||  |||| || ||   |
 CCACCCCAGC--TCC--AGGCTCAGGACCCTGTGGATCTGGGAGTGTGGCATCACTGCCAAGGGCT--GCGG
  880           890       900       910       920       930         940

   800       810        820          830          840         850
 GG-TTACACCTGTAATCTCA-GCCCTTGG-GAGCC--CAG-AG--CAGGATTGCTG--AATGGTCTGGAGCA
 || |     | ||   |||| | ||  || |||||   || ||  |||  | || |  || |  |||| | |
 GGATCTGTGCCGTGTCCTCAGGGCCAAGGAGAGCCTGAAGGAGCTCAGCCTGGCCGGCAACGAGCTGGGGGA
      950       960       970       980       990      1000      1010

860       870        X
 GGTCGTCTCGTTCCAGTCGAC
  |  |    || || | |  |
 TGAGG----GTGCCCGACTGCTGTGTGAGAC
       1020      1030      1040


7. US-08-162-407-1 (1-879)
   Q05150        Modified human adipsin gene with leader sequence.

 ID   Q05150 standard; DNA; 835 BP.
 AC   Q05150;
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DT   05-NOV-1990  (first entry)
DE   Modified human adipsin gene with leader sequence.
KW   Adipsin; complement D; obesity; lupus erythrymatosis;
KW   rheumatoid arthritis; ds.
FH   Key             Location/Qualifiers
FT   CDS             11..769
FT   /*tag=  a
FT   misc_RNA        1..84
FT   /*tag=  b
FT   /label=leader sequence
PN   WO9006365-A.
PD   14-JUN-1990.
PF   21-NOV-1989; 005374.
PR   30-NOV-1988; US-277963.
PA   (BETH-) Beth Israel Hospita.
PA   (DANA-) Dana-Farber Cancer Inst.
PA   (META-) Metabolic Biosystems Inc.
PI   Flier JS, Spiegelman BM, Rosen BM, White RT;
DR   WPI; 90-209777/27.
DR   P-PSDB; R05773.
PT   Human protein having adipsin and complement D activity -
PT   used in diagnosis and control of metabolically caused obesity
PT   and for treating infection.
PS   Claim 2; Fig 3; 43pp; English.
CC   Abs raised to the gene product may be used in diagnosis of
CC   metabolically caused obesity. The protein may also be used to
CC   treat and prevent obesity and bacterial, viral, parasitic and
CC   neoplastic cell infection.
SQ   Sequence   835 BP;   128 A;   295 C;   294 G;   118 T;

Initial Score    =    129  Optimized Score   =    270  Significance =  7.47
Residue Identity =    50%  Matches           =    322  Mismatches   =   247
Gaps             =     73  Conservative Substitutions           =     0

 270       280       290       300       310       320       330       340
   AAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATG
             ||| || |  | | || |||| | |  ||   |    | ||  | |||      ||| || |
             GGATCC-CACCAT-GCACAGCTCCGTGTACTTC----GCAG-TTCTGG-TCCTCCTAGGA-G
             X        10         20        30             40         50

         350       360       370         380       390       400
   CAAACGCTTCTGGAGGACGTCAACACCGAGAT-ACAT-TTTGTCACCTCATGTACCTTCCAGC-CCCT--AC
   |   |||  |||     || |  | ||| | |   ||  | | |  |  |    ||     || | ||   |
   CGGCCGC--CTGCGCCGCG-CGGCCCCGTGGTCGGATCCTGGGCGGCAGAGAGGCCGAGGCGCACGCTCGGC
        60          70         80        90       100       110       120

  410        420       430       440        450       460         470
   CAGA-ATGTCTGCGATTCGTCCAGACCAACATCTCCCACCT-CCTGAAGGACACCTG--CACACAGC--TGC
   |  | |||   ||| |  || |||   |||  | | |||||    | |||   ||||    |  |||  ||
   CTTACATG---GCG-TCGGTGCAGCTGAACGGCGCGCACCTGTGCGCAGGCGTCCTGGTGGCGGAGCGGTGG
        130           140       150       160       170       180       190

          480       490          500       510       520        530
   TTGCT----CTGAAGCCCTGTATCG-GGA--AGGCCTGCCAGAATTTCTCTCGGT-GCCTGGAGGTGCA---
    ||||      |  || |||  | | |||   ||||  |  |||  |  |  | |  |||||  | |||
   GTGCTGAGCGCGGCGCACTGCCTGGAGGACGCGGCCGACGGGAAGGT-GCAGGTTCTCCTGGGCGCGCACTC
          200       210       220       230        240       250       260

        540       550       560       570          580        590       600
   ---GTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCC---CATAGCCCTA-GAAGCCACGGAGC
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      ||  ||||||||  ||||||  |  |||   | | |   |||   ||  |||| |    | ||   |||
   CCTGTCGCAGCCGGAGCCCTCCAAGCGCCTG-TACGACGTGCTCCGCGCAGTGCCCCACCCGGACAGCCAGC
         270       280       290        300       310       320       330

          610       620       630       640       650        660       670
   TCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACT-GGTGCTGCTGGCA
    || | | | ||| ||  |  | ||  |||| || | ||||  |  |     |||||| ||  ||||||
   -CCGACACCATCGACCACG--ACCTCCTGCTGCTACAGCTGTCGGAGAAGGCCACACTGGGCCCTGCTGTGC
         340       350         360       370       380       390       400

         680       690          700       710       720         730
   GCCGCCTGGGGCCTTCGCTG-GC--AAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGG--GTGCCCCTCC
   ||| |||   ||| | || | ||    |  || |   ||    |||| ||   | ||| |  ||| ||  |
   GCCCCCT---GCCCTGGCAGCGCGTGGACCGCGACGTGGCACCGGGAACT---CTCTGCGACGTGGCCGGCT
            410       420       430       440          450       460

  740       750       760       770        780        790       800
   CCTCCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACT-CAGC-CAGGGTCTTATCTCGGTTACACC-TG
       |     | |  |  || |||     |      | || |||| |  | |||| |   | |  |||  |
   GGGGCATAGTCAACCACGCGGGCCGCCGCCCGGACAGCCTGCAGCACGTGCTCTTGCCAGTGCTGGACCGCG
   470       480       490       500       510       520       530

   810        820       830       840       850       860          870
   TAATCT-CAGCCCTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTCGT-CTCG--TTCCAGT
     | || || ||    || || |  | || ||  ||   ||   |  | ||  |  || | ||     || |
   CCACCTGCAACC----GGCGCACGCACCACGACGGCGCCATCACCGAGCGCTTGATGTGCGCGGAGAGCAAT
 540       550           560       570       580       590       600

      X
   CGAC
   || |
   CGCCGGGACAGCTG
   610       620


8. US-08-162-407-1 (1-879)
   Q03566       Human adipsin/D cDNA hg 31-40.

ID   Q03566 standard; cDNA; 847 BP.
AC   Q03566;
DT   30-JUL-1990  (first entry)
DE   Human adipsin/D cDNA hg 31-40.
KW   CAT; hybrid protein; Human adipsin/D;ss.
OS   Homo sapiens.
PN   WO9001540-A.
PD   22-FEB-1990.
PF   09-AUG-1989; U03417.
PR   11-AUG-1988; US-231224.
PA   (CALB-) Calif Biotechn Inc.
PI   Hilliker S, White R;
DR   WPI; 90-083499/11.
DR   P-PSDB; R05421.
PT   Heterologous protein expression on prokaryotic host -
PT   using 3' truncated chloramphenicol acetyl transferase gene to
PT   stably express hybrid protein.
PS   Example; Fig 10; 67pp; English.
CC   When inserted into an expression vector, pTrpCAT 72,
CC   the construct gave 10-15% levels of fusion protein upon
CC   induction in W3110 cells.
CC   See also Q03557 to Q05366; and Q04767.
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SQ   Sequence   847 BP;   132 A;   291 C;   299 G;   125 T;

Initial Score     =    129  Optimized Score  =    261  Significance =  7.47
Residue Identity =    49%  Matches          =    311  Mismatches   =   245
Gaps             =     74  Conservative Substitutions             =     0

        280     X 290       300       310       320       330       340
      TTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAACG
                  |||   |  | | || |    |  |  |  | ||  | |||   | ||  |  ||   ||
                AATTC---GGGCGGGGCAGTTCTGGTCCTCCTAGGA--GCGGC--CGCCTGCGCCGC--GCG
                X          10        20        30            40        50

      350       360       370       380       390       400       410
      CTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTG
         |  | || ||  | | | | |   ||    | | |     | ||  ||  | || |||    |||   |
      -GCCCCGTGGTCG-GATC-CTGGGCGGCAGAGAGGC-CGAGGCGCACGCTC--GGCCTTAC----ATG---G
            60          70        80         90       100             110

    420       430       440        450       460         470             480
      CGATTCGTCCAGACCAACATCTCCCACCT-CCTGAAGGACACCTG--CACACAGC--TGCTTGCT----CTG
      || |  || |||   |||  | | |||||    | |||   ||||    |  |||  ||  ||||      |
      CG-TCGGTGCAGCTGAACGGCGCGCACCTGTGCGCAGGCGTCCTGGTGGCGGAGCGGTGGGTGCTGAGCGCG
            120       130       140       150       160       170       180

           490          500       510       520        530             540
      AAGCCCTGTATCG-GGA--AGGCCTGCCAGAATTTCTCTCGGT-GCCTGGAGGTGCA------GTGCCAGCC
        || |||  | | |||   ||||  |  |||  |  |  | |  |||||  | |||      ||  |||||
      GCGCACTGCCTGGAGGACGCGGCCGACGGGAAGGT-GCAGGTTCTCCTGGGCGCGCACTCCCTGTCGCAGCC
          190       200       210        220       230       240       250

         550       560       570          580        590       600       610
      GGACTCCTCCACCCTGCTGCCCCCAAGGAGTCC---CATAGCCCTA-GAAGCCACGGAGCTCCCAGAGCCTC
      |||  ||||||  |  |||   | | |   |||   ||  |||| |    | ||   ||| || | | | ||
      GGAGCCCTCCAAGCGCCTG-TACGACGTGCTCCGCGCAGTGCCCCACCCGGACAGCCAGC-CCGACACCATC
         260       270        280       290       300       310        320

           620       630       640       650        660       670       680
      GGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACT-GGTGCTGCTGGCAGCCGCCTGGGGC
      | ||  |  | ||  |||| || | ||||  |  |     |||||| ||  ||||||   ||| |||   ||
      GACCACG--ACCTCCTGCTGCTACAGCTGTCGGAGAAGGCCACACTGGGCCCTGCTGTGCGCCCCCT---GC
         330         340       350       360       370       380          390

          690          700       710       720         730       740       750
      CTTCGCTG-GC--AAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGG--GTGCCCCTCCCCTCCCATCCCT
      | | || | ||    |  || |   ||    |||| ||   | ||| |  ||| ||  |     |     |
      CCTGGCAGCGCGTGGACCGCGACGTGGCACCGGGAACT---CTCTGCGACGTGGCCGGCTGGGGCATAGTCA
            400       410       420          430       440       450       460

             760       770        780        790       800        810
      AGGATTCGAGCCTTGTGCATCGTTGACT-CAGC-CAGGGTCTTATCTCGGTTACACC-TGTAATCT-CAGCC
      |  |  || |||     |      | || |||| |  | ||||  |   | |  |||  |  | || || ||
      ACCACGCGGGCCGCCGCCCGGACAGCCTGCAGCACGTGCTCTTGCCAGTGCTGGACCGCGCCACCTGCAACC
             470       480       490       500       510       520       530

     820       830       840       850       860          870        X
      CTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTCGT-CTCG--TTCCAGTCGAC
          || || |  | || ||  ||   ||   |  | ||  |  || | ||     || ||| |
      ----GGCGCACGCACCACGACGGCGCCATCACCGAGCGCTTGATGTGCGCGGAGAGCAATCGCCGGGACAGC
               540       550       560       570       580       590 X     600
```

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      TG


9. US-08-162-407-1 (1-879)
   Q05149       Human adipsin gene from the clone phg31.

  ID   Q05149 standard; DNA; 1093 BP.
  AC   Q05149;
  DT   05-NOV-1990  (first entry)
  DE   Human adipsin gene from the clone phg31.
  KW   Adipsin; complement D; obesity; lupus erythrymatosis;
  KW   rheumatoid arthritis; ds.
  FH   Key             Location/Qualifiers
  FT   CDS             1..750
  FT   /*tag=  a
  PN   WO9006365-A.
  PD   14-JUN-1990.
  PF   21-NOV-1989; 005374.
  PR   30-NOV-1988; US-277963.
  PA   (BETH-) Beth Israel Hospita.
  PA   (DANA-) Dana-Farber Cancer Inst.
  PA   (META-) Metabolic Biosystems Inc.
  PI   Flier JS, Spiegelman BM, Rosen BM, White RT;
  DR   WPI; 90-209777/27.
  DR   P-PSDB; R05772.
  PT   Human protein having adipsin and complement D activity -
  PT   used in diagnosis and control of metabolically caused obesity
  PT   and for treating infection.
  PS   Disclosure; .
  CC   Abs raised to the gene product may be used in diagnosis of
  CC   metabolically caused obesity. The protein may also be used to
  CC   treat and prevent obesity and bacterial, viral, parasitic and
  CC   neoplastic cell infection.
  SQ   Sequence   1093 BP;   190 A;   343 C;   383 G;   177 T;

Initial Score     =    128  Optimized Score  =    261  Significance =  7.41
Residue Identity =    49%  Matches          =    312  Mismatches   =   244
Gaps             =     74  Conservative Substitutions             =     0

        280     X 290       300       310       320       330       340
      TTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAACG
                  |||   |  | | || |    |  |  |  | ||  | |||   | ||  |  ||   ||
                AATTC---GGGCGGGGCAGTTCTGGTCCTCCTAGGA--GCGGC--CGCCTGCGCGGC-GCCG
                X          10        20        30            40        50

      350       360       370       380       390       400       410
      CTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTG
      |  |  | || ||  | | | | |   ||    | | |     | ||   |  | ||||||    |||   |
      C--CCCGTGGTCG-GATC-CTGGGCGGCAGAGAGGC-CGAGGCGCAC--GCGCGGCCCTAC----ATG---G
            60          70        80         90         100           110

    420       430       440        450       460         470             480
      CGATTCGTCCAGACCAACATCTCCCACCT-CCTGAAGGACACCTG--CACACAGC--TGCTTGCT----CTG
      || |  || |||   |||  | | |||||    | |||   ||||    |  |||  ||  ||||      |
      CG-TCGGTGCAGCTGAACGGCGCGCACCTGTGCGCAGGCGTCCTGGTGGCGGAGCAGTGGGTGCTGAGCGCG
            120       130       140       150       160       170       180

           490          500       510       520        530             540
      AAGCCCTGTATCG-GGA--AGGCCTGCCAGAATTTCTCTCGGT-GCCTGGAGGTGCA------GTGCCAGCC
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       || |||  | | |||   ||||  |  |||  |  |  | |  |||||  | |||      ||  |||||
     GCGCACTGCCTGGAGGACGCGGCCGACGGGAAGGT-GCAGGTTCTCCTGGGCGCGCACTCCCTGTCGCAGCC
         190       200       210        220       230       240       250

        550       560       570          580        590       600       610
     GGACTCCTCCACCCTGCTGCCCCCAAGGAGTCC---CATAGCCCTA-GAAGCCACGGAGCTCCCAGAGCCTC
     |||  ||||||  |  |||   | | |   |||   ||  |||| |    | ||   ||| || | | | ||
     GGAGCCCTCCAAGCGCCTG-TACGACGTGCTCCGCGCAGTGCCCCACCCGGACAGCCAGC-CCGACACCATC
        260       270        280       290       300       310        320

          620       630       640       650        660       670       680
     GGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACT-GGTGCTGCTGGCAGCCGCCTGGGGC
     | ||  |  | ||  |||| || | ||||  |  |     |||||| ||  ||||||   ||| |||   ||
     GACCACG--ACCTCCTGCTGCTACAGCTGTCGGAGAAGGCCACACTGGGCCCTGCTGTGCGCCCCCT---GC
        330         340       350       360       370       380          390

         690          700       710       720        730       740        750
     CTTCGCTG-GC--AAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTG-GGGTGCCCCTCCCCTCCCAT-CCCT
     | | || | ||    |  || |   ||    |||| ||   | ||| |  |   ||  |     |||   |
     CCTGGCAGCGCGTGGACCGCGACGTGGCACCGGGAACT---CTCTGCGACTTGGCCGGCTGGGGCATAGTCA
           400       410       420          430       440       450       460

            760       770        780        790       800        810
     AGGATTCGAGCCTTGTGCATCGTTGACT-CAGC-CAGGGTCTTATCTCGGTTACACC-TGTAATCT-CAGCC
     |  |  || |||     |      | || |||| |  | ||||  |   | |  |||  |  | || || ||
     ACCACGCGGGCCGCCGCCCGGACAGCCTGCAGCACGTGCTCTTGCCAGTGCTGGACCGCGCCACCTGCAACC
            470       480       490       500       510       520       530

    820       830       840       850       860          870        X
     CTTGGGAGCCCAGAGCAGGATTGCTGAATGGTCTGGAGCAGGTCGT-CTCG--TTCCAGTCGAC
         || || |  | || ||  ||   ||   |  | ||  |  || | ||     || ||| |
     ----GGCGCACGCACCACGACGGCGCCATCACCGAGCGCTTGATGTGCGCGGAGAGCAATCGCCGGGACAGC
              540       550       560       570       580       590 X     600

     TG


 10. US-08-162-407-1 (1-879)
     Q30966       Encodes vitamin K dependent carboxylase.

  ID   Q30966 standard; DNA; 2452 BP.
  AC   Q30966;
  DT   25-MAR-1993  (first entry)
  DE   Encodes vitamin K dependent carboxylase.
  KW   vitamin K dependent carboxylase; factor VII; factor IX; factor X;
  KW   protein C; protein S; prothrombin; VKD carboxylase; diagnosis; liver;
  KW   cancer; carcinoma; tumour; increased undercarboxylated prothrombin;
  KW   ss.
  OS   Synthetic.
  FH   Key             Location/Qualifiers
  FT   CDS             87..2360
  FT   /*tag=  a
  PN   WO9219636-A.
  PD   12-NOV-1992.
  PF   08-MAY-1992; U03853.
  PR   08-MAY-1991; US-697427.
  PR   09-SEP-1991; US-756250.
  PA   (UYNC-) UNIV NORTH CAROLINA.
  PI   Stafford DE;
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DR   WPI; 92-398792/48.
DR   P-PSDB; R28954.
PT   DNA coding for vitamin=K-dependent carboxylase - for prodn. of
PT   transformed cells producing carboxylated vitamin=K-dependent
PT   proteins, e.g. clotting factors
PS   Claim 1; Page 36; 55pp; English.
CC   This sequence encodes a vitamin K-dependent carboxylase. The 1.6kb
CC   insert from lambdaZAP-CARB1.6 was used to screen a human cDNA
CC   library. No clones however, coded for the entire sequence of the gamma
CC   glutamyl carboxylase. They did allow comparison of liver carboxylase to
CC   the carboxylase of another tissue. A second cDNA library constructed
CC   using HEL cells (human erythroleukaemia) was screened and a clone
CC   isolated. This contained the entire coding sequence  of the human
CC   carboxylase and some upstream and downstream sequences.
SQ   Sequence   2452 BP;    541 A;    654 C;    640 G;    617 T;

Initial Score    =    124  Optimized Score  =    375  Significance =  7.14
Residue Identity =    48%  Matches          =    461  Mismatches   =   363
Gaps             =    135  Conservative Substitutions              =     0

              X          10        20              30        40        50
              GTCGA---CTGGAACGAGACGACCTGCTCT---GT---CACAGGCATGAG-GGGTCCCCGGC
              | | |   |||| ||  || |   ||| ||   ||   |||  ||| | |  | || ||  |
    TGGGCTGTATGGCTATTCCTGGGACATGATG--GTGCACTCCCGTTCCCACCAGCACGTGAAGATCACCTAC
         1270 X    1280      1290        1300      1310      1320      1330

          60        70        80        90        100         110       120
    AGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCT-CCCTGTTGCTGC--TGTTGCTGCTGCTGAG
     | |||| | |  ||||||  | |  ||   ||  |  |||    | ||    |   || |  | ||    |
    CGTGATGGCCGCACTGGCG--AACTGGGCTACCTTAACCCTGGGGTATTTACACAGAGTCGGCGATGGAAGG
         1340      1350        1360      1370      1380      1390      1400

              130       140       150       160            170       180
    TCCTTG----CCTGCGGGGGACACCTGACTGTTACTTCAGCCAC---AGTCCCA--TCTCCTCCAACT---T
      | ||    | ||| |  |  |  || |  || | | |||| |     |||||  | |  |   |||
    ATCATGCAGACATGCTGAAGCAATATGCCACTTGCCTGAGCCGCCTGCTTCCCAAGTATAATGTCACTGAGC
         1410      1420      1430      1440      1450      1460      1470

           190       200       210       220       230       240       250
    CAAAG-TGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTC
    |  || |  | ||| || | |||  |  ||| |   | |  | ||  |||| ||  | |    |  | | ||
    CCCAGATCTACTTT-GATATTTGGGTCTCCATC-AATGACCGCTT--CCAG-CAGAG-GATTTTTGACCCTC
       1480       1490      1500       1510        1520        1530

         260       270        280       290       300       310       320
    AGGACGAGAAGCACTGCAAGGC-CTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACT
      |  || |     |||| | | ||||   | ||| |||   || || | |||| |  | | |||   || |
    GTGTGGACA--TCGTGCAGGCCGCTTGGTCACCCT-TTCAGCGCACATC-CTGGGTGCAACCACTCTTGA-T
 1540        1550      1560      1570       1580       1590      1600

        330        340       350       360        370         380       390
    GTGGCAGGGT-CTAAGATGCAAACGCTTCTGGAGGACGTCAACA-CCGAGATA--CATTTTGTCACCTCATG
    |   | |  | |   || |   | | | | |||   |   | || || ||| |  ||   ||  |  |  |
    GGACCTGTCTCCCTGGAGGGCCAAGTTACAGGAAATCAAGAGCAGCCTAGACAACCACACTG--AGGTGGTC
    1610      1620      1630      1640      1650      1660        1670

          400       410       420       430       440       450       460
    TACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTG
    | | || |||    | || |   | ||||  || |   |||      |     |   ||||    ||||  |
    TTCATTGCAG-ATTTCCCTG---GACTGCACTTGG---AGAATTTTGTGAGTGAAGACCTGGGCAACACTAG
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  1680       1690         1700         1710      1720      1730      1740

      470                   480       490        500       510       520
  CACACAGCTGCT-----------TG-CTCTGAAGCCCTGTATCGGGA-AGGCCTGCCAGAATTTCTCTCG-G
  ||  ||||||||           || || || || | |||  | | | ||     ||||| | | ||  | |
  CATCCAGCTGCTGCAGGGGGAAGTGACTGTGGAG-CTTGTGGCAGAACAGAAGAACCAGACTCT-TCGAGAG
       1750      1760      1770       1780      1790      1800       1810

        530        540       550       560       570       580       590
  TGCCTGGAGGTGCAG-TGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGC
   |     |  ||||| |||| || ||      |||    | ||    | |  | || | ||||||    ||
  GGAGAAAAAATGCAGTTGCCTGCTGGTGAGTACCA-TAAGGTGTATACGA-CA-TCACCTAGCCCTTCTTGC
       1820      1830      1840       1850      1860        1870      1880

       600       610       620       630       640         650       660
  CACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGC--TGCCTCTCACACTGGTG
   ||  |  | |    | ||  | | |  || ||   |  | |||  |||  ||    |||  || |
  TAC--ATGTAC----GTCTATGTCAA--CA-CTACAGAGCTTGC-ACTGGAGCAAGACCTGGCATA-----T
              1890      1900         1910       1920      1930

       670       680       690       700       710       720       730
  CTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGC-C
  ||||  | |      |   |     | |||  || || ||    |  |||    || | | ||| | | |||
  CTGCAAGAA-----TTAAAGGAAAAGGTGGAGAATGG-AAGTGAAACAGGGCCTCTACCCCCAGAGCTGCAG
 1940           1950      1960       1970      1980      1990      2000

      740       750         760           770       780       790
  CCTCCCCTCCCATCCCTAG--GATTCGAGCCTTGTG----CATCGTTGACTCAGCCAGGGTCTTATCTCGGT
  ||||   |   |     ||   |   | ||| || |    || |  ||  |||| |    |||||   ||
  CCTCTGTTGGAAGGGGAAGTAAAAGGGGGCCCTGAGCCAACACCTCTGGTTCAGAC-CTTTCTTA-GACGCC
     2010      2020      2030      2040      2050       2060       2070

800             810       820                830        840            850
  TACA------CCTGTAATCTCAGCCCTTGGGA-----GCC----CA-GAGCAGGATT-----GCTGAATGGT
   |||      || | |   | | | |  | ||      ||    || ||||  ||||     |||   || |
  AACAAAGGCTCCAGGAGATTGAACGCCGGCGAAATACTCCTTTCCATGAGC--GATTCTTCCGCTTCTTGTT
     2080      2090      2100      2110      2120        2130      2140

             860       870        X
  -CTGGAGC---AGGTCGTCTCGTTCCAGTCGAC
   |   |||   | ||| | |||   |||     |
  GCGAAAGCTCTATGTC-TTTCGCCGCAGCTTCCTGATGACTTG
     2150       2160      2170    X 2180


11. US-08-162-407-1 (1-879)
    Q25061        Clone 2918.4.

ID   Q25061 standard; DNA; 1102 BP.
AC   Q25061;
DT   15-NOV-1992  (first entry)
DE   Clone 2918.4.
KW   RFLP; probe p29G8; beta-lymphoblastoid cell line; LG2; HLA-DRbeta;
KW   transplant; transfusion; paternity; Raji cell line; 2918.8; ss.
OS   Synthetic.
PN   US5110920-A.
PD   05-MAY-1992.
PF   05-DEC-1984; 678255.
PR   22-JAN-1982; US-341902.
PR   07-JAN-1983; US-456373.
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PR   05-DEC-1984; US-678255.
PR   30-AUG-1988; US-238619.
PA   (CETU ) CETUS CORP.
PI   Erlich HA;
DR   WPI; 92-175244/21.
PT   New DNA probes specific to single class II HLA locus - useful in
PT   HLA typing e.g. to evaluate paternity and transplant or
PT   transfusion compatibility and to diagnose disease susceptibility
PS   Disclosure; Page 14; 21pp; English.
CC   The sequence given is clone 2918.4 which was derived from a
CC   beta-lymphoblastoid cell line LG2 derived cDNA library using an
CC   18-mer probe based on the published amino acid sequence for the
CC   conserved amino acids 20-25 of the HLA-DRbeta cDNA clone from the Raji
CC   cell line.  This probe was hybridized to the cDNA library above
CC   and two sequences were isolated, the sequence given and another clone
CC   designated 2918.8.  These two clones were found to represent different
CC   loci.
CC   The 18-mer probe could be useful in HLA typing based on RFLPs.  It can
CC   be utilized in paternity disputes or for determining transplant or
CC   transfusion compatability.  It can also be used to make disease
CC   correlations to diagnose diseases or predict susceptibility to
CC   diseases.
SQ   Sequence   1102 BP;    241 A;    281 C;    321 G;    251 T;
SQ   8 Others;

Initial Score    =    123  Optimized Score   =    382  Significance =  7.07
Residue Identity =    49%  Matches           =    477  Mismatches   =   349
Gaps             =    137  Conservative Substitutions             =     0

            X        10        20          30        40        50
            GT-CGACTGGAACGAGACGACCT--GCTCTGTCACAGGCATGAGGGGTCCCCGGCAGAGATG
            ||   ||| ||  | |  || ||       | | | |||  || |||   ||||  |   | |
  AGCGCTGACAGTGACACT-GATGGTGCTGAGCTNNNNNNNGGCCCCGGC-TG-GGGACACCCGACCACGTTT
  40        50         60        70        80          90       100

 60        70        80         90       100       110          120
  ACAGTGCTGGCGCCAGCCTGGAGCCCAAAT-TCCTCCCTGTTGCTGCTGTTGCTGCTGCTG---AG-TCCTT
     |||   ||   ||  ||  | |   || | |     |  |  || | ||| | |||||   || | | |
  CTTGTGGCAGCTTAAGTTTGAATGTCATTTCTTCAATGGGACGGAGCGGGTGCGGTTGCTGGAAAGATGCAT
  110       120       130       140       150       160       170

   130          140       150       160        170       180         190
  GCCT--GCGGG-GGACACCTGACTGTTACTTCAGCCAC-AGTCCCATCTCCTCCAACTTCA-AAG-TGAAG-
     |   |  | |||  || |   | | |  |||| ||  |    |   ||      || |  || ||  |
  CTATAACCAAGAGGAGTCC-GTGCGCTTCGACAGCGACGTGGGGGAGTACCGGGCGGTTGAGGAGCTGGGGC
180       190        200       210       220       230       240       250

             200        210       220            230       240
  ---TTTA--GAGAGTTGACT-GACCACCTGCTTAAAGATTACC-----CAGTCACTGTGGCC--GT---CAA
      | |    ||||  ||| || || |  |  || ||  ||     |||  |  | ||||  ||   |||
  GGCCTGATGCCGAGT--ACTGGAACAGC--CAGAAGGACCTCCTGGAGCAG-AAGCGGGGCCAGGTGGACAA
         260         270         280       290        300       310

    250       260       270       280       290       300       310
  T--CTTCAGGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTG
  |  || || ||| | |   |||  | ||  |||  |||   ||||  ||  |||||| |  | ||||     |
  TTACTGCA-GAC-ACA---ACT--ACGGGGTTGGTGAG-AGCTTCACAGTGCAGCGCCGAGTTGAGCCTAAG
  320         330            340        350       360       370       380

  320       330       340       350       360       370       380
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    AAGACTGTGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCA
      |||||||      || ||||  ||   ||  ||| || ||  ||||  |  | |    | ||| |  |
    GTGACTGTGTATCCTTCAAAGACCCA---GCCCCTGCAGCACCACAACCTCCTGGTCTGCTCTGTGA-GTGG
          390       400          410       420       430       440

  390       400         410          420       430       440       450
    TGTACCTTCCAGCC--CCTACCAG-AATGT--CTGCGATTCGTCCAGACCAACATCTCCCACCTCCTG---A
    | | |  ||||| |  | |   ||  | ||   | ||   || ||||    | |   |     |  ||   |
    T-TTCTATCCAGGCAGCATTGAAGTCAGGTGGTTCCGGAACGGCCAGGAAGAGAAGGCTGGGGTGGTGTCCA
  450        460       470       480       490       500       510       520

        460          470         480        490       500       510
    AGGACACCTG---CACACAGCTGCTTG--CTCTGAAG-CCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTC
     ||   ||||   || |  |  | |||  |  |  || |||||    | || |  |||  |  | ||| |||
    CGG--GCCTGATCCAGAATGGAGATTGGACCTTCCAGACCCTG----GTGATG--CTGGAAATAGTTC-CTC
             530       540       550       560             570       580

  520       530       540       550       560       570       580        590
    GGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTA-GAA
    || |    |||||  |   || |||  | |    |||||   ||    | ||   || || ||    | | |
    GGAGTGGAGAGGTTTA-CACCTGCC-AAGTGGAGCACCCAAGTG-TGACGAGCCCTCTCACAGTGGAATGGA
        590        600        610       620        630       640       650

                 600         610        620        630           640
    G-CCACGG-----AGCT-CCCAGAGC-CTCGGCCCAG-GCAG-CTGTTGC-TCCTGCTG---CTGCTGCTGC
    |  |||||     | || | ||||||     ||  || | || | |  || || |||||   ||||| || |
    GAGCACGGTCTGAATCTGCACAGAGCAAGATGCTGAGTGGAGTCGGGGGCTTCGTGCTGGGCCTGCT-CTTC
         660       670       680       690       700       710        720

   650       660       670       680       690       700         710
    CTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGA--GGGGGGAGCT
    || |    | || |||| |  || |  | |  ||  |  |     ||||| ||    |||     |  | |
    CT-TGGGGCCGG-GCTGTT--CATCTACTTCAGGAATCAG-----AAAGGACACTCTGGACTTCAGCCAACA
         730        740         750            760       770       780

   720        730       740           750       760          770       780
    CCA-CCCTGGGGTGCCCCTCCCCT---CC-CATCCCTAGGATTCGAGCCTTGTG---CATCGTTGACTCAGC
      |  |||| | ||     |   |   || |||  |  |||   || |||| ||   || | ||| |  |
    GGATTCCTGAGCTGAAATGCAGATGAACCACAT-TCAAGGA--AGAACCTTCTGTCCCAGCTTTG-CAGAAT
     790       800       810        820         830       840        850

         790       800       810        820             830       840
    CAGGGTCTTATCTCGGTTACACCTGTAATCTCAGCC-CTTGGGAG------CCCAGAGCAGGATTGCTGAAT
     |    ||| ||  | ||    | || || ||  || |  | |||      | |||  |  | ||||| | |
    GAAAAGCTT-TCCTGCTT--GGCAGTTAT-TCTTCCACAAGAGAGGGCTTTCTCAGGACCTGGTTGCT-ACT
       860        870         880        890       900       910        920

    850           860        870        X
    GGTCTGG----AGCAGGTCGT-CTCGTTCCAGTCGAC
    |||  ||     ||||    |  || | ||    | |
    GGTTCGGCAACTGCAGAAAATGTTCCTCCCTTGTGGCTTCCTCAGCT
          930       940       950       960


12. US-08-162-407-1 (1-879)
    N70128         Novel DNA encoding a polypeptide having mouse gran

 ID   N70128 standard; DNA; 1363 BP.
 AC   N70128;
 DT   22-OCT-1990  (first entry)
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DE   Novel DNA encoding a polypeptide having mouse granulocyte
DE   colony-stimulating factor (b-CSF) activity is new
KW   Mouse granulocyte colony stimulating factor; lymphokine; interleukin.
OS   Mouse.
FH   Key             Location/Qualifiers
FT   CDS             68..157
FT   /*tag=  a
FT   /product=Leader peptide
FT   mat_peptide     158..694
FT   /*tag=  b
PN   J62269693-A.
PD   24-NOV-1987.
PF   19-MAY-1986; 112506.
PR   19-MAY-1986; JP-112506.
PA   (CHUS) Chugai Pharmaceutical Kk.
DR   WPI; 88-004545/01.
DR   P-PSDB; P70114.
PT   New deoxyribonucleic acid -
PT   is prepd. by forming mRNA from mammal cells producing
PT   polypeptide(s) with mouse granulocyte colony stimulating factor
PT   activity
PS   Disclosure; Fig 1(A) Page 491; 12pp; Japanese.
CC   The CDS for the mature peptide (see FT) is claimed (claims 5 and 6). It
CC   was prepd. as follows. mRNA is prepd. from mammal cells capable of
CC   producing polypeptides having G-CSF activity and double stranded cDNA is
CC   produced from the mRNA by conventional methods. Polypeptides having mouse
CC   G-CSF activity are obtd. as 14-75S fractions by the sucrose
CC   density-gradient centrifugation method.
SQ   Sequence   1363 BP;   279 A;   403 C;   368 G;   313 T;

Initial Score    =    123  Optimized Score    =    387  Significance =  7.07
Residue Identity =    50%  Matches            =    488  Mismatches   =   325
Gaps             =    154  Conservative Substitutions              =     0

              X       10              20            30         40        50
              GTCGACTGGAACGA--GAC---G-ACCTGCT-CTGT--CACAG-GCATGAGGGGTCCCCGGC
              | ||  || | | |  | |   | | ||||| ||||  || || |||  |  ||||   ||
    TCTGCCCAGAGGCGCATGAAGCTAATGGCCCTGCAGCTGCTGCTGTGGCAAAGTGCACTA-TGGTC--AGGA
   80        90       100       110       120       130        140

          60           70           80         90        100       110
    AGAGATGACAGT--GCTGG-CGC---CAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGC-TGCTGC
     |||| | |  |   |||| | |   ||||     |||   || ||| |||  |||  | |  || | ||||
    CGAGAGGCCGTTCCCCTGGTCACTGTCAGCGCTCTGCCACCATCCCTGCCT-CTGC-CCCGAAGCTTCCTGC
   150       160       170       180       190        200        210

     120          130       140        150       160       170       180
    -TGAGTCCTT---GCCTGCGGGGGACA-CCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAA
     | ||||| |   ||  | | || | | || | |        ||||  |  ||    || ||  | |
    TTAAGTCCCTGGAGCAAGTGAGGAAGATCCAGGC--------CAGCGGC--TCGGTGCTGCTGGAGCAGTTG
   220       230       240       250                 260       270       280

       190       200       210            220       230       240
    AGTGAAGTTTAGAGAGTTGACTGACC---ACCTGCT--TAAAGATTACCCAGTCACTGTGG--CCGTCAATC
     |||     || | || ||  | |||   |   |||  |   | |   ||| || ||| ||  ||   |  |
    TGTGCCACCTACA-AGCTGTGTCACCCCGAGGAGCTGGTGTTGCTGGGCCACTCTCTGGGGATCCCGAAGGC
           290        300       310       320       330       340       350

  250        260        270        280         290       300       310
    TT-CAGGACGAGAAGCACT-GCAAGGCCTTG-TGGAGCCTC--TTCCTAGCCCAGCGCTGGATAGAGCAACT
```

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 || |  ||   |  || || || ||||| ||  | || | |  | ||||  ||||| |   |  | ||  ||
 TTCCCTGAGTGGCTGCTCTAGCCAGGCCCTGCAGCAGACACAGTGCCTAAGCCAGCTCCACAGTGGGC-TCT
       360       370       380       390       400       410        420

  320       330       340       350       360        370       380
 GAAGACTGTGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAAC-ACCGAGATACATTTTGTCACCT
    | || |  || |||||    ||||  | | | | | | |  ||  |  ||  |   |       |||||
 ---GCCTCTACCAAGGTCT--CCTGCAGGCTC-TATCGGGTATTTCCCCTGCCCTGGCCC------CCACCT
         430         440        450       460       470             480

 390       400       410       420         430       440       450
 CATGTACCTTCCAGCCCCTACCAGAATGTCTGCGA--TTCGTCCAGACCAACATCTCCCACCTCCTGAAGGA
   || | ||| |  |    | | | |||| ||| |  || | |||  ||| |||||  || |   ||  | |
 --TGGA-CTTGCTTC----AGCTGGATGT-TGCCAACTTTG-CCA--CCACCATCTGGCAGCAGATG--GAA
         490           500        510          520       530         540

 460       470       480        490        500       510           520
 CACCTGCACACAGCTGCTTGCTCTGAAGCCC-TGTATCG-GGAAGGCCTGCCAGAATTTCT--CT--CGGTG
  ||||       ||  | | || || |||||    |  | |  | ||| |||   | ||||  ||  | | |
 AACCTAGGGGTGGC-CCCTACTGTGCAGCCCACACAGAGCGCCATGCCAGCCTTCACTTCTGCCTTCCAGCG
       550        560       570       580       590       600       610

      530       540       550       560        570            580
 CCTGG-AGGTGCAGTGCCAGCCGGACTCCTCCACCCTGC-TGCCCCCAAGGAG-----TCCCATAGCCCTAG
 || || ||| |  ||| |  | || |   ||   |||||  | |  |  ||||     || | | || ||
 CCGGGCAGGAG--GTGTC--CTGGCCATTTCGTACCTGCAGGGCTTCCTGGAGACGGCTCGCCTTGCTCTGC
      620           630       640       650       660       670       680

590       600       610       620       630        640          650
 AAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCT-GCTGCT---GCTGCCTCTCACA
 |  ||||   |  || ||| |||  |  |||  |||  ||  ||| | | | |  |    ||   | | | |
 A--CCACTTGG--CCTAGA-CCT--GAGCAGAAAGCCCTT--TCCAGATAGTTTATTTATCTCTATTTAATA
            690          700       710         720       730       740

  660       670       680       690         700       710       720
 CTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAG--GGCAAGAAGGAGGGGGGAGCTCC---ACC
  |  |||   |   ||||  ||      ||    | |||||  |  || | ||||     |||| |   | |
 TTTATGCATATTTAAGCCTACT-----ATTTAAAGACAAAGACGAGAAAATGGAGCTCTAAGCTTCTAGATC
     750       760            770       780       790       800       810

     730              740       750             760       770         780
 CTGGGGTGCCCCTCC-------CCTCCCATCCCTAG------GATTCGAGCCTTGTGCATCGT--TGACTCA
  |    | | | |||         || | | | |||      ||    || ||  ||  || |  ||
 ATTCTCTCCACTTCCGAGTTTTGTTCTCCTGCTTAGAGCAGAGAGAGAAGGCTCTTGTGTCCTCCTGTGGAG
        820       830       840       850       860       870       880

        790        800       810       820         830        840
 GCCAGGGTCTTATCTCGGT-TACACCTGTAATCTCAGCCCT-TGGGAGC-CCAGAGCA-GGATTGCTGAATG
 |||||||    |  | |||  | |||    || | |  |||   |  || |||| |||   | | |||  ||
 GCCAGGGAAGGAGATGGGTAAATACCAAGTAT-TGATTCCTGCTGCTGCTCCAG-GCACCCAGTTCTG--TG
      890       900       910        920       930        940         950

850             860          870         X
 GTCTGGAGC------AGGTC-GT--CTCGTTCC-AGTCGAC
 | | | | |      |  || ||    | | ||  |  ||
 G-CAGTACCCCCAAAAAATCAGTGAGCCCTGCCGTGCTGAGGCACCATCTC
         960       970       980       990      1000
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13. US-08-162-407-1 (1-879)

```
   Q10613       Rianodin receptor gene.

ID   Q10613 standard; DNA; 15672 BP.
AC   Q10613;
DT   26-APR-1991  (first entry)
DE   Rianodin receptor gene.
KW   Rianodin receptor gene; calcium release modulator; tranquiliser;
KW   antagonist; ss.
OS   Oryctolagus cuniculus.
FH   Key             Location/Qualifiers
FT   CDS             593..15553
FT   /*tag=  a
FT   /product= rianodin receptor
FT   GC_signal       351..356
FT   /*tag=  b
FT   /note= "feature unlabelled in specification"
FT   GC_signal       407..452
FT   /*tag=  c
FT   /note= "feature unlabelled in specification"
FT   CAAT_signal     392..396
FT   /*tag=  d
FT   /note= "feature unlabelled in specification"
FT   misc_feature    503..510
FT   /*tag=  e
FT   /note= "feature unlabelled in specification"
FT   misc_feature    514..521
FT   /*tag=  f
FT   /note= "feature unlabelled in specification"
FT   polyA_signal    15388..15393
FT   /*tag=  g
PN   J03011098-A.
PD   18-JAN-1991.
PF   07-JUN-1989; 144569.
PR   07-JUN-1989; JP-144569.
PA   (MITU) Mitsubishi Kasei Corp.
DR   WPI; 91-062003/09.
DR   P-PSDB; R10834.
PT   New rianodin receptor, genes encoding it and its prepn. - useful as
PT   calcium release modulator for tranquillisers and for assaying
PT   calcium antagonists.
PS   Disclosure; Fig 1; 18pp; Japanese.
CC   RNA contg. poly(A) was prepared from rabbit skeletal muscle
CC   endoplasmic reticulum.  From the obtd. poly(A) mRNA, a cDNA bank
CC   corresp. to it was prepared by random primer method, oligo (dT)
CC   primer method, and primer extension method.  A cDNA was obtained by
CC   screening with a DNA probe (see Q10614-15).  By introducing the obtd.
CC   cDNA into an expression vector, vector pRRS7 was formed.
CC   The product is said to be involved in calcium release from
CC   sarcoplasmic reticulum which triggers constriction of skeletal muscle.
CC   Therefore, the receptor is useful as tranquilliser and assay series for
CC   screening of calcium antagonist.
SQ   Sequence   15672 BP;    3139 A;    4909 C;    4955 G;    2669 T;

Initial Score     =    122  Optimized Score    =    402  Significance =  7.00
Residue Identity  =    51%  Matches            =    496  Mismatches   =   326
Gaps              =    144  Conservative Substitutions             =     0

                X       10        20         30        40        50
                GTCGACTGGAACGAGACGACCTG-CTCTGTCACAGGCATGAGGGGTCCCCGG----CA--GA
                | |  |  || ||  | | || | ||| |   |     |||| |  || |||    ||  ||
   GATGAAGTCGGGCCCCGAGATCGTCAAGGCCGGCCTCCGCTCCTTCTTTGAGAGCGCCTCGGAGGACATCGA
        9690 X    9700      9710      9720      9730      9740      9750

      60             70          80         90        100          110
   GATGACAGTG-----CTGGCGCC--AGCCTGGAG-CCCAAATTC-CTCCCTGTTGCTG---CTGTTGCTGCT
   || ||  |||     || ||| |   ||  || | ||||    | | | | | ||  |    ||   | |
   GAAGATGGTGGAGAACTTGCGGCTGGGCAAGGTGTCCCAGGCGCGCACGCAGGTGAAGGGCGTGGGCCAGAA
      9760      9770      9780      9790      9800      9810      9820

     120        130       140       150       160         170       180
   GCTGAGTCCT-TGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTC--CCATCTCCTCCAACTTCA-
    || |  |||   ||  || ||  |  ||| | ||  | ||| ||||  ||  ||| | | ||   |  ||
   CCTCA--CCTACACCACCGTGGCCCTGCTGCCCGT--CCTCA-CCACGCTCTTCCAGCACATCGCCCAGCAC
    9830        9840      9850        9860       9870      9880      9890

       190       200            210       220       230       240       250
   AAGTGAAGTTTAGAGAGT-----TGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCT
    |||   |    ||  ||     ||  ||||   | | |       |||| |  || ||| || | || |||
   CAGTTCGGCGACGA-CGTCATCCTGGATGACGTGCAGGTGTCTTGCTACCGA-ACATTGT-GCAG-CA-TCT
       9900       9910      9920      9930      9940       9950

          260       270           280       290       300        310
   TCAGGACGAGAAGCACTGCAAG--GCCTT--GTGGAGCCTCTTCCTAGCCCAGCGC-TGGATAGAGCAACTG
    |     | | | |||  ||||    |||  |||||    || |   | ||||| | |||| || ||  |||
   ACTCTCTGGGGACCAC--CAAGAACACTTATGTGGAAAAGCTAC---GGCCAGCCCTTGGAGAGTGC--CTG
9960      9970        9980      9990     10000        10010     10020

   320         330       340       350       360         370         380
   AAGACTG--TGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAAC--ACCGAGATACA--TTTGTC
     | | |  |||||| | | | |       |  | ||||||  | ||| |  | |||| ||||    ||| |
   --GCCCGCCTGGCAGCGGCCATGCCTGTGGCCTTCCTGGAG--CCTCAGCTGAACGAG-TACAACGCTTG-C
      10030     10040     10050     10060       10070      10080      10090

       390       400       410       420       430       440       450
   ACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAG
    ||   |  |||  | || | |  |  ||      ||||  | ||| |       || || ||  | || ||
   TCCGTGTACACCACCAAGTCTCCCCGGGA------GCGAGCCATCCTG---GGGCTCCCCAACAGCGTGGAG
        10100     10110           10120     10130        10140     10150

          460        470          480       490       500       510
   GACA-----CCTG-CACACAGCTGCTTGCT---CTGAAGCCCTGTATCGGGAAGGCCTGCCAGAAT--TTCT
   || |     |||| ||  | | |||| | |   || | | |    ||||||  || ||| | || |
   GAGATGTGTCCTGACATCCCGGTGCTGGATCGGCTCATGGCAGACATCGGG--GGGCTGGCCGAGTCCGGGG
     10160     10170     10180     10190     10200       10210     10220

    520       530         540       550        560        570       580
   CTCGGTGCCTGGAGGTGCAG--TGCCAGCCGGACTCCTCCACCC-TGCT-GCCCCCAAGGAGTCCCATAGCC
   | || | |  |||| ||| |   | || |  ||   | |  ||| ||||   |  | |   | |||   |
   CCCGCTACACGGAGATGCCGCACGTCATCGAGATCACGCTGCCCATGCTCTGCAGCTACCTGCCCCGCTG--
     10230     10240     10250     10260     10270     10280     10290

      590       600       610           620       630       640        650
   CTAGAAGCCACGGAGCTCCCAGAGCC----TCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGC-TGCCTC
    | | || | ||| || |   | |||     | |||| | | || |  || ||  | ||  ||||  | ||
   GTGGGAG-CGCGG-GCCCGAGGCGCCCCCTCCCGCCCTGCCTGCCGGCGC-CCCCCCGC-CCTGCACGGCTG
     10300       10310     10320     10330     10340       10350     10360

         660       670          680        690         700            710
   TCACACTGGTGCTGCTGGCAGC---CGCCTGGGG-CCTTCGCTGGCA--AAGGGCAAGAA---GG--AGGGG
   ||||    |  |  ||  || |   | | |||||  | ||    |||  |  | ||| ||   ||  |  |
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    TCACCTCCGACCACCT--CAACTCACTCTTGGGGAACATCTTGCGCATCATTGTCAACAACCTGGGCATTGA
        10370       10380     10390     10400     10410     10420     10430

         720       730       740       750       760       770       780
    GGAGCTCCACCCTGGGGTGCCCCTCCCCTCCCATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCCA
     |||  ||| |||| | ||   |  |       |  || |  |||  |||  |  ||||| |||  | | |
    CGAG-GCCA-CCTG-GATGAAGCGGC-------TTGCT-GTGTTC--GCCCAGCCCATCG-TGAGCCGGGCG
          10440      10450             10460       10470      10480

       790         800       810       820           830          840
    GGGTCTTATCTC--GGTTACACCTGTAATCTCAGCCCTTGGG----AGCCCA---GAGCAGGATTGCTGAAT
     || || | |||  |  | | |   | ||| |  || | |||     || ||   | |||||   | ||  |
    CGGCCTGAGCTCCTGCATTCCCACTTCATCCCCACCATCGGGCGGCTGCGCAAGCGGGCAGGCAAGGTG-GT
10490     10500     10510     10520     10530     10540     10550      10560

    850           860         870          X
    GGTC----TGGAGCAGGT-CGTCTCG-TTCCA--GTCGAC
    || |     ||||||| | || || |   |||  | |||
    GGCCGAGGAGGAGCAGCTGCGGCTGGAGGCCAAGGCCGAGGCCGAGGAGG
         10570     10580     10590     10600     10610


14. US-08-162-407-1 (1-879)
    Q37813       Sequence encoding the alpha 1C human calcium chann

 ID   Q37813 standard; cDNA; 5904 BP.
 AC   Q37813;
 DT   30-JUN-1993  (first entry)
 DE   Sequence encoding the alpha 1C human calcium channel subunit.
 KW   Human calcium channel subunit; diagnosis; agonist; antagonist;
 KW   Lambert Eaton syndrome; ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             1..5904
 FT   /*tag=  a
 PN   WO9304083-A.
 PD   04-MAR-1993.
 PF   14-AUG-1992; U06903.
 PR   15-AUG-1991; US-745206.
 PR   10-APR-1992; US-868354.
 PA   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
 PI   Brenner R,  Ellis SB,  Feldman DH,  Harpold MM,  Mccue AF,
 PI   Williams ME;
 DR   WPI; 93-093936/11.
 DR   P-PSDB; R33547.
 PT   DNA encoding specific human calcium channel sub-units - used for
 PT   identifying calcium channel agonists and antagonists and
 PT   diagnosing Lambert Eaton syndrome
 PS   Disclosure; Page 102-109; 150pp; English.
 CC   Numerous alpha 1C-specific DNA clones were isolated.
 CC   Characterisation of the sequence revealed the alpha 1C coding
 CC   sequence, the alpha 1C initiation of translation sequence, and an
 CC   alternatively spliced region of alpha 1C. Q37814 and Q37815 encode
 CC   two possible amino terminal ends of the alpha 1C protein. Q37816
 CC   encodes an alternative exon for the IV S3 transmembrane domain.
 SQ   Sequence   5904 BP;    1360 A;    1726 C;    1551 G;    1266 T;
 SQ   1 Others;

Initial Score    =    120  Optimized Score  =    396  Significance =  6.87
Residue Identity =    50%  Matches          =    481  Mismatches   =   348
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Gaps              =    123  Conservative Substitutions          =     0

            X       10        20          30          40        50
            GTCGACTGGAACGAGACGAC-CTGC-TCTGTCACA--GGCATGAGGGGTCCCCGGCA--GAG
            | | ||   | | |  | || | ||  |||  | |   ||| |    | |   | ||  |
  CGGGGAGGTTGACCACCCCATC-ATCCAACCCCGCAGCTGGGAGAACAGCAAG-TTTGACTTTGACAATGTT
3310      3320      3330       3340      3350      3360       3370

    60           70         80        90        100       110         120
  ATGACAG---TGCTGGCGC-CAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTG--CTGCTGAGT
   || |||   || |||| | |  |   |   |||  || |     || ||    | |||||  | |||   |
  CTGGCAGCCATGATGGCCCTCTTCACCGTCTCCACCTT-CGAAGGGTGGCCAGAGCTGCTGTACCGCTCCAT
3380      3390      3400      3410       3420      3430      3440

         130       140       150       160       170       180       190
  C--CTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAGT
  |  ||  |   |||  ||||   | |   | || || | || ||        ||||| ||||    | |  |
  CGACTCCCACACGGAAGACAAGGGCCCCAT-CTACAACTACCGTGTGGAGATCTCCATCTTCTTCATCA--T
3450     3460      3470       3480      3490      3500      3510

       200       210       220       230       240               250
  TTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGC--CGTCA--ATC----TTCAGGA
   || |   |    | | | ||| ||| | ||| | |   |   || |||  |||||   ||    |||||||
  CTACATCAT--CATCATCGCCTTCTTCATGATGAACATCTTCGTG-GGCTTCGTCATCGTCACCTTTCAGGA
3520        3530      3540      3550      3560       3570      3580

         260       270           280       290        300        310
  ------CGAGAAGCACTGCAAGGCCT-TG---TGGAGCCTCTTCCTAGC-CCAGCGC-TGGATAGAGCAACT
         ||| || | | ||||  || ||   |||| |     || |||  ||| || |||| | |    ||
  GCAGGGGGAGCAGGAGTACAAGAACTGTGAGCTGGA-CAAGAACC-AGCGACAGTGCGTGGA-ATACGCCCT
 3590      3600      3610      3620       3630       3640       3650

   320       330       340       350       360       370       380
  GAAGACTGTGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTC
   ||| |   |||     |  || | ||     | |   || ||  || ||||   | | | | ||  || |
  CAAGGC-CCGGCCCCTGCGGAGGTACA-----TCCCCAAGAAC--CAGCACCAGTACAAAGTGTGGTACGTG
  3660       3670      3680           3690        3700      3710      3720

 390       400       410          420        430       440         450
  ATGTACCTTCCAGCCCCTACCAGAA--TG-TCTGCG-ATTCGTCCAGACCAACATCTCCCACCT--CC-TGA
   |  ||  |||| |  || | || |  || | | ||   || ||| |  ||||| |  |  |||  || ||
  GTCAAC--TCCACCTACTTCGAGTACCTGATGTTCGTCCTCATCCTGCTCAACACCATCTGCCTGGCCATGC
          3730      3740      3750      3760      3770      3780      3790

      460       470       480         490         500       510       520
  AGGACACCTGCACACAGCTGCTTGCTCTGAA--GCCCTG--TATCGGGAAGGCCTGCCAGAATTTCTCTCGG
  || ||  | || || ||||||| || ||  ||  ||| ||   |||   ||  | |||      ||| || |
  AGCACTACGGC-CAGAGCTGCCTGTTCAAAATCGCCATGAACATCCTCAA--CATGC----TCTTCACTGGC
        3800       3810      3820      3830        3840          3850

        530        540         550       560       570       580
  TGCCTGGAGGTGCAG-TGCCAGCCGGA--CTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAG----CCCT
    | |    ||| || ||  | || ||  ||| |    ||| |    |||||||  | |  |||    ||||
  CTCTTCACCGTGGAGATG--ATCCTGAAGCTCAT--TGCCTTC-AAACCCAAGGGTTACTTTAGTGATCCCT
   3860      3870        3880        3890       3900      3910      3920

   590        600       610       620       630       640       650
  AGAA-GCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCCTCTCACAC
   ||| |     || || ||  |   |||     ||||||   |  |  ||  | |  | |  |  ||| ||
  GGAATGTTTTTGA-CTTCCTCA---TCGTAATTGGCAGC--ATAAT--TGACG-TCATTCT--CAGTCAGAC
```

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      3930       3940         3950        3960         3970        3980

  660        670       680       690       700       710          720
  TGGTGCTGCTG-GCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTC---CACCCT
  |  | | ||||  ||  | |   |  |   | ||   || |   | |||       | | |||   |||| |
  TAATCCAGCTGAACATACCCAATGCTCTCCCTCTATGAACGCAGAGGAAAACTCCCGCATCTCCATCACCTT
     3990      4000      4010      4020      4030      4040      4050

    730       740         750            760            770       780
  GGGGTGCCCCTCCCCTCCCATCC--CTAG-GATTC----GAGCCTT-----GTGCATCGTTGACTCAGCCAG
       |||  | ||    ||| |  || | ||  |    ||||| |     | |||||   ||| | ||
  CTTCCGCCTGTTCCGGGTCATGCGTCTGGTGAAGCTGCTGAGCCGTGGGGAGGGCATC-CGGACGCTGCTGT
   4060      4070      4080      4090      4100      4110       4120

    790       800       810       820          830       840       850
  GGTCTTATCTCGGTTACACCTGTAATCTCAGCCCT-TG-GGAGC-CCAGAGCAGGATTGCTGAATGGTC-TG
  || | |   ||   |   | |  |  | | ||||| || ||  | || || |  || |||||  |  || |
  GGACCTTCATCAAGT--CCTTCCAGGCCCTGCCCTATGTGGCCCTCCTGATCGTGA-TGCTG-TTCTTCATC
  4130      4140        4150      4160      4170      4180        4190

      860       870        X
  GAGCAGGTCGTCTCGTTCCAGTCGAC
   |   |||  ||  | | |||  |
  TACGCGGTGATCGGGATGCAGGTGTTTGGGAAAATT
    4200      4210      4220      4230


15. US-08-162-407-1 (1-879)
    Q13798          Zea mays 15 kD seed storage protein gene, pZein15K

 ID   Q13798 standard; DNA; 1747 BP.
 AC   Q13798;
 DT   10-DEC-1991  (first entry)
 DE   Zea mays 15 kD seed storage protein gene, pZein15K.
 KW   Promoter; beta-zein; polyadenylation signal; zmP; zmS; ss.
 OS   Zea mays.
 FH   Key               Location/Qualifiers
 FT   CDS               360..899
 FT   /*tag=  a
 FT   /label= seed_storage_protein
 FT   /note= "15 kD"
 PN   WO9113993-A.
 PD   19-SEP-1991.
 PF   14-FEB-1991; U00887.
 PR   05-MAR-1990; US-489175.
 PA   (UPJO ) UPJOHN CO.
 PI   Slightom JL, Chee PP;
 DR   WPI; 91-295647/40.
 DR   P-PSDB; R14108.
 PT   Seed specific expression cassettes - having specific gene
 PT   regulatory elements for prodn. of proteins in plant seed storage
 PT   bodies
 PS   Disclosure; Page 28-30; 58pp; English.
 CC   The nucleotide sequence of the beta-zein gene reported by Pedersen
 CC   only extends ca. 233 bp 5' of the translation initiation.
 CC   To obtain more of the beta-zein promoter, a second gene, pZein15K,
 CC   was isolated.  The sequence contains an additional 110 bp of 5'
 CC   flanking DNA, giving a total promoter region of ca. 350 bp to the
 CC   translation initiation codon.  Analysis of many zein type genes
 CC   has shown that sequences responsible for controlling the
 CC   developmental expression of seed specific genes are located within
 CC   these 350 bp.
 CC   The promoter (zmP) and polyadenylation signal (zmS) were used in the
 CC   construction of an expression cassette.
 CC   See also Q13801.
 SQ   Sequence   1747 BP;    487 A;    412 C;    402 G;    446 T;

Initial Score     =    119  Optimized Score  =    376  Significance =  6.80
Residue Identity  =    49%  Matches          =    466  Mismatches   =   353
Gaps              =    131  Conservative Substitutions             =     0
```

```
            X       10          20        30               40        50
            GTCGACTGGA-ACGAG-ACGACCTGCTCTGTCA---CAGG-CAT---GAGGGGTCCCCGGCA
            ||   ||  | | | | | ||  | |  || ||   |  | |||    ||  |   |
  GCATTACAAAGTTAGCTTCACAAGCGTATGA-ATTCATTGACAACCCTTGACATCTAAAGTTGATTCATATG
  100       110       120        130       140       150       160

       60         70        80         90          100        110
  GAGATGACAG-TGCTGGCGCCAGCCTGGA-GCCCAAATTCCT---CCCTGTTGCTGC-TGTTGCTGCTGCTG
   | | || || |    |  | |  ||| |   |||||| | |   |  |||| |  | |  |||  |
  TATAAGAAAGCTTAATGATCTA-TCTGTACATCCAAATCCATGTACTATGTTTCCACGTCATGCAACGCAAC
 170       180       190        200       210       220       230

120       130       140          150       160           170       180
  AGTCCTTGCCTGCGGGGGACACC--TGACT-GTTACTTCAGCCACA---GTCCCA-TCTCCTCCAACTTCAA
  | |||    |  |  ||  || |  | | | | ||  ||  |||||   |  | | ||||   || | || |
  ATTCCAAAAC--CATGGATCATCTATAAATGGCTAGCTC--CCACATATGAACTAGTCTCTATCATCATCCA
240         250       260       270         280       290       300

     190       200       210       220       230       240       250
  AGTGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGA
  | |  || | ||  |   | | |      ||| || |||  | |  |||       | |   | | | | ||
  A-TCCAGATCAGCAAAGCGGCAG------TGCGTAGAGAGGATC--GTC----GAACAGAACAGCATGAAGA
   310       320             330       340             350       360

   260       270       280        290         300        310       320
  CGAGAAGCACTGCAAGGCCTTGTG-GAGCCTCTTCCTAGC--CCAGCG-CTGGATAGAGCAACTGAAGACTG
   |   | |  | |  |  | ||||   | ||||  | |||  |||||| ||    |  |||  ||    |||
  TGGTCATC-GTTCTCG-TCGTGTGCCTGGCTCTGTC-AGCTGCCAGCGCCTCTGCAATGCAGATG--CCCTG
   370        380        390       400        410       420         430

     330       340       350       360       370         380        390
  TGGCAGGGTCTAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGAT-AC-ATTTTG-TCACCTCATGTA
     | | | |   | ||| |  |||  || | | ||    | |||   | || |   || |   | |  |
  CCCCTGCG-CGGGGCTGC-AGGGCT--TGTACGGCGCTGGCGCCGGCCTGACGACGATGATGGGCGCCGGCG
      440        450          460       470       480       490       500

      400        410       420            430          440       450
  CCTTCCAGCCCCTAC-CAGAATGTCTGCG--ATTC---GTCCAGACC---AACATCTCCCACCTCCT--GAA
     |  | ||||||| | || |  ||| |  |  |   || ||| ||     |  |  |  ||| ||  |
  GGCTGTA-CCCCTACGCGGAGTACCTGAGGCAGCCGCAGTGCAGCCCGCTGGCGGCGGCGCCCTACTACGCC
         510       520       530       540       550       560       570

     460        470       480       490         500       510       520
  GGACACCTGCACAC-AGCTGCTTGCTCTGAAGCCCTGTATCGGGA--AGGCCTGCCAGAATTTCTCTCGGTG
  ||      ||| || |||  | ||  |   ||||  |   ||| |  ||  ||||||| |        ||
  GGGTGTGGGCAGACGAGCGCCATGTAC--CAGCC--GCTCCGGCAACAGTGCTGCCAGCAGCAGATGAGGAT
       580       590         600         610       620       630       640

      530       540        550         560       570       580       590
```

```
CCTGGAGGTGCAGTGCCAGCCGGA-CTCCTCC--ACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGC
  |||| ||||||| |    || | |  || |  |   || |||  |    | || ||   |||      ||
GATGGACGTGCAGTCCGTCGCGCAGCAGCTGCAGATGATGATGCAGCTTGAGCGTGCCGCTGCC------GC
       650       660       670       680       690       700

     600       610       620       630       640       650       660
CACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACTGGTGCT
|| | |||      ||||| |  | || |||||  || | | || || || || ||  ||  ||||   |
CA-GCAGC------AGCCT-GTACGAGCCAGCT-CTGATGCAGCAGCAGCAGCAGCTGCTGGCACTCCAG--
  710              720       730        740       750       760

   670       680         690       700         710       720
GCTGGCAGCCGCCTGGGGCCTT--CGCTGGCAAAGGGCAAGAAGG--AGGGGGGAGCTCCAC-----CCTG-
| |  || || | |  |||| |   | ||||  ||  || |  ||  | ||| |  ||| ||     || |
GGTCTCAACCCCAT--GGCCATGATGATGGCGCAGAACATGCCGGCCATGGGTGGACTCTACCAGTACCAGT
770       780         790       800       810       820       830

    730          740       750            760        770       780
---GGGTGCCC--CT-CCCCTCCCATCCCT-AGGATTC----GAGCC-TTGTGCATCGTTGACTCAGCCAGG
    | |||||  || || | || | ||||  ||  ||      ||| ||  ||  |    ||| |  ||
ACCAGCTGCCCAGCTACCGCACCAACCCCTGTGGCGTCTCCGCTGCCATTCCGC-CCTACTACTGATTCA--
840       850       860       870       880       890        900

 790       800        810       820        830        840       850
GTCTTATCTCGGTTA-CACCTGTAATCTCAGCCCTTGGGAGC-CCAGA-GCAGGATTGCTGAATGGTCTGGA
 |  ||| | ||  | | ||| | ||| || ||||    | |   | | | |  | ||| | |  | |   |
-TGATATTTGGGAAATCTCCTCT-ATC-CATCCCTCTCTATCTATATATGTAATAATGCAGTA-AGACGACA
  910       920        930        940       950       960        970

  860       870        X
GCAGGTCGTCTCGTTCCAGTCGAC
 ||  |  ||  ||       |||
-CACATTATCATGTGTGGTATGACCAATAATATA
    980       990      1000
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq1nsqinv.res made by  on Wed 5 Apr 95 20:44:54-PDT.


Query sequence being compared:US-08-162-407-1' (1-879)
Number of sequences searched:                  57621
Number of scores above cutoff:                  4502

     Results of the initial comparison of US-08-162-407-1' (1-879) with:
   Data bank : N-GeneSeq 17, all entries

 10000-    *
      - ***
N     -
U 5000-
M     -
B     -     *
E     -      *   *
R     -       **
      -         * ***  *
```

```
O     -              **
F 1000-                  *
      -                 *    *
S     -                   **
E  500-                     *
Q     -                       **
U     -*                        *
E     -                            *
N     -                          **
C     -                             *
E     -                              *
S  100-                                **
      -                               *
      -                                  *
    50-                                   *
      *
      -                                    *  *    *
      -                                     *    *
      -                                        *
      -                                           *
      -                                      *  *   **
    10-
      -                                                *
      -
     5-
      -
      -                                                  ***
      -                                               * *          *
      -
      -
      -                                                       * **   *
     0-------------------------------------------------------------------
      |    | |    | |   |  |   |  |   |  |  |   |  |   |  |   | |    |
SCORE 0    |15    |31   | 46   | 62   | 77  |  93  | 108  | 124 |  139
STDEV      0      1     2      3      4     5      6      7     8

                                PARAMETERS

Similarity matrix         Unitary     K-tuple                         4
Mismatch penalty                1     Joining penalty                30
Gap penalty                  1.00     Window size                    32
Gap size penalty             0.33
Cutoff score                    2
Randomization group             0

Initial scores to save         45     Alignments to save          15
Optimized scores to save        0     Display context             10
                                SEARCH STATISTICS

Scores:                    Mean         Median      Standard Deviation
                             18            14         14.33

Times:                     CPU                      Total Elapsed
                       00:03:49.01                  00:03:49.00

Number of residues:                   24347505
Number of sequences searched:            57621
Number of scores above cutoff:            4502
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Cut-off raised to 11.
Cut-off raised to 17.
Cut-off raised to 25.
Cut-off raised to 31.
Cut-off raised to 36.
Cut-off raised to 40.
Cut-off raised to 44.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                          Init. Opt.
Sequence Name      Description                        Length Score Score   Sig. Frame
----------------------------------------------------------------------------------
                      ****  8 standard deviations above mean ****
   1. Q29269         Human calcium channel 27980/1   6232   139   406    8.44    0
   2. Q51731         Plasmid pCisEBON for subcloni  10596   134   385    8.09    0
   3. N91772         Human androgen receptor cDNA.   3569   133   399    8.02    0
                      ****  7 standard deviations above mean ****
   4. Q43423         Sequence encoding the 10E3B (    739   129   275    7.75    0
   5. Q30999         Notch clone hN3k full length    3234   128   272    7.68    0
   6. N90369         DNA sequence of alpha-2 plasm   1521   123   355    7.33    0
                      ****  6 standard deviations above mean ****
   7. Q04035         Stem cell leukaemia (SCL) gen   4091   117   391    6.91    0
   8. Q05330         Stem cell leukaemia (SCL) gen   4199   117   391    6.91    0
   9. Q37817         Sequence encoding the alpha 1   7362   116   405    6.84    0
  10. N60309         Equine IFN-omega-1 from pAH61   2109   115   340    6.77    0
  11. Q03541         Chinese hamster IMPDH.          1620   114   387    6.70    0
  12. Q45955         mRXR-beta.                      2285   113   386    6.63    0
  13. Q43031         Collagen-like polymer DCP2-C2    432   112   204    6.56    0
  14. Q43032         Collagen-like polymer DCP3-C2    756   112   315    6.56    0
  15. Q37818         Sequence encoding the alpha 1   7175   112   404    6.56    0
  16. Q45335         Human TLE-3 gene.               2357   110   389    6.42    0
  17. Q62177         Human TLE-3 gene.               2357   110   389    6.42    0
  18. Q65395         Osteogenic protein hOP2 gene.   6418   108   370    6.28    0
  19. Q13608         ACV synthetase gene, pcbAB.    11601   108   392    6.28    0
  20. Q48231         Vector containing ACVS gene.   13058   108   392    6.28    0
  21. Q24474         Precursor ET-3 cDNA sequence.   2233   107   391    6.21    0
  22. Q11255         Endothelin-3 precursor.         2299   107   396    6.21    0
  23. Q11943         Nucleotide sequence of HIV-1    9192   107   373    6.21    0
  24. N92768         HIV-2 variant HIV-D194 clone.   9473   107   387    6.21    0
  25. N93063         Sequence encoding hybrid prot   1383   106   291    6.14    0
  26. Q06029         Sequence encoding recombinant   1774   105   375    6.07    0
                      ****  5 standard deviations above mean ****
  27. Q20924         C10-E13 DNA fragment encoding    559   103   243    5.93    0
  28. Q23091         Antigen ac-6b gene.              619   103   237    5.93    0
  29. N50390         Bovine interferon alpha C.       840   103   306    5.93    0
  30. N92097         Combined open reading frames    5300   103   375    5.93    0
  31. N90327         Hepatitis C virus composite p   5360   103   375    5.93    0
  32. N92103         Combined open reading frames    6905   103   375    5.93    0
  33. N92106         Combined open reading frames    7310   103   375    5.93    0
  34. N90336         Composite hepatitis C virus (   7310   103   375    5.93    0
  35. Q10566         Hepatitis C virus strain 1 DN   9185   103   375    5.93    0
  36. Q05956         Sense strand of the compiled    9185   103   375    5.93    0
```

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37. Q21744       Compiled HCV cDNA.                9400   103   376   5.93   0
38. Q05955       Hepatitis C virus open readin     8316   102   375   5.86   0
39. Q12864       Human Cytotoxic Cell Protease      849   101   235   5.79   0
40. Q05617       Exon 1 of porcine leukaemia i     1140   101   223   5.79   0
41. Q63870       Feline T cell protein CD4 cDN     1422   101   409   5.79   0
42. N60077       DNA sequence of the env regio     2607   101   382   5.79   0
43. N80220       Sequence of Mycobacterium tub     2640   101   317   5.79   0
44. Q14753       HIV-1 BA-L clone.                 3807   101   375   5.79   0
45. Q43662       Acetobacter cdg3 operon.          4131   101   293   5.79   0

1. US-08-162-407-1' (1-879)
   Q29269       Human calcium channel 27980/11.

ID    Q29269 standard; DNA; 6232 BP.
AC    Q29269;
DT    03-MAR-1993  (first entry)
DE    Human calcium channel 27980/11.
KW    Plasmid pR14-5.3.3.1; Ca-flux assay; ss.
OS    Homo sapiens.
FH    Key             Location/Qualifiers
FT    polyA_signal    6215..6220
FT    /*tag=  a
FT    repeat_unit     1..252
FT    /*tag=  b
FT    /standard_name= Alu_repeat
FT    /note= "possible cloning artefact"
FT    CDS             253..6048
FT    /*tag=  c
FT    /note= "amino acids 358 to C-terminus
FT    i.e. Domains II to IV"
FT    misc_difference 3746
FT    /*tag=  d
FT    /note= "undefined"
PN    EP-507170-A.
PD    07-OCT-1992.
PF    23-MAR-1992; 104970.
PR    04-APR-1991; DE-110785.
PA    (FARB ) BAYER AG.
PI    Franz J, Rae P, Unterbeck A, Weingaertner B;
DR    WPI; 92-333446/41.
DR    P-PSDB; R27649.
PT    Cloned human neuronal calcium channel sub-types - useful in
PT    calcium flux assays to screen for neurone-specific calcium
PT    channel ligands
PS    Claim 2; Page 63-77; 101pp; German.
CC    Human neuroblastoma cell line, hippocampus, frontal and temporal
CC    cortex and visual cortex cDNA banks were screened with a probe
CC    containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
CC    pR14-5.3.3.1 overlaps with clone p1247-14.1.1.1 (see Q29263). The
CC    following differences are observed between the two sequences
CC    (nucleotide and position in pR14-5.3.3.1 given in brackets):
CC    1.Cytosine at position 520 (T: 3507); no change in deduced amino
CC    acid sequence. 2.Cytosine at position 775 (G; 3768); no change in
CC    deduced AA sequence. 3.Cytosine at position 1617 (T;4611).
CC    4.Adenosine at position 2360 (G; 5353). 5.deletion of 6 nucleotides
CC    at position 708 (CGGAAA; 3695-3700). 6. deletion of an Adenosine
CC    residue at position 1013 which leads to a stop codon at position
CC    1028-1030. 7. at position 3240 there are a further 2199 nucleotides
CC    of the 3'UTR which are absent from pR14-5.3.3.1. (The deletion of
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CC    Adenosine at position 1013 is thought to be a cloning artefact).
CC    The sequence can be inserted into a eukaryotic expression vector for
CC    use in transforming suitable host cells. Cell lines producing human
CC    neuronal calcium channel proteins can be used for screening for Ca
CC    channel ligands (agonists or antagonists). See also Q29259-Q29275.
SQ    Sequence   6232 BP;    1250 A;    1914 C;    1827 G;    1240 T;
SQ    1 Others;

Initial Score     =    139  Optimized Score  =    406  Significance =  8.44
Residue Identity  =    51%  Matches          =    490  Mismatches   =   334
Gaps              =    122  Conservative Substitutions              =     0

              X       10        20        30          40        50
            GTCGA-CTGGAACGAGACGACCTGCTCCAGACCAT-TCAG-CA-ATCCTGCTCTG-GGCTCC
             || || ||||  || |||| |  ||    | || |   || || | || | ||| |||| |
    GCCGCTGGTGGTGGAGCTGGGCCGCGACGGCGCGGGGGCCCGTGGGAGGCAAAGCCCGACCTGAGGCTGC
        1480 X   1490      1500      1510      1520      1530     1540

    60        70        80         90        100       110         120
    CAAGGGCTGAGATTACAGGTGTAACC-GAGATAAG--ACC-CTGGCTGAGTCAACGATGCACAAG-GCTCGA
      ||| |   ||   |  ||  | ||   |   ||  ||| | |||   | | || | | ||||| | |
    GGAGGCCCCCGAGGGC--GTCGACCCTCCGCGCAGGCACCACCGGCACCG-CGAC-AAGGACAAGACCCCCG
      1550      1560      1570      1580      1590      1600      1610

       130         140       150       160       170       180      190
    ATCCTAGGGA-TGGGA--GGGGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCCCTTTGCCAGCG
       |  ||||   |||  | | || ||| ||| | || ||||  |      ||    |||||    ||||
    CGGCGGGGGACCAGGACCGAGCAGAGGC-CCCGAAGGCGGAGAGCGGGGAGCC-CGGTGCCCGGGAGGAGCG
        1620      1630     1640       1650      1660      1670      1680

         200       210       220       230       240       250       260
    AAGGC-CCCAGGCGGCTGCCAGCAGC-ACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCCTG
       ||  || | | || |||| |||| |  ||   | | |||  | | ||  || ||||| | || |||
    GCCGCGGCCCGACCGCAGCCA-CAGCAAGGAGGCCGCGGGGCCCCCGGAGGCGC-GGAGCGAGCGCGGCCGA
        1690      1700     1710      1720      1730       1740      1750

        270       280       290       300       310       320       330
    GGCCGAGGCTCTGGGAGC-TCCG-TGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAG-GGTGGAGGAG
    |||| |||| | | | ||  |||  |||  |   |||   | | ||||  || || || | | |  ||||
    GGCCCAGGCCCCGAGGGCGGCCGGCGGCACCACCGGC---GCGGCTCCCCGGAGGAGGCGGCCGAGCGGGAG
        1760      1770     1780        1790      1800      1810      1820

         340       350      360       370       380       390
    TCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGC-AGGCCTTC-CCGATAC--AGGGC-TTCA
     || |  | ||| || |   | |||||| || |  || |  || ||| | | |||   | |||||  |
    CCCCGACGCCACCGCGCGCACCGGCACC-AG-G--ATCCGAGCAAGGAGTGCGCCGGCGCCAAGGGCGAGCG
         1830      1840     1850          1860      1870      1880

  400       410      420       430         440       450       460
    GAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAG--GTGGGAGATGTTGGTCTGGACGAATCGCAGACATTC
    | ||  || ||   | |  ||   ||    || |    |||||  |  |  | ||  ||   || | |
    GCGCGCGCGGCACCGCGGCGGCCCCCGAGCGGGGCCCCGGGAGGCGGAGAGCGGG--GAGGAGCCGGCGCGG
 1890      1900     1910      1920      1930      1940      1950

  470       480      490       500       510       520       530       540
    TGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTGACGTCCTCCAGAAGCGTTTGCAT
     || |  ||  |   || |||  ||| | ||   ||  || ||  | ||      |  ||||| |   ||
    CGGCACCGG--GCCCGGCACA--AGGCG-CAGCCTG-CTCACGAGGCTG------TGGAGAAG-GAGACCA-
 1960        1970       1980       1990       2000            2010
```

```
         550         560       570       580       590               600
  CTTAG-ACCCTGCCAC--AGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAG--GCT------CCAC
  |  || |    |||||  ||      | ||   ||      ||  | | ||||| ||  |||      ||||
  CGGAGAAGGAGGCCACGGAGAAGGAGGCTGAGATAGTGGAAGC-CGACAAGGAAAAGGAGCTCCGGAACCAC
 2020      2030      2040      2050      2060       2070      2080

       610       620        630       640         650       660       670
  AAGGCCTTGCAGTGCTTCT-CGTCCTGAAGATTGACGGCCACAGTGAC--TGGGTAATCTTTAAGCAGGTGG
   || ||  | ||     ||  | |||| |||   |  |  || |||||  |||||    |  |  ||  ||
  CAGCCCCGGGAGCCACACTGTGACCTGGAGA-CCAGTGGGACTGTGACTGTGGGTCCCATGCACACA-CTGC
2090      2100      2110       2120      2130      2140      2150

        680       690       700       710       720       730
  TCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTGGCTGAAGTAACAGTCAG----G
   ||| || || |||  |         |||| |||||  ||   | | | || || ||  ||| ||||
  CCAG-CACCTGTCTCCA---------GAAGGTGGAG--GAACAGCCAGAGGATGCAG--ACAATCAGCGGAA
2160       2170               2180        2190      2200         2210

740       750            760       770         780             790
  TGTCCCCCGCA--GGCA---AGGACTCAGCAGCAGCAACAGCA--GCA------ACAGGGAGGAATTTGGGC
   ||| | ||||  ||||   ||  | ||| | | | ||||  |  | |       ||| || |     ||||
  CGTCACTCGCATGGGCAGTCAGCCCCCAG-ACCCG-AACACTATTGTACATATCCCAGTGATGCTGACGGGC
  2220      2230      2240       2250       2260      2270      2280

 800       810        820             830       840       850
  TCCAGGCTGGCGCCAG-CACTGTC-ATCTCTG-----CCGGGGACCCCTCATGCCTGTGACAG----AGCAG
   |    || | |  || ||| |||  || | |      || |||||    | |||    | ||    || ||
  CC---TCTTGGGGAAGCCACGGTCGTTCCCAGTGGTAACGTGGACCTGGAAAGCCAAGCAGAGGGGAAGAAG
     2290      2300      2310      2320      2330      2340      2350

860       870        X
  GTCGTCTCGTTCCAGTCGAC
  |  |  | |   | |  |||
  GAGG--TGGAAGCGGATGACGTGATGAGGA
     2360      2370  X   2380


2. US-08-162-407-1' (1-879)
   Q51731       Plasmid pCisEBON for subcloning huHGF variants.

 ID   Q51731 standard; DNA; 10596 BP.
 AC   Q51731;
 DT   31-MAY-1994  (first entry)
 DE   Plasmid pCisEBON for subcloning huHGF variants.
 KW   Hepatocyte Growth Factor; HGF; variant; mutein; in vitro mutagenesis;
 KW   proteolysis resistant; liver; malignancy; CMV-driven;
 KW   Cytomegalovirus; episomal expression plasmid; ss.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   enhancer        1..611
 FT   /*tag=  a
 FT   /note= "CMV enhancer/promoter"
 FT   promoter        758..775
 FT   /*tag=  b
 FT   /label= SP6_promoter
 FT   misc_feature    845..849
 FT   /*tag=  c
 FT   /note= "SP6 RNA start"
 FT   misc_feature    902..966
 FT   /*tag=  d
```

```
FT   /function= cloning_linker
FT   polyA_signal    967..1107
FT   /*tag=  e
FT   /note= "SV40 poly A"
FT   misc_feature    1108..1531
FT   /*tag=  f
FT   /function= SV40_origin
FT   misc_feature    1580..4189
FT   /*tag=  g
FT   /label= EBNA-1
FT   misc_feature    4190..6374
FT   /*tag=  h
FT   /function= oriP
FT   repeat_region   4295..4887
FT   /*tag=  i
FT   /note= "family of repeats"
FT   misc_structure  5866..5978
FT   /*tag=  j
FT   /note= "dyad region"
FT   terminator      6375..6457
FT   /*tag=  k
FT   /label= HSV_TK_terminator_3'-end
FT   CDS             6975..7975
FT   /*tag=  l
FT   /phenotype= neomycin_resistance
FT   /note= "Tn5 neomycin_phosphotransferase gene"
FT   promoter        7975..8112
FT   /*tag=  m
FT   /label= TK_promoter
FT   misc_feature    8114..8594
FT   /*tag=  n
FT   /function= M13_ori
FT   misc_RNA        8595..10414
FT   /*tag=  o
FT   /label= delta_2a
PN   WO9323541-A.
PD   25-NOV-1993.
PF   17-MAY-1993; U04648.
PR   18-MAY-1992; US-884811.
PR   18-MAY-1992; US-885971.
PA   (GETH ) GENENTECH INC.
PI   Godowski PJ,  Lokker NA,  Mark MR;
DR   WPI; 93-386573/48.
PT   Hepatocyte growth factor variants - are resistant to proteolytic
PT   cleavage into its two-chain form, used to treat malignancies
PT   associated with HGF receptor
PS   Example 1; Fig 6; 87pp; English.
CC   Plasmid pCisEBON (a pRK5 derivative) is an episomal CMV driven
CC   expression plasmid. HuHGF variants with enhanced receptor binding
CC   activity were produced by site-directed mutagenesis. Stable
CC   populations of preferred HGF variants were obtained by transfecting
CC   human embryonic kidney 293 cells and then these were subcloned in
CC   pCisEBON. See R52940-R52949 for examples of pref. HGF variants.
SQ   Sequence   10596 BP;    2625 A;    2571 C;    3024 G;    2376 T;

Initial Score    =    134  Optimized Score  =    385  Significance =  8.09
Residue Identity =    48%  Matches          =    461  Mismatches   =   379
Gaps             =    108  Conservative Substitutions          =     0

              X       10         20         30        40         50         60
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            GTCGACTGGAACGAG-ACGACCTGCTCCA-GACCATTCAGCAATCCTGCTCTGGGCTCCCAA
               ||  || | ||| | ||   |   || || ||   || |          ||||    |
  GGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCA-GGAGGAGGGGCAGGAGGGGC-AGGAG
       2260 X    2270      2280      2290       2300      2310       2320

          70        80           90        100        110       120
  GGGCTGAGATTACAGGTGTA-ACCGAG--ATAAGACCCTG-GCTGAGTCA-ACGATGCACAAGGCTC-GAAT
  |||| |      |||| | |    |||    | || |  | |  | | ||   |  |||  |||  | | |
  GGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAG
       2330      2340      2350      2360      2370      2380      2390

   130        140        150       160       170       180         190
  CCTAGGGATGGG-AGG-GGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCC--CTTTGCCAGCGA
  |    ||| ||| ||| | ||| | |      || || ||     |         | |      | ||| ||
  CAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAG-GA
     2400      2410      2420      2430      2440      2450      2460

         200       210       220       230          240       250
  AGGCC----CCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCA---GCAGCAGCAGGAGCAACAGCTG
   || |     |||| ||  |   |||| | |||   ||| ||||| |   |||| |||||||| |   || |
  GGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
    2470      2480        2490      2500      2510      2520      2530

260        270       280       290       300       310       320       330
  CCTGGGC-CGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTGGAGG
     ||||  ||||  |  |||||   | ||     ||||  |  |||  |    ||||||| |||| | |||
  GAGGGGCAGGAGGGGC-AGGAGC-AGGAGG-----AGGGGCA--GGA-GCAGGAGGGGCAGGAGGG-GCAGG
    2540      2550        2560             2570       2580      2590

         340       350       360       370       380       390        400
  AGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGG-GCTTCAGA
  ||   ||| ||  | | |    |||| | |  ||| |      | |||       |   |||| ||   ||
  AG--GGGCAGGAGCAGGAGGGGCAGG-AGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGG
     2600      2610       2620      2630      2640      2650      2660

        410         420       430         440        450          460
  GCAAGCAGCTG--TGTGCAGGTGTCCTTCAGGAGGTG--GGAG-ATGTTGGTCTGGACG---AATCGCA-GA
  |  || ||| |   | ||||| |     ||||||| |  |||| | |  || | ||| |   |   ||| ||
  GGCAGGAGCAGGAGGGGCAGGAG-----CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGA
    2670      2680           2690      2700      2710      2720      2730

     470       480            490        500       510       520
  CATTCTGGTAGGGGCTGGA-----AGGTACATGAGGTG-ACAAAATGTATCTCGGTGTTGACGTCC---TCC
      | || |||||| |||     |||  || |||| | |  |   | |    ||    || |  |     |
  GGGGCAGG-AGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGC
        2740      2750      2760      2770      2780      2790      2800

  530       540        550         560       570       580       590
  AGAAGCGTTTGCATCTTAGAC-CCTGC--CACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAGG
  || ||     |||     | |    ||   |  | |   ||  ||   |  ||| |  |||| ||| || ||
  AGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGA-GCAG-GAGGGGC-AGG-AGGGG
      2810      2820      2830      2840      2850        2860        2870

   600       610        620        630       640       650       660
  CTCCACAAGGCCTTGCA-GTGCTTCTCG-TCCTGAAGATTGACGGCCACAGTGACTGGGTAATCTTTAAGCA
  |   |  |||    ||| | |   |  |  |  || ||  | | |   ||| ||  ||| |       ||||
  CAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAG-GA-GGGGCA-----GGAGCA
        2880      2890      2900      2910      2920             2930

   670        680       690       700         710        720         730
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  GGTGGT-CAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAG--GAGATGGGACT-GTGGCTGAAGT--AAC
  || |||  || |     || |     ||  | || |  || |  |||  || | | | ||| |  ||  |
  GGAGGTGGAGGCCGGGGTCGAGGAGGCA-GTGGAGGCCGGGGTCGAGGAGGTAGTGGAGGCCGGGGTCGAGG
   2940      2950      2960       2970      2980      2990      3000

         740       750       760       770       780         790       800
  AGTCA--GGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAA--CAGGGAGGAATTTGGGCTC
  ||  |  || | || |||  |   |||||   | |  ||| |  |  | ||  |  | | ||    |||
  AGGTAGTGGAGGCCGCCGGGGTAGAGGAC-GTGAAAGAGCCAGGGGGGGAAGTCGTGAAAGAGCCAGGGGGA
  3010      3020      3030       3040      3050      3060      3070

                 810           820       830         840       850
  CAGG--------CTGGCGCCA----GCACTGTCATCTCTGCCG-GGGAC-CCCTCATGCCTGTGACAGAGCA
   |||         ||| |  |    || | |   || | |  |   | |  | |||| |  ||  |  | |
  GAGGTCGTGGACGTGGAGAAAAGAGGCCCAGGAGTCCCAGTAGTCAGTCATCATCATCCGGGTCTC-CACCG
 3080      3090      3100      3110      3120      3130      3140

 860       870         X
  GGTCGTCTCGTTCCA-GTCGAC
   |  | | |  |||| || ||
  CGCAGGCCCCCTCCAGGTAGAAGGCCATTTTT
3150      3160      3170      3180


3. US-08-162-407-1’ (1-879)
   N91772       Human androgen receptor cDNA.

 ID   N91772 standard; cDNA; 3569 BP.
 AC   N91772;
 DT   19-MAR-1990  (first entry)
 DE   Human androgen receptor cDNA.
 KW   Human androgen receptor; monoclonal antibody; ploycional antibody;
 KW   cancer; probe.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             363..3122
 FT   /*tag=  a
 PN   WO8909791-A.
 PD   19-OCT-1989.
 PF   13-APR-1989; U01548.
 PR   14-APR-1988; US-182646.
 PA   (UYNC-) University of North Carolina.
 PI   French FS, Wilson EM, Joseph DR, Lubahn DB;
 DR   WPI; 89-324206/44.
 DR   P-PSDB; P93109.
 PT   DNA encoding androgen receptor protein - useful for transforming
 PT   eukaryotic hosts for protein expression and subsequent antibody prodn.
 PS   Disclosure; Fig. 4; 41pp; English.
 CC   Complementary DNA sequences derived from the cDNA may be used as probes
 CC   detect the presence of androgen receptor (AR mRNA in tumour cells, and to
 CC   detect AR gene defects using DNA hybrisidation assays.
 SQ   Sequence   3569 BP;   796 A;   1008 C;   975 G;   790 T;

Initial Score.   =     133  Optimized Score    =    399  Significance =  8.02
Residue Identity =     52%  Matches            =    495  Mismatches   =   323
Gaps             =     130  Conservative Substitutions                =     0

             X       10         20        30        40        50        60
             GTCGACTGGAACGAGAC-GACCTGCTCCAGACCATTCAGCAATCCTGCTCTGGGCTCCCAAG
             || |  ||||| ||  | | |  |||| ||   ||   | | | | | |  |||||   |||
  GGTAAGGGAAGTAG-GTGGAA-GATTCAGCCAAGCTCAAG--GAT--GGAAGTGCAG-TTAGGGCTGGGAAG
      330   X    340        350       360           370        380

          70           80          90       100       110         120
  GG-CTGAGAT-TACAG--GTGTAA--CCGAGATAAGACCCTGGCTGAGTCAACGATGCACA--AGGCTCGAA
  || ||    |   | |  ||  ||  || |   | || | |  | || ||   | | || |    || ||||
  GGTCTACCCTCGGCCGCCGTCCAAGACCTACCGAGGAGCTTTCCAGAATC--TGTTCCAGAGCGTGCGCGAA
 390       400       410       420       430         440       450

     130       140       150        160         170       180       190
  -TCCTAGGGATGGGAGGGGAGGGGCACCC-CAGGGTG-GAGCTC-CCCCCTCCTTCTTGCCCTTTGCCAGCG
   |  |   ||     ||     |||||||  |||  | |||| |  | |||||     |||  ||  | ||
  GTGATCCAGAACCCGGGCCCCAGGCACCCAGAGGCCGCGAGCGCAGCACCTCC-CGGCGCCAGTTTGCTGCT
 460       470       480       490       500       510        520

      200       210       220       230       240       250       260
  AAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCCTGGG
     ||  || || || | |||||||| |||    ||  |||||||||||||||| |||| |||| ||  | |
  GCTGCAGCA-GCAGCAG-CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAAGAG
530        540        550       560       570       580       590

    270       280        290          300       310       320       330
  CCGAGGCTCTGGGAGC-TCCGTGGCTTCTAGGG---CTATGGGACTCCTTGGGGGCAGCAGGGTGGAGGAGT
   | || | | || |||  | |  ||  | ||||     ||||  ||||    |  || |   || |||  |
  ACTAGCCCCAGGCAGCAGCAGCAGCAGC-AGGGTGAGGATGGTTCTCCCCAAGCCCATC---GTAGAG--GC
600       610       620        630       640       650          660

      340         350       360       370       380       390       400
  CCGGCTGGC-AC-TGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGGGCTTCAGAGC
  ||  | ||| || ||  |||  | | |   | || ||   |  |||     ||  |  | |  ||  || ||
  CCCACAGGCTACCTGGTCCTGGATG-AGGAACAGCAACCTTCACAG-----CCGCAGTCGGCCCTGGAGTGC
    670       680       690        700       710            720       730

      410       420       430       440       450        460       470
  AAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACG-AATCGCAGACATTCTG--G
   | |  | | | | ||||  | | |  |||   ||||  |  |   ||| ||  | |   |   | | |  |
  CACC--CCGAGAG-AGGTTGCGTCCCAGAGCCTGGAGCCGCCG---TGGCCGCCAGCAAGGGGCTGCCGCAG
          740        750       760       770          780       790

       480         490         500        510       520       530
  TAGGGGCTGGAAGGTAC--ATGAGG-TGAC-AAAATGTATC-TCGGTGTTGACGTCCTCCAGAAGCGTTTGC
   ||  ||  | |  | |  | |||| ||||  |  ||   | ||   |||| |  ||| | |  ||     |
  CAGCTGCCAGCACCTCCGGACGAGGATGACTCAGCTGCCCCATCCACGTTGTC--CCTGCTG-GGC---CCC
  800       810       820       830       840       850          860

540         550        560       570          580       590       600
  ATCTTAGACC--CTGCCACAG-TCTTCAGTTGCTCT---ATCCAGCGCTGGGCTAGGAAGAGGCTCCA--CA
  | |||   ||  ||    ||| |  || | ||  ||   |  || | ||| || |||   || | |||  ||
  A-CTTTCCCCGGCTTAAGCAGCTGCTCCGCTGACCTTAAAGACATC-CTGAGCGAGG-CCAG-CACCATGCA
       870       880       890       900        910        920        930

      610       620        630            640       650       660
  AGGCCTTGCAGTGCTTC-TCGTCCTGAAG----AT-TGACGGCCACAGTGACTGGGTAATCTTTAAGCAGG-
  |  |||| ||  ||  |  |  |  ||||    ||  ||  |||  |||  |  |||  | |   | | |||
  ACTCCTT-CA--GCAACAGCAGCAGGAAGCAGTATCCGAAGGCAGCAG-CAGCGGGAGAGC--GAGGGAGGC
         940         950       960       970        980         990

  670         680            690           700       710       720
  -TGGTCAG-TC-AACT--CTCTAA--AC-TTCACTT----TGAAGTTGGAGGAGATGGGACTGTGGC--TGA
   | |   | ||  |||  ||| ||  ||  | ||||     | | || ||  |  |  |||   | |   ||
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```
   CTCGGGGGCTCCCACTTCCTCCAAGGACAATTACTTAGGGGGCACTTCGACCATTTCTGACAACGCCAAGGA
  1000      1010      1020      1030      1040      1050      1060

        730          740         750        760       770       780
   ----AGTAA--CAGT-CAGGTGTCCCCCG--CAG-GCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAG
        ||||  ||||   |||||||   |  | | |   |||  | |  | |||| | | ||   ||||  |
   GTTGTGTAAGGCAGTGTCGGTGTCCATGGGCCTGGGTGTGGAGGC-GTTGGAGCATCTG-AG-TCCAGG--G
1070      1080      1090      1100      1110       1120        1130

  790       800       810       820          830       840       850
   GAATTTGGGCTCCAGGCTGGCGCCAGCACTGT---CATCTCTGCCGGGGACCCCTCATGCCTGTGACAGAGC
   |||     ||| | ||  || |   ||| |||   |  | ||   |||    || |  | ||||| |    |
   GAA---CAGCTTCGGG--GG-GATTGCA-TGTACGCCCCACTTTTGGGAGTTCCACCCG-CTGTG-CGTCCC
      1140        1150        1160      1170      1180       1190

   860       870        X
   AGGTCGTCTCGTTCCAGTCGAC
   |  || |   |  ||| | | |
   A-CTCCTTGTGCCCCATTGGCCGAATGCAAAG
1200       1210      1220      1230


4. US-08-162-407-1’ (1-879)
   Q43423        Sequence encoding the 10E3B (mouse) transcription

 ID   Q43423 standard; cDNA; 739 BP.
 AC   Q43423;
 DT   01-DEC-1993  (first entry)
 DE   Sequence encoding the 10E3B (mouse) transcription cofactor ("DCoH")
 DE   protein.
 KW   Transcription cofactor; intermolecular interaction; ss.
 OS   Homo sapiens
 PN   WO9312133-A.
 PD   24-JUN-1993.
 PF   15-DEC-1992; U10866.
 PR   17-DEC-1991; US-809436.
 PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
 PI   Crabtree GR,  Mendel DB;
 DR   WPI; 93-214087/26.
 PT   Transcriptional cofactors - in which intermolecular interactions
 PT   between transcription factors are enhanced, useful to regulate
 PT   co-ordinated gene expression, e.g. for gene therapy
 PS   Disclosure; Page 59; 79pp; English.
 CC   The transcriptional cofactors (DCoH) are relatively small peptides
 CC   having a domain of between 20-50 AAs which is lipophilic. They
 CC   normally exist as dimers in solution and are conserved across
 CC   mammalian species. The cofactors bind to at least one of the HNF-1-
 CC   alpha dimer and HNF-1-beta and their heterodimers.
 SQ   Sequence   739 BP;    202 A;    179 C;    169 G;    189 T;

Initial Score    =    129  Optimized Score  =    275  Significance =  7.75
Residue Identity =    49%  Matches          =    339  Mismatches   =   252
Gaps             =     93  Conservative Substitutions             =     0

          250       260       270       280        290       300       310
   GCAGCAGGAGCAACAGCTGCCTGGGCCGAGGCTCTGGGAGCTCC-GTGGCTTCTAGGGCTATGGGACTCCTT
             ||   ||||   | ||||||     | |||  || |   || | |   ||  ||| ||   |
             CACAGGCTG--AGCGCCGAG-----GAGAGGACCAGCTACTGCCAAACCTGAGGG-CT--GT
             X         10              20        30        40          50
        320       330        340       350          360       370
  GGGGGCAGCAGGGTGGAGGAGTCCG-GCTGGCACTGCACCTCCAGGCA---CCGAGAGAAATTCT--GGCAG
  ||||   | |  | | || || ||| | ||   ||  | || || |||   ||     |||  ||    |||
  GGGG--TGGAATGAGTAGAAGGCCGAGATG---CT--ATCTTCAAGCAGTTCCATTTTAAAGACTTCAACAG
          60        70        80             90       100       110

  380       390       400          410        420        430         440
  GCCTTCCCGATACAGGGCTTCAG-AG-CAAGCA-GCTG-TGTGCAGG-TGTCCTTCAGGA--GGTGGGAGAT
  | |||   | | || | |   || || |  ||| ||||    || ||    || ||  ||  |||   |  |
  GGCTTTTGGCTTCATGACAAGAGTAGCCCTGCAGGCTGAAAAGCTGGACCACCATCCCGAGTGGTTTAACGT
  120       130       140       150       160       170       180

        450        460          470       480       490        500
  GTTGGTC-TGGACGA-ATCGC--AGA-CATTCTGGTAGGGGCTGGAAGGTACATG-AGGTGACA-AAATGTA
  ||    |  || | | ||| |   || ||  |  | | | || ||    |   || | | || | |||  |
  GTACAACAAGGTCCATATCACCTTGAGCACCCATGAATGTGCCGG--TCTTTGTGAACGGGATATAAACCTG
190       200       210       220       230         240       250

  510       520       530        540         550       560       570
  TCTCGGTGTTGACGTCCTCCAGAAGC-GTTTGCAT--CTTAGACCCTGCCACAGTCTTCAGTTGCTCTATCC
   | | |  |   ||    | ||  || || |  ||  | |||| |   ||  | |||| | |||||
  GC-CAGCTTCATCG--AACAAGTCGCCGTGTCTATGACATAGATCTACCCTGACTCTT-ATTTGCTTGGGGG
260        270         280       290       300       310        320

   580       590       600        610       620        630       640
  AGCGCTGGGCTAGGAAGAGGCTCC-ACAAGGCCTTGCAGTGCTTCTCGTCC-TGAAGATTGACGGCCACAGT
  |  |   | || ||| ||||  || |  | |     ||  |   || | || ||     ||||     ||||
  AAGGAGTGACT-GGAGGAGGAACCTAGGAAGGGAACCAAGGAGGCTGGCCCTTGCTCCCTGACTCTTTCAGT
  330        340       350       360       370       380       390

   650       660         670         680               690       700
  GACTGGGTAATCTTTAAGCA----GGTGGTCA--GTCAAC-----TCTCT-AAAC--TTCACTTTGAAGTTG
  |||       ||  || |||    ||  ||||  ||||||        || | ||  ||| || ||    |
  GACCACCACCTCCCTATGCAGAAGGGATGTCAATGTCAACAGCAGGGACTGAGACCTTTCTCTGTGCCACTC
 400       410       420       430       440       450       460       470

     710       720       730       740       750       760       770
  GAGGAGATGGGACTGTGGCTGAAGTAACAGTCAGGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGC
         ||| || || |  | || ||| | |  ||      ||   |      || | || ||   |  |
  TCCTCACTGGGGCTCTGCC--ATGTTACACTAATTTG-AATAAGCTCTCCCTTTTTCTGTAG-AGTTCC--C
         480         490       500        510       520        530

   780       790       800        810         820       830       840
  AGCAACAGGGAGGAATTTGGGCTCCAGGCTGGC-GCCAGCAC--TGTCATCTCTGCCGGGGACCCCT--CA-
  |||  |    || |||    | |||||||||||  |  |  |  | ||  | ||  |  |  |   |  ||
  AGCCTC----AGTAAT----GTTCCAGGCTGGCTTCTTGTTCCTTTTCTACCCTTTCTAGTTCATTTTCCAA
   540               550       560       570       580       590       600

         850       860            870          X
  --TGCCTGTGACAGAGCAGGTCGT-----CTCGTTCCAG-TC-GAC
    |  ||||||| | |||| | | |     | |  | ||| ||  ||
  GGTAGCTGTGATAAAGCATGACATAAAAGCCCAATTCAGATCCTACTAATAAAACA
         610       620         630       640     X 650

5. US-08-162-407-1' (1-879)
   Q30999         Notch clone hN3k full length clone.

 ID   Q30999 standard; DNA; 3234 BP.
 AC   Q30999;
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DT   01-APR-1993  (first entry)
DE   Notch clone hN3k full length clone.
KW   Human; Notch; plasmid; cDNA; clone; hN2k; expression library;
KW   adhesion domain; Drosophilla; epidermal growth factor; EGF;
KW   EGF-like; homologous; repeat; ELR; ELR-11; ELR-12; PCR;
KW   polymerase chain reaction; primer; cloning vector; Delta; Serrate;
KW   neurogenic; toporythmic; homotypic; heterotypic; differentiation;
KW   quantitation; antibody; ss.
OS   Homo sapiens.
PN   WO9219734-A.
PD   12-NOV-1992.
PF   01-MAY-1992; U03651.
PR   03-MAY-1991; US-695189.
PR   14-NOV-1991; US-791923.
PA   (INDV ) UNIV INDIANA FOUND.
PA   (UYYA ) UNIV YALE.
PI   Artavanis-Tsakonas S, Blaumueller CM, Fehon RG, Muskavitch MAT;
PI   Rebay I, Shepard SB;
DR   WPI; 92-398861/48.
PT   Human Notch and Delta DNA and protein sequences - used for study
PT   and manipulation of differentiation processes
PS   Claim 132; Fig 23; 239pp; English.
CC   The sequence given represent the full length nucleotide sequence of
CC   human Notch contained in plasmid cDNA clone hN3k.  A human expression
CC   library was constructed and screening assays were carried out on the
CC   basis of positive binding to the adhesion domain of Notch, ie. the
CC   region that is homologous to Drosophilla epidermal growth factor
CC   (EGF)-like (homologous) repeat (ELR)-11 and -12.  Alternatively the
CC   sequence could be isolated by amplification using polymerase chain
CC   reaction (PCR) primers.  The isolated gene may be inserted into a
CC   cloning vector and expressed.  The Notch gene and also the Delta and
CC   Serrate neurogenic genes are designated "toporythmic" genes.  The
CC   proteins they encode are involved in specific homo- or heterotypic
CC   interactions crucial to differentiation.  The quantitation of mRNA
CC   for human Notch and Delta and adhesive molecules, and study of its
CC   expression are possible using the DNA and antibodies raised against
CC   the Notch and Delta proteins.
SQ   Sequence   3234 BP;    608 A;    1130 C;    999 G;    497 T;

Initial Score    =    128  Optimized Score    =    272  Significance =  7.68
Residue Identity =    49%  Matches            =    326  Mismatches   =   252
Gaps             =     75  Conservative Substitutions              =     0

              X       10         20          30           40          50
              GTCGACTGGAACGAGACG-ACCTG--CTCCAGACCATTCAG---CAAT-CCTGC-TCTGGGC
               ||  | ||   | |  | ||| |  | || || ||  |||   |  | |||||  |  |||
    CAATACAACCCTCTGCGGGGGAGTGTGGCACCAGGCCCCCTGAGCACACAGGCCCCCTCCCTGCAGCATGGC
      2610    X 2620      2630      2640      2650      2660      2670

        60            70         80        90          100       110
    TCCCAAGG---GCTG-AGATTACAGGTG-TAACCGAGATAAGACCCTG--GCTGAGTCAACGATGCACAAGG
         |||   |||| | | ||    || |  | | |    | ||| |  | |||| | || | || |  |
    ATGGTAGGCCCGCTGCACAGTAGCCTTGCTGCCAGCGCCCTGTCCCAGATGATGAG-CTACCAGGC-CCTGC
    2680      2690      2700      2710      2720      2730       2740

  120       130       140       150             160       170       180
    CTCGAATCCTAGGGATGGGAGGGGAGGGGCACC----CCAG--GGTGGAGCTCCCCCCTCCTTCTTGCCCTT
    |  | | ||   || |||      ||   ||||     |||     | || | | ||| |     |  |
    CCAGCACCC---GGCTGGCCACCCAGCCTCACCTGGTGCAGACCCAGCAGGTGCACCCACAAAACTTACAGA
    2750         2760      2770      2780      2790      2800      2810
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      190       200       210        220       230       240        250
  TGC--CAGCGAAGGCCCCAGGCGGCTGCCA-GCAGCACCAGTGTGAGAGGCAGCAGCAG-CAGCAGGAGCA-
  |||  ||||  |  |  ||| | ||   ||  ||||| |||    | || | ||||| | || ||  | ||
  TGCAGCAGCAGAACCTGCAGCCAGCAAACATCCAGCAGCAG---CAAAGCCTGCAGCCGCCACCACCACCAC
   2820      2830      2840      2850         2860      2870      2880

          260       270       280       290       300       310       320
  -ACAGCTG--CCTGGGCCGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCT-TGGGGGCAGC
   ||||| |  ||| |||    ||||  | ||| | | |||  |  ||||   | |  ||||  | ||  |||
  CACAGCCGCACCTTGGCGTGAGCTC-AGCAGC-CAGCGGCCACCTGGGC-CGGAGCTTCCTGAGTGGAGAGC
    2890      2900       2910       2920      2930       2940      2950

         330       340       350       360       370       380        390
  AGGGTGGAGGAGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGA-TACA
   | |    | || |  || | |||||  || ||| ||| |  | |   | |   |    || ||| |  | |
  CGAGCCAGGCAGACGTGCAGCCACTGGGCC-CCA-GCAGCCTG-GCGGTGCACACTATTCTGCCCCAGGAGA
     2960      2970      2980        2990       3000      3010      3020

          400       410        420         430       440       450
  GGGC--TTCAGAGCAAGCAGCTG-TGTGCAGG-TG-TCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAAT
  |  |    | |  || |  ||||   | |  | || |||  |  | |   | ||     | ||  ||||
  GCCCCGCCCTGCCCACGTCGCTGCCATCCTCGCTGGTCCCACCCGTGACCGCAG-CCCAGTTCCTGACGCCC
      3030      3040      3050      3060      3070       3080      3090

 460        470       480       490       500       510       520
  CGCAGACA-TTCTGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTGACGTCCTCCAG
  | |   ||   | | ||    || |      | || |  ||||| |     | | |     ||  ||| |||
  CCCTCGCAGCACAGCTA-CTCCTCG------CCTGTG--GACAACA---CCCCCAG---CCACCACCTACAG
     3100      3110             3120        3130            3140      3150

530       540        550       560       570       580          590
  AAGCGTTTGCATCTTA-GACCCTGCCACAGTCTTCAGTTGCTCTATCCAGCGCTGGGC---TAGGA-AGAGG
    || | | | | | | |    ||   |  ||||| | | || | |  || |||   |   |  ||  || |
  GTGCCTGTTCCTGTAATGGTAATGATCCGATCTTCGGATCCT-TCTAAAG-GCTCATCAATTTTGATCGAAG
        3160      3170      3180      3190        3200      3210      3220

   600       610       620
  CTCCACAAGGCCTTGCAGTGCTTCT
  |||| | |  | | |
  CTCC-CGACTCATGG
         3230   X

6. US-08-162-407-1' (1-879)
   N90369       DNA sequence of alpha-2 plasmin inhibitor deriv.

 ID   N90369 standard; DNA; 1521 BP.
 AC   N90369;
 DT   18-OCT-1989  (first entry)
 DE   DNA sequence of alpha-2 plasmin inhibitor deriv.
 KW   Alpha-2 plasmin inhibitor deriv.; antithrombin-active
 KW   serine protease inhibitor; thrombin.
 OS   Escherichia coli
 FH   Key             Location/Qualifiers
 FT   CDS             142..1497
 FT   /*tag=  a
 FT   misc_feature    1..6
 FT   /*tag=  b
 FT   misc_feature    7..24
```

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FT   /*tag=  c
FT   misc_signal     25..141
FT   /*tag=  d
PN   EP-236013-A.
PD   02-AUG-1989.
PF   19-JAN-1989; 100851.
PR   28-JAN-1988; JP-15762.
PA   Hoechst Japan Ltd.
PI   Toba M, Tone M, Kikuno R, Hashimoto T;
DR   WPI; 89-221985/31.
PT   Alpha-2 plasmin inhibitor deriv. - having reactive site cleavable with
PT   plasmin deleted or replaced to give protein active in inhibiting blood
PT   coagulation.
PS   Disclosure; ; 16pp; English.
CC   The DNA encodes an alpha-2 plasmin inhibitor (API) deriv., with the
CC   normal API reactive site cleavable with plasmin deleted or replaced
CC   with that of antithrombin active serine protease inhibitor cleavable with
CC   thrombin. It is active in inhibiting blood coagulation, and can be used
CC   in preventitive treatment or therapy of cardiovascular disturbances or
CC   diseases. The DNA sequence is expressed in plasmid p-alpha-AP216.
CC   Misc. feature b is the EcoRI site from the EcoRI linker used in the
CC   cloning; c is a non-coding region upstream of the 5' end; and d
CC   corresponds to the peptide contd. only in the alpha-2-PI (the signal
CC   peptide coding portion or anchor portion). When the host is an animal
CC   cell, the gene carrying the anchor portion is incorporated into the
CC   vector, but when host is prokaryotic, this gene is deleted, and an ATG
CC   codon is added, then incorporated. See also P90534 for encoded peptide,
CC   and P90537.
SQ   Sequence   1521 BP;   296 A;   503 C;   435 G;   287 T;

Initial Score     =    123  Optimized Score  =    355  Significance =  7.33
Residue Identity  =    50%  Matches          =    426  Mismatches   =   318
Gaps              =    102  Conservative Substitutions              =     0

     80        90       100       110       120       130         140
    GTAACCGAGATAAGACCCTGGCTGAGTCAACGATGCACAAGGCTCGAATCCTAGGGAT--GGGAGGGGAGGG
               ||  ||  ||||  | ||  |  | ||| ||| |   ||   ||| |   || |   ||
              GAATTCC--GGCT--GGCAGGGGAGAACATGGCGCTGCTCTGGGGGCTCCTGGTGCTCAGCT
              X         10          20         30         40         50

    150       160        170         180       190       200       210
    GCACCCCAGGGTG-GAGCTCCCCCCTCCTTCT--TGCCCTTTGCCAGCGAAGGCCCCAGGCGGCTGCCAGCA
    |    || |  ||  ||  |||  |||| | |  | |||| ||   || | ||  ||    ||||| ||||
    G--GTCCTGCCTGCAAGGCCCCTGCTCCGTGTTCTCCCCTGTGAGCGCCATGGAGCCCTTGGGCTGGCAGC-
      60        70        80        90       100       110       120

     220       230       240       250        260       270       280
    GCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAG-CAACAGCTGCCTGGGCCGAGGCTCTGGGAGCTCCGTG
      || || |     ||| | | ||| |||||| | |  ||  | ||     | ||  |  || | |   | |
    TAACTAGCG-----GGCCGAACCAGGAGCAGGTGTCCCCACTTACCCTCCTCAAG--TTGGGCAACCAGGAG
    130            140       150       160       170         180       190

    290       300        310       320       330         340       350
    GCTTCTAGGGCTATGGGACT-CCTTGGGGGCAGCAGGGTGGAGGAGTC--CGGCTGGCACTGCACCTCCAG-
     ||  |  ||| |   |||| || ||  |  ||        |||||||  | || |  ||  |||| ||||
    CCTGGT--GGCCA---GACTGCCCTGAAG--AG--TCCCCCAGGAGTCTGCAGCAGAGACCCCACC-CCAGA
           200          210           220       230       240        250

      360       370         380         390         400       410       420
    GCACCGAGAGAAATTCTGG--CAGGCCTTCCCG--ATACAGGGC--TTCAGAGCAAGCAGCTGTGTGCAGGT
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     |||  ||   | |  ||||  | |||| |   |   | ||  ||    | |  |   | | || |  ||
     GCA--GACCCACAGGCTGGCCCGGGCCATGATGGCCTTCACTGCCGACCTGTTCTCCCTGGTG-GCTCAAAC
          260       270       280       290       300       310        320

           430       440       450       460       470       480       490
     GTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAGACATTCTGGTAGGGGCTGGAAGGTACATGA
     ||||  | |          ||  | |||    |  |  |  | |   ||||    | ||  |     ||  |
     GTCCACCTGCCCCAACCTCATCCT-GTCACCCCTGAGTGTGGCC---CTGGCGCTGTCT-CACCTGGCACTA
         330       340        350       360          370        380       390

         500       510       520        530        540         550       560
     GGTGACAAAATGTATCTCGGTGTTGACG-TCCTCCAGAAGC-GTTTGCA-TCTTA-GACCCTGCCACAGTCT
     ||||   | |   | | || ||  || | | |  |||  || |   |||  || | | ||||||| |   |
     GGTGCTCAGAACCA-CACGTTGCAGAGGCTGCAACAGGTGCTGCACGCAGGCTCAGGGCCCTGCCTCCCCCA
            400        410       420       430       440       450       460

                 570       580       590       600       610       620
     TCAGTTG------CTCTATCCAGCGCTGGGCTAGGAAGAGGCTCCACAAGGCCTTGCAGTGCTTCTCGTCCT
     || | ||      ||||  |  |  ||||||   |  |  | |||  |  | ||  ||| | |   | | |
     TCTGCTGAGCCGCCTCTGCCAGGACCTGGGCCCCGGCG-CGTTCC-GACTGGCTGCCAG-GATGTACCTGCA
           470       480       490        500        510        520       530

     630         640            650        660         670       680
     GAA--GATTGACGGCCACAG-TGA----CTGG-GTAATCTTTA-AGC-AGGTGGTCAGTCAACTCTC-TAAA
     |||  ||||  |   || ||  ||    ||||   ||||   | ||| |  |||   | |||  | | | |
     GAAAGGATTTCCCATCAAAGAAGATTTCCTGGAACAATCCGAACAGCTATTTGG---GGCAAAGCCCGTGAG
            540       550       560       570       580          590

    690       700       710       720       730          740            750
     CTTCACTTTGAAGTTGGAGGAGATGGGACTGTGGCTGAAGTAACAGTCA---GGTG-----TCCCCCGCAGG
     | | ||    |||  |||  ||||  |||  ||||  ||  | ||  ||   ||||       || || |||
     CCTGACGGGAAAGCAGGA--AGAT--GAC-CTGGC--AAACATCAACCAATGGGTGAAGGAGGCCACGGAGG
   600       610         620            630       640       650       660

          760       770       780        790        800       810        820
     CAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAG-GAATTTG-GGCTCCAGGCTGGCGCCA-GCACTGTC
       | || |||| |    |       ||  | || ||  |   ||  ||| |       |||||  ||||  |
     GGAAGATTCAGGAATTCCTCTCTGGGCTGCCGGAAGACACCGTGTTGCTTCTCCTCAACGCCATCCACTTCC
        670       680       690       700       710       720       730

              830       840        850        860       870         X
     A---TCTCTGCCGGGGACCCCTCATG-CCTGTGACAGA-GCAGGTCGTCTCGTTCCA-GTCGAC
     |   | ||||  | ||| |     || || | | |  |  |||   | ||| |||||  | |||
     AGGGTTTCTG--GAGGAACAAGTTTGACCCGAGCCTTACCCAGAGAGACTCCTTCCACCTGGACGAGCAGTT
      740         750       760       770       780       790       800

     CA


7. US-08-162-407-1’ (1-879)
    Q04035           Stem cell leukaemia (SCL) gene.

  ID   Q04035 standard; cDNA; 4091 BP.
  AC   Q04035;
  DT   10-SEP-1990  (first entry)
  DE   Stem cell leukaemia (SCL) gene.
  KW   Stem cell leukaemia; leukaemia; SCL; AML; ALL;
  KW   haematopoietic; aplastic anaemias; ds.
  OS   Homo sapiens.
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 FH   Key                 Location/Qualifiers
 FT   CDS                 1..618
 FT   /*tag=  a
 PN   US7437819-A.
 PD   6-MAR-1990.
 PF   17-NOV-1989; 437819.
 PR   17-NOV-1989; US-437819.
 PA   (USSH) Nat Inst of Health.
 PI   Kirsch IR, Begley CG;
 DR   WPI; 90-132045/17.
 DR   P-PSDB; R04127.
 PT   Human stem cell leukaemia (SCL) gene -
 PT   and haematopoietic growth and differentiation factor encoded by
 PT   it, for diagnosing haematopoietic malignancy and bone marrow
 PT   disorders.
 PS   Disclosure; p; English.
 CC   SCL gene is associated with stem cell leukaemia manifesting myeloid
 CC   and lymphoid differentiation capabilities. Gene allows recognition
 CC   of the disorders, and gene product has uses similar to those of
 CC   known growth factors.
 SQ   Sequence   4091 BP;   961 A;   1008 C;   1025 G;   1097 T;

Initial Score     =    117  Optimized Score    =    391  Significance =  6.91
Residue Identity  =    50%  Matches            =    480  Mismatches   =   338
Gaps              =    129  Conservative Substitutions                =     0

               X       10        20        30        40         50        60
               GTCGACTGGAACGAGACGACCTGCTCCAGACCATTCAGCA-ATCCTGCTCTGGGCTCCCAAG
                ||  |  ||| ||||   ||| | || | ||||  || | |||    ||| ||   |||||
     GGACAAGAAGCTCAGCAAGAATGAGA--TCCTCCGCCTGGCCATGAAGTATATCAACTTCTTGG---CCAAG
           290 X     300         310       320       330       340

             70         80        90       100       110       120       130
     -GGCTGAGATTA-CAGGTGTAACCGAGATAAGACCCTGGCTGAGTCAACGATGCACAAGGCTCGAATCCTAG
       ||| | || | |||| | |   |||     |||| | |   | ||| ||    |||||  |   |  | |
     CTGCTCA-ATGACCAGGAGGA--GGAG--GGCACCCAGCC--GGCCAA-GACTGGCAAGGACCCTGTGGTGG
    350        360         370         380          390       400       410

               140       150       160              170       180
     G----GATGGGAGGGGAGGGGCACCCCAGGGTGGAGCTCCCC-------CCTCCTTCTTGCC---CTTTGCC
     |    | |||| | ||||| |       ||| || || ||||       |||||| |  | |   |||| ||
     GGGCTGGTGGGCGTGGAGGTGGGGGAGGGGGCGGCGCGCCCCCAGATGACCTCCTCCAAGACGTGCTTTCCC
          420       430       440       450       460       470       480

   190       200       210       220       230       240         250
     AGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGG--AGCAAC----A
       | ||  | |||    |||| | ||||| ||  ||   | ||||||  ||||  | ||  ||| ||    |
     --CCAA--CTCCA----GCTG-CGGCAGCTCC-CTGGATGCGGCAGC--CAGC--CCGGACAGCTACACGGA
            490            500        510       520           530       540

       260       270       280       290        300       310       320
     GCTGCCTGGGCCGAGGCTCTGGGAGCTCCGTGGCTTC-TAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTG
     |  ||| | ||| | || |  |  || |   |||| | |   || |||   || | ||  | |   | || |
     GGAGCCCGCGCCCAAGCACACG--GCCCGCAGGCTCCATCCTGCCATG---CTGCCTGCCGCC--GATGGAG
          550       560         570       580          590       600

      330         340       350          360        370       380       390
     GAGGAGTCCG--GCTGGCACTGCACCTCCAGG--CA-CCGAGAG-AAATTCTGGCAGGCCTTCCCGATACAG
       ||    ||  | |||  |||  || |||||  || ||  |||    ||||   ||||      |||   |
     CCGGCCCTCGGTGATGGGTCTGGGCCACCAGGATCAGCCAGGAGGGCGTTCT--TAGGCTGCTGGGATGGTG
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  610       620       630       640       650         660       670

       400             410       420       430       440       450
  GGCTTCAGAGCAAG------CAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGAC-GAA
  |||||||| ||| |      |||   || || | | ||   ||  ||| ||  ||  ||   ||   | | |
  GGCTTCAGGGCAGGTGGGGTCAGAATTGGGCGGCTCTCAAGCA--AGGCGGTCGA-CTTCAACTTTCCTGGA
  680       690       700       710       720         730        740

  460       470       480       490         500       510        520
  TCGCAGACATTCTGGTAGGGGCTGGAAGGTACATGAGG-TGAC-AAAATGTATCTCGGTGTTG-ACGTCCTC
  |  | || | | ||| |  | ||  |  |  | || || || |     ||| ||  |     | |||   |
  TGTCTGA-ACTTTGGGA-AGCCTTTACTGACCCTGGGGCTGGCTTTTCTGTTTCCTGTACCAGTACGAGAT-
   750        760        770       780       790       800       810

   530        540              550       560       570       580
  CAGAAGCGT-TTGCA---TCTTAG--AC--CCTGCCACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCT-AG
  |||||   |   |||   |  |||  ||    ||  | || |  ||   | ||| |||  | ||   || ||
  CAGAAAAATGGAGCAAAGTGGTAGGTACTTTTTGTGA-AGACGGCA--CGGTCT-TCC--CTCTTCCCTCAG
    820       830       840       850        860            870       880

  590       600       610         620        630        640        650
  --GAAGAGGCTCCACAAGGCCTTGCAGTGCT--TCTCGTC-CTGAAGATTGAC-GGCCACAGTGA-CTGGGT
      | |  || | ||||   |   || |||    | ||| |||    | | | ||     | || |   ||
  TCCCAAATCCTTCCCAAG---TAAGAG-GCTGGAGTTGTCACTGCTTTTGGCCTGGAGTTTGGGATCCCTGT
        890          900        910       920       930       940

     660        670       680       690       700       710       720
  AATCTTTAAG-CAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTGG--C
    |   |||| |  | |||  |||| |||||  | ||      |   |  |     |    | || | |  |
  CTTTCCTAAGACCTGGGGT-TGTCAGCTCTC--ATCTGAGGCATCCAGCAGTCTCTGCCTTGCCTTTAGCCC
950       960        970         980       990      1000      1010

      730       740        750       760       770        780       790
  TGAAGTAACAGTCAGGTGTCCCCCG-CAGGCAAGGACTCAGCAGCAGCAACAGCA-GCAACAGGGAGGAATT
        | | | | || ||  || |   ||  |   ||   ||     |   | |  ||| ||      |||
  CTCCCAAGCTGGCTGGGGTGGCCTGTGTGGGCACTTCTGTCCATATTTATAGGTACCCAATAGCTGCCCATT
1020      1030      1040      1050      1060      1070      1080      1090

         800       810       820        830       840       850
  ---TGGGCTCCAGGCTGGCGCCAGCACTGTCAT-CTCTGCCGGGGACCCCTCATGCCTGTGACAGAG---CA
     || || |||  ||    ||||  || |  |  ||   |  |    ||  ||| |||   |||||   ||
  TCGTGAGCCCCA-TCTTCACCCAGGCCTATGTTGATCCATCCAGCTTGCCAGATG-CTG---CAGAGTCACA
        1100       1110      1120      1130      1140          1150

 860       870        X
  GGTCGTCTCGTTCCAGTCGAC
   | | ||  | | |  ||  |
  AG-CCTCGAGGTGCCTTCTTCAGGGCCTGGT
  1160      1170      1180

8. US-08-162-407-1' (1-879)
   Q05330        Stem cell leukaemia (SCL) gene.

ID   Q05330 standard; DNA; 4199 BP.
AC   Q05330;
DT   10-SEP-1990  (first entry)
DE   Stem cell leukaemia (SCL) gene.
KW   Stem cell leukaemia; leukaemia; SCL; AML; ALL;
KW   haematopoietic; aplastic anaemias; ds.
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OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             85..726
FT   /*tag=  a
PN   US7437819-A.
PD   6-MAR-1990.
PF   17-NOV-1989; 437819.
PR   17-NOV-1989; US-437819.
PA   (USSH) Nat Inst of Health.
PI   Kirsch IR, Begley CG;
DR   WPI; 90-132045/17.
DR   P-PSDB; R05857.
PT   Human stem cell leukaemia (SCL) gene -
PT   and haematopoietic growth and differentiation factor encoded by
PT   it, for diagnosing haematopoietic malignancy and bone marrow
PT   disorders.
PS   Disclosure; p; English.
CC   SCL gene is associated with stem cell leukaemia manifesting myeloid
CC   and lymphoid differentiation capabilities. Gene allows recognition
CC   of the disorders, and gene product has uses similar to those of
CC   known growth factors.
SQ   Sequence   4199 BP;   966 A;   1052 C;   1036 G;   1137 T;   8 Others;

Initial Score    =    117  Optimized Score  =    391  Significance =  6.91
Residue Identity =    50%  Matches          =    480  Mismatches   =   338
Gaps             =    129  Conservative Substitutions          =     0

            X       10        20        30        40         50        60
            GTCGACTGGAACGAGACGACCTGCTCCAGACCATTCAGCA-ATCCTGCTCTGGGCTCCCAAG
             ||  |  ||| ||||   ||| | || | ||||  || | |||    ||| ||   |||||
  GGACAAGAAGCTCAGCAAGAATGAGA--TCCTCCGCCTGGCCATGAAGTATATCAACTTCTTGG---CCAAG
390       400       410         420       430       440       450

          70         80        90       100       110       120       130
  -GGCTGAGATTA-CAGGTGTAACCGAGATAAGACCCTGGCTGAGTCAACGATGCACAAGGCTCGAATCCTAG
    ||| | || | |||| | |   |||     |||| | |   | ||| ||    |||||  |   |  | |
  CTGCTCA-ATGACCAGGAGGA--GGAG--GGCACCCAGCC--GGCCAA-GACTGGCAAGGACCCTGTGGTGG
   460        470         480         490          500       510       520

            140       150       160              170       180
  G----GATGGGAGGGGAGGGGCACCCCAGGGTGGAGCTCCCC-------CCTCCTTCTTGCC---CTTTGCC
  |    | |||| | ||||| |       ||| || || ||||       |||||| |  | |   |||| ||
  GGGCTGGTGGGCGTGGAGGTGGGGGAGGGGGCGGCGCGCCCCCAGATGACCTCCTCCAAGACGTGCTTTCCC
         530       540       550       560       570       580       590

190       200       210       220       230       240         250
  AGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGG--AGCAAC----A
    | ||  | |||    |||| | ||||| ||  ||   | ||||||  |||| | ||  ||| ||    |
  --CCAA--CTCCA----GCTG-CGGCAGCTCC-CTGGATGCGGCAGC--CAGC--CCGGACAGCTACACGGA
           600            610        620         630         640       650

    260       270       280       290        300       310       320
  GCTGCCTGGGCCGAGGCTCTGGGAGCTCCGTGGCTTC-TAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTG
  |  ||| | ||| | || |  |  || |   |||| | |   || |||   || | ||  | |   | || |
  GGAGCCCGCGCCCAAGCACACG--GCCCGCAGGCTCCATCCTGCCATG---CTGCCTGCCGCC--GATGGAG
         660       670         680       690          700         710

   330         340       350          360         370       380       390
  GAGGAGTCCG--GCTGGCACTGCACCTCCAGG--CA-CCGAGAG-AAATTCTGGCAGGCCTTCCCGATACAG
    ||    ||  | |||  |||  || |||||  || ||  |||    ||||   ||||      |||   |
    CCGGCCCTCGGTGATGGGTCTGGGCCACCAGGATCAGCCAGGAGGGCGTTCT--TAGGCTGCTGGGATGGTG
      720       730       740       750       760         770       780

         400             410       420       430       440       450
    GGCTTCAGAGCAAG------CAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGAC-GAA
    |||||||| ||| |      |||   || || | | ||   ||  ||| ||  ||  ||   ||   | | |
    GGCTTCAGGGCAGGTGGGGTCAGAATTGGGCGGCTCTCAAGCA--AGGCGGTCGA-CTTCAACTTTCCTGGA
      790       800       810       820         830        840       850

    460       470       480       490         500       510        520
    TCGCAGACATTCTGGTAGGGGCTGGAAGGTACATGAGG-TGAC-AAAATGTATCTCGGTGTTG-ACGTCCTC
    |  | || | | ||| |  | ||  |  |  | || || || |     ||| ||  |     | |||   |
    TGTCTGA-ACTTTGGGA-AGCCTTTACTGACCCTGGGGCTGGCTTTTCTGTTTCCTGTACCAGTACGAGAT-
       860        870        880       890       900       910       920

     530        540              550       560       570       580
    CAGAAGCGT-TTGCA---TCTTAG--AC--CCTGCCACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCT-AG
    |||||   |   |||   |  |||  ||    ||  | || |  ||   | ||| |||  | ||   || ||
    CAGAAAAATGGAGCAAAGTGGTAGGTACTTTTTGTGA-AGACGGCA--CGGTCT-TCC--CTCTTCCCTCAG
        930       940       950       960          970          980

    590       600       610         620        630        640        650
    --GAAGAGGCTCCACAAGGCCTTGCAGTGCT--TCTCGTC-CTGAAGATTGAC-GGCCACAGTGA-CTGGGT
        | |  || | ||||   |   || |||    | ||| |||    | | | ||     | || |   ||
    TCCCAAATCCTTCCCAAG---TAAGAG-GCTGGAGTTGTCACTGCTTTTGGCCTGGAGTTTGGGATCCCTGT
  990      1000         1010       1020      1030      1040      1050

       660        670       680       690       700       710       720
    AATCTTTAAG-CAGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTGG--C
      |   |||| |  | |||  |||| |||||  | ||      |  ||  |     |    | || | |  |
    CTTTCCTAAGACCTGGGGT-TGTCAGCTCTC--ATCTGAGGCATCCAGCAGTCTCTGCCTTGCCTTTAGCCC
   1060      1070       1080        1090      1100      1110      1120

        730       740        750       760       770        780       790
    TGAAGTAACAGTCAGGTGTCCCCCG-CAGGCAAGGACTCAGCAGCAGCAACAGCA-GCAACAGGGAGGAATT
          | | | | || ||  || |   ||  |   ||   ||     |   | |  ||| ||      |||
    CTCCCAAGCTGGCTGGGGTGGCCTGTGTGGGCACTTCTGTCCATATTTATAGGTACCCAATAGCTGCCCATT
    1130      1140      1150      1160      1170      1180      1190

           800       810       820        830       840       850
    ---TGGGCTCCAGGCTGGCGCCAGCACTGTCAT-CTCTGCCGGGGACCCCTCATGCCTGTGACAGAG---CA
       || || |||  ||    ||||  || |  |  ||   |  |    ||  ||| |||   |||||   ||
    TCGTGAGCCCCA-TCTTCACCCAGGCCTATGTTGATCCATCCAGCTTGCCAGATG-CTG---CAGAGTCACA
  1200      1210       1220      1230      1240      1250          1260

   860       870        X
    GGTCGTCTCGTTCCAGTCGAC
     | | ||  | | |  ||  |
    AG-CCTCGAGGTGCCTTCTTCAGGGCCTGGT
      1270      1280    X 1290

9. US-08-162-407-1' (1-879)
   Q37817          Sequence encoding the alpha 1B-1 human calcium cha

 ID    Q37817 standard; cDNA; 7362 BP.
 AC    Q37817;
 DT    30-JUN-1993  (first entry)
 DE    Sequence encoding the alpha 1B-1 human calcium channel subunit.
 KW    Human calcium channel subunit; diagnosis; agonist; antagonist;
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 KW    Lambert Eaton syndrome; ss.
 OS    Homo sapiens.
 FH    Key                 Location/Qualifiers
 FT    CDS                 144..7163
 FT    /*tag=  a
 PN    WO9304083-A.
 PD    04-MAR-1993.
 PF    14-AUG-1992; U06903.
 PR    15-AUG-1991; US-745206.
 PR    10-APR-1992; US-868354.
 PA    (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
 PI    Brenner R,  Ellis SB,  Feldman DH,  Harpold MM,  Mccue AF,
 PI    Williams ME;
 DR    WPI; 93-093936/11.
 DR    P-PSDB; R33549.
 PT    DNA encoding specific human calcium channel sub-units - used for
 PT    identifying calcium channel agonists and antagonists and
 PT    diagnosing Lambert Eaton syndrome
 PS    Disclosure; Page 111-120; 150pp; English.
 CC    DNA encoding the alpha 1B subunit was isolated by screening a
 CC    human basal ganglia cDNA library with  fragments of the rabbit
 CC    skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
 CC    A portion of one of the positive clones was used to screen an IMR32
 CC    cell cDNA library. Clones that hybridized to the basal ganglia
 CC    DNA prove were used to further screen an IMR32 cell cDNA library
 CC    to identify overlapping clones that in turn were used to screen a
 CC    human hippocampus cDNA library. In this way, a sufficient series of
 CC    clones to span nearly the entire length of the nucleotide sequence
 CC    encoding the human alpha 1B subunit was obtained. PCR amplification
 CC    of specific regions of the IMR32 cell alpha 1B mRNA yielded
 CC    additonal segments of the alpha 1B coding sequence. A full-length
 CC    alpha 1B DNA clone was constructed by ligating portions of the
 CC    partial cDNA clones (see Q37817, Q37818). Alpha 1B-1 and alpha
 CC    1B-2 are derived by alternative splicing of the alpha 1B subunit
 CC    transcript.
 SQ    Sequence   7362 BP;    1446 A;    2276 C;    2214 G;    1426 T;

Initial Score    =    116  Optimized Score  =   405   Significance =  6.84
Residue Identity =    51%  Matches          =   491   Mismatches    =  331
Gaps             =    126  Conservative Substitutions               =    0

              X        10        20        30          40         50
              GTCGA-CTGGAACGAGACGACCTGCTCCAGACCAT-TCAG-CA-ATCCTGCTCTG-GGCTCC
              || || ||||  || |||| |  ||    | || |   || || | || |  ||| |||| |
    GCCGCTGGTGGTGGAGCTGGGCCGCGACGGCGCGCGGGGGCCCGTGGGAGGCAAAGCCCGACCTGAGGCTGC
   2590      2600      2610      2620      2630      2640      2650

     60        70        80         90          100       110         120
    CAAGGGCTGAGATTACAGGTGTAACC-GAGATAAG--ACC-CTGGCTGAGTCAACGATGCACAAG-GCTCGA
      ||| |   ||   |  ||  | ||   |   ||  ||| | |||   | | || | | |||||  | |
    GGAGGCCCCCGAGGGC--GTCGACCCTCCGCGCAGGCACCACCGGCACCG-CGAC-AAGGACAAGACCCCCG
 2660      2670        2680      2690      2700       2710       2720

       130          140       150       160       170       180       190
    ATCCTAGGGA-TGGGA--GGGGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCCCTTTGCCAGCG
       |  ||||   |||  | | || ||| ||| | || ||||  |      ||    |||||      ||||
    CGGCGGGGGACCAGGACCGAGCAGAGGC-CCCGAAGGCGGAGAGCGGGGAGCC-CGGTGCCCGGGAGGAGCG
   2730      2740      2750       2760      2770       2780      2790

           200       210        220       230       240       250       260
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  ---AAGGCCCCAGGCGGCTGCCAGCAGC-ACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCC
       |||| ||  | || |||| |||| |  ||   | | |||  | | ||  ||  ||||| | || |||
  GCCGCGGCCGCA--CCGCAGCCA-CAGCAAGGAGGCCGCGGGGCCCCCGGAGGCGC-GGAGCGAGCGCGGCC
 2800        2810       2820      2830      2840      2850       2860

        270       280         290       300       310       320        330
  TGGGCCGAGGCTCTGGGAGC-TCCG-TGGCTTCTAGGGCTATGGACTCCTTGGGGGCAGCAG-GGTGGAGG
    |||| |||| | | ||  |||  |||  |   |||   | | ||||  || ||  || |  | |  ||
  GAGGCCCAGGCCCCGAGGGCGGCCGGCGGCACCACCGGC---GCGGCTCCCCGGAGGAGGCGGCCGAGCGGG
   2870      2880      2890      2900         2910      2920      2930

         340       350       360       370        380        390
  AGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGC-AGGCCTTC-CCGATAC--AGGGC-TT
  || || |  | ||| || |   | |||||| || |  || |  || |||  | | |||   |  |||||
  AGCCCCGACGCCACCGCGCGCACCGGCACC-AG-G--ATCCGAGCAAGGAGTGCGCCGGCGCCAAGGGCGAG
    2940      2950      2960          2970      2980      2990      3000

  400       410       420       430         440       450       460
  CAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAG--GTGGGAGATGTTGGTCTGGACGAATCGCAGACAT
  | | ||  || ||   | |  ||   ||    || |    |||||  |  |  | ||  ||   || | |
  CGGCGCGCGCGGCACCGCGGCGGCCCCCGAGCGGGGCCCCGGGAGGCGGAGAGCGGG--GAGGAGCCGGCGC
      3010      3020      3030      3040      3050        3060      3070

  470       480       490       500       510       520       530
  TCTGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTGACGTCCTCCAGAAGCGTTTGC
     || |  ||  |   || |||  ||| | ||   ||  || ||  | ||      |   ||||| |   |
  GGCGGCACCGG--GCCCGGCACA--AGGCG-CAGCCTG-CTCACGAGGCTG------TGGAGAAG-GAGACC
      3080        3090         3100       3110            3120       3130

540        550         560       570       580       590               600
  ATCTTAG-ACCCTGCCAC--AGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAG--GCT------CC
  | |  || |    |||||  ||      | ||   ||      ||  | | ||||| ||  |||      ||
  A-CGGAGAAGGAGGCCACGGAGAAGGAGGCTGAGATAGTGGAAGC-CGACAAGGAAAAGGAGCTCCGGAACC
        3140      3150      3160      3170       3180      3190      3200

         610       620        630       640         650       660
  ACAAGGCCTTGCAGTGCTTCT-CGTCCTGAAGATTGACGGCCACAGTGAC--TGGGTAATCTTTAAGCAGGT
  || || ||  | ||     ||  | |||| |||   |  |  || |||||  |||||    |  |  ||  |
  ACCAGCCCCGGGAGCCACACTGTGACCTGGAGA-CCAGTGGGACTGTGACTGTGGGTCCCATGCACACA-CT
       3210      3220      3230       3240      3250      3260       3270

670       680       690       700       710       720       730
  GGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGACTGTGGCTGAAGTAACAGTCAG---
  |  ||| || || |||  |         |||| |||||  ||   | | | || || ||  ||| ||||
  GCCCAG-CACCTGTCTCCA---------GAAGGTGGAG--GAACAGCCAGAGGATGCAG--ACAATCAGCGG
        3280               3290        3300      3310        3320

  740       750            760       770         780             790
  -GTGTCCCCCGCA--GGCA---AGGACTCAGCAGCAGCAACAGCA--GCA------ACAGGGAGGAATTTGG
     ||| | ||||  ||||   ||  | ||| | | | ||||  |  | |       ||| || |     ||
  AACGTCACTCGCATGGGCAGTCAGCCCCCAG-ACCCG-AACACTATTGTACATATCCCAGTGATGCTGACGG
3330     3340      3350      3360        3370      3380      3390

   800       810        820             830       840       850
  GCTCCAGGCTGGCGCCAG-CACTGTC-ATCTCTG-----CCGGGGACCCCTCATGCCTGTGACAG----AGC
  || |    || | |  || ||| |||  || | |      || |||||    | |||    | ||    ||
  GCCC---TCTTGGGGAAGCCACGGTCGTTCCCAGTGGTAACGTGGACCTGGAAAGCCAAGCAGAGGGGAAGA
3400        3410      3420      3430      3440      3450      3460

  860       870        X
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  AGGTCGTCTCGTTCCAGTCGAC
  |||  |  | |   | |  |||
  AGGAGG--TGGAAGCGGATGACGTGATGAGGA
3470        3480      3490


10. US-08-162-407-1' (1-879)
    N60309          Equine IFN-omega-1 from pAH61.

 ID   N60309 standard; DNA; 2109 BP.
 AC   N60309;
 DT   10-JUN-1991  (first entry)
 DE   Equine IFN-omega-1 from pAH61.
 KW   IFN-omega-1; equine; interferon; ss.
 OS   Equus cabalus.
 FH   Key             Location/Qualifiers
 FT   CDS             1421..2005
 FT   /*tag=  a
 FT   /product= IFN-omega-1
 FT   sig_peptide     1421..1490
 FT   /*tag=  b
 FT   mat_peptide     1491..2005
 FT   /*tag=  c
 PN   EP-186098-A.
 PD   02-JUL-1986.
 PF   17-DEC-1985; 116083.
 PR   18-DEC-1984; DE-446122.
 PA   (BOEH ) BOEHRINGER INGELHEIM.
 PI   Himmler A, Hauptmann R, Hauel N, Adolf G, Swetley P.
 DR   WPI; 86-170649/27.
 DR   P-PSDB; P60400.
 PT   New equine and canine interferon - and recombinant DNA molecules
 PT   coding for them, and transformed cells.
 PS   Disclosure; Fig 12; 149pp; German.
 CC   Microorganisms transformed with the recombinant sequence produce IFN
 CC   which is useful therapeutically in veterinary medicine.
 CC   See also N60306-13 and N60938.
 SQ   Sequence   2109 BP;    609 A;    476 C;    471 G;    553 T;

Initial Score     =    115  Optimized Score   =    340  Significance =  6.77
Residue Identity  =    52%  Matches           =    407  Mismatches   =   273
Gaps              =     98  Conservative Substitutions               =     0

            X       10        20        30        40          50
            GTCGACTGGAACGAGACGACCTGCTCCAGACCATTCAGCAAT--CCTGCTCTG-GGCTCCCA
              ||  || ||| ||| || ||||  |    || | | ||||  | | ||| | | || ||
  CTCTCAATCTCCCGTCT-CAACCAGAAGAGCTGCGTCTTGGCACTTACCAATGGCTTTCTCAGTGTCTTCC-
       1380 X     1390      1400      1410      1420      1430      1440

 60        70         80           90        100       110           120
  AGGGCTGAGATTACAGGTG-TAAC--CGAGATAAGAC-CCTGGCTGAGTCAACGA--TGC--ACAAGGCTCG
     | ||  | |   |||| |  |  | ||    | | |||   |||| |  |||  |||   | || || |
  -CTGATGGCACTGGTGGTGATCTCCTCCAGCCCCGTCTCCTCCATGAG-CTGCGACCTGCCTGCGAGCCTTG
        1450      1460      1470      1480       1490      1500      1510

      130       140                 150       160       170       180
  AATCCTAGGGATGGGAGGGG------AGGG----GCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCCCTT
  |   || | ||  | ||| |      || |    |||||  | || |    || | |||||||| || |
  A---CTTGAGAAAGCAGGAGACCCTCAGAGTTCTGCACCAGATGGAGACAATCTCTCCTCCTTCCTGTCTGA
          1520      1530      1540      1550      1560      1570      1580
     190       200       210       220       230        240       250
  TGC-CAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAG-CAGCAGCAGCAGGAGCAACA
   || |||   || |  ||||   |  |||| |||| | |  ||  ||||||    |||  ||    || ||
  AGCACAGGACAGACTTCAGG-TTCCCCCAGGAGCAGCTGGATGGCAGGCAGTTCCCAGAGGCCCAGGCCACG
        1590      1600       1610      1620      1630      1640      1650

     260        270       280       290       300       310       320
  GCTG-CCT-GGGCCGAGGCTCTGGGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGGT
   ||| |||   |  || ||||  | || ||    || |||    | |  |  | | | |   || ||  ||
  TCTGTCCTCCAGGAGATGCTCCAGCAGATCGTCAGCCTCTTCCAC-ACAGAGCGC-TCGTCTGCTGCCTGGA
       1660      1670      1680      1690       1700       1710      1720

    330       340       350        360        370       380       390
  GGAGGAGTCCGGCTGGCACTGCACCTCCAGGCAC-CGA-GAGAAATTCTGGCAGGCCTTCCCGATACAGGGC
    | || | | |||||  |  | ||||  || || | |  || |   ||||| || |||   | | ||  |
  ACACGACT-CTGCTGGACCGACTCCTCGCGGGACTCCATCAGCA--GCTGGAAGACCT---CAACACCTGCT
        1730      1740      1750      1760        1770         1780

     400       410       420         430       440       450       460
  TTCA-GAGCAAGCAGCTGTGTGCAGGTGTCCTTC--AGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAGA
  |  | |||||  |||  | | | | |  |||  |   |||  || | |    |   |||| ||    |  |
  TGGATGAGCAGACAG--GAGAGGAAGAATCCGCCCTGGGAACTGTG-GGCCCTACACTGGCCGTGAAGAGGT
 1790      1800        1810      1820      1830       1840      1850

     470       480       490        500        510         520       530
  CATTCTGGTAGGGGCTGGAAGGTACATGA-GGTGACAAAATGTA-TCTCGGTG--TTGACGTCCTCCAGAAG
    ||| || ||   |  |   |||| |||  | ||  ||||  | |  | |||  | |  |     ||||
  ACTTCAGG-AGAATC-CGTCTGTACCTGACAGAGAAGAAATACAGTGACTGTGCCTGGGAGATTGTCAGA--
  1860       1870       1880      1890      1900      1910      1920

       540        550       560       570         580       590
  CGTTTGCATC-TTAGACCCTGCCACAGTCTTCAGTTGCTCTATCCAGC--GCTGGGCTAGGAA-GA-GGCT-
   ||   |||| | ||| ||| |     ||||||  |   | | || ||  |   || |||||| || || |
  -GTGGACATCATGAGATCCTTC-----TCTTCA--TCAGCAAACCTGCAAGGAAGGTTAGGAATGAAGGATG
     1930      1940           1950        1960      1970      1980

  600            610       620       630       640       650       660
  -CCACAAGG-----CCTTGCAGTGCTTCTCGTCCTGAAGATTGACGGCCACAGTGACTGGGTAATCTTTAAG
     ||  ||     ||||| | || ||||| | |  |  | ||  |||||   ||     | |  |||  |
  GAGACCTGGGGTCACCTTGAAATGATTCTCCTAC--ACTACTG--GGCCA---TG-----GCACCCTTGCA-
1990      2000      2010      2020          2030              2040

     670       680         690       700       710       720       730
  CAGGTGGTCAGTCAACTCTCTAAA--CTTCACTTTGAAGTTGGAGGAGATGGGACTGTGGCTGAAGTAACAG
  |  ||  | |||||  | |  |||  ||    |||    || |   | ||   ||| |   |||| |
  CCTGTCTTTAGTCA--TTTCAAAAGGCTCTTATTTCTGCTTTGGTCATAT---ACT-TTATTGAATTC
 2050      2060        2070      2080      2090          2100        X

     740
  TCAGGT
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11. US-08-162-407-1' (1-879)
    Q03541       Chinese hamster IMPDH.

 ID   Q03541 standard; DNA; 1620 BP.
 AC   Q03541;
 DT   31-AUG-1990  (first entry)
 DE   Chinese hamster IMPDH.
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 KW   Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
 KW   guanosine monophosphate; ss.
 OS   Cricetulus sp.
 PN   WO9001545-A.
 PD   22-FEB-1990.
 PF   02-AUG-1989; U0344.
 PR   12-AUG-1988; US-232302.
 PA   (ARCH-) Arch. Dev. Corp.
 PI   Collart FR, Huberman E;
 DR   WPI; 90-083504/11.
 DR   N-PSDB; Q03541.
 PT   DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
 PT   used to detect high levels of enzyme activity of tumour cells,
 PT   esp. hepatomas, and to produce guanosine monophosphate.
 PS   Claim 8; Fig 2; 51pp; English.
 CC   The sequence can be used to quantitatively detect IMPDH encoding
 CC   DNA or RNA by hybridisation, eg in normal and malignant cells,
 CC   esp. hepatomas.
 CC   See also Q03540.
 SQ   Sequence   1620 BP;   423 A;   369 C;   421 G;   406 T;    1 Others;

Initial Score    =    114  Optimized Score   =   387   Significance =  6.70
Residue Identity =    49%  Matches           =   463   Mismatches   =   368
Gaps             =    107  Conservative Substitutions               =     0

            X       10           20         30           40         50
            GTCGACTGGAAC--GAGACG-ACCTGCTCCAGACC--ATTCA-GCAATCCTGCTCTGGGCTC
            | |    ||| |  | || | |  |  |  |  ||  |  || |||   || || |||  ||
  GTAGVCCTTAGCCCCAAGGATCGTGTGAGGGATGTTTTTGAAGCCAAAGCCAGGCATGGCTTCTGTGGTATC
380       390       400       410       420       430       440       450

    60        70        80        90       100       110           120
  CCAAGGGCTGAGATTACAGGTGTAACCGAGATAAGACCCTGGCTGAGTCAACGATGC-ACAAGG---CTCGA
  || |   |  |||| |||||    |  | ||   ||  |||| || | || |  | |  |||||    | ||
  CCCA--TCACAGAT-ACAGGCCGGATGGGGAGTCGA--CTGG-TG-GGCATCATTTCTTCAAGGGATATTGA
          460        470       480          490        500       510

       130       140       150       160       170       180       190
  -ATCCT-AGGGATGGGAGGGGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCCCTTTGCCAGCGA
    | || | ||| || || | | |  |    |  || |||| ||     |           ||||   | |
  TTTTCTCAAGGA-GGAAGAGCATGACCGTTTCTTGGAGGAGATCATGACAAAGAGGGAAGATTTG---GTGG
   520        530       540       550       560       570       580

     200          210       220       230       240        250       260
  AGGCCC---CAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAG-CAGGAGCAACAGCTGCC-
   |||||   |||||  |   | | || |      ||| |  | ||||| ||||  |  ||  | || ||||
  TGGCCCCTGCAGGCATCACTCTGAAGGAGGCAAATGAAATTCTGCAGC-GCAGTAAAAAGGGAAAGTTGCCC
     590       600       610       620       630        640       650

         270        280       290       300       310       320       330
  -TGGGCCGAGGCTCTG-GGAGCTCCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGCAGGGTGGAGGA
   | |     |    ||  ||||  || ||    |  |||  |  |  |||  |  | || |  || ||  |
  ATTGTGAATGAAAATGATGAGCT-GGTAGCCATCATTGCTCGGACAGACCT--GAAGAAGAATCGT-GATTA
    660       670        680       690       700         710        720

          340        350       360       370       380       390       400
  GTC--CGGCTGGCACTG-CACCTCCAGGCACCGAGAGAAATTCTGGCAGGCCTTCCCGATACAGGGCTTCAG
    |   ||||  ||  |   ||   | |||  |  |  |  |  ||||| | ||     |   | |  | |
  CCCATTGGCTTCCAAAGATGCCAAAAAGCA--GCTACTATGTGGGGCAGCCATTGGTACTCATGAGGATGAC
      730       740       750         760       770       780       790
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           410         420       430       440       450       460
    AGCAAGCAGCTG--TGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAG----AC-
    |   |   ||||    | | ||  || | | ||  ||||  |  || | | |||||   || |||    ||
    AAGTATAGGCTGGACTTACTGG-CTCTTGCTGG-TGTGGATGTAGTGGTTTTGGACTCTTCCCAGGGAAACT
        800       810        820        830       840       850       860

        470       480          490       500       510       520       530
    --ATTCTGGTAGGGGCT-GGA--AGGTACATGAGGTGACAAAATGTATCTCGGTGTTGACGTCCTCCAGAAG
      ||| |   |     |  ||  |  |||||||   || |||   || | |  | |  | ||| |   | ||
    CCATTTTCCAAATCAATATGATCAAATACATGA-AAGAGAAA---TACCCCAATCTCCAAGTCAT--TGGAG
        870       880       890        900          910       920

         540       550         560       570       580       590       600
    CGTTTGCATCTTAGACCCTGC--CACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAGGCTCCAC
         |||   ||| | ||||  | ||  |   ||   ||| ||  | ||| ||  | |||    ||||  |
    -----GCAATGTAGTCACTGCTGCTCAAGC-CAAGAACCTC-ATAGA-CGCAGGTGT-GGA---TGCTCTGC
       930       940       950        960         970        980

           610       620       630       640         650        660
    AAG--GCCTTGCAGTGCTTCTCGTCCTGAAGATTGACGGCCACAGT--GACTG-GGTAATCTTTAAGCAGGT
     ||  | | ||  |||    ||   ||| |  |   | |  |  ||  | ||| |||   |   |||||
    GAGTTGGCATGGGGTGTGGTTCCATCTGCA-TTACTCAGGAAGTGTTGGCCTGTGGTCGGCCCCAAGCAACA
  990      1000      1010       1020      1030      1040      1050      1060

  670           680       690        700       710       720       730
    GGTCAGT---CAA-CTCTCTAAACTTCACTTTG-AAGTTGGAGGAGATGGGACTGTGGCTGAAGTAA-CAGT
    |  ||||   |||  | |||  | |   ||  |    |||| |    ||  | ||  | || || || |
    G--CAGTGTACAAGGTTTCT-GAGTATGCTCGGCGCTTTGGTGTTCCTGTTATTGCTGATGGAGGAATCCAA
            1070       1080      1090      1100      1110      1120

      740       750       760       770       780       790       800
    CAGGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTTGGGCTCCAGGCTG
     | |||   |     | ||| | ||  |  ||      |||  | ||||  | ||   ||||||||    ||
    AATGTGGGTCATATTGCCAAAG-CTTTG--GCTCTTGGAGCTTCTACAGTCATGA---TGGGCTCCCTCTTG
 1130      1140      1150         1160      1170      1180         1190

     810       820       830          840              850        860
    GC-GCCAGCACTGTCATCTCTGCCGGGGA---CCCCTCA--TG----CCTG-TGACAGAGCA-GGTCGTCTC
    || |||| ||| |    | |||  | | |   |  ||||  ||    || | | | | || |  || || |
    GCTGCCACCACCGAAGCCCCTGGTGAGTACTTCTTCTCAGATGGGATCCGGCTAAAAAAGTACCGTGGTATG
     1200      1210      1220      1230      1240      1250      1260

    870        X
    GTTCCAGTCGAC
    | | |  | ||
    GGTTCTCTTGATGCCATGGACA
   1270      1280


12. US-08-162-407-1’ (1-879)
    Q45955        mRXR-beta.

 ID   Q45955 standard; DNA; 2285 BP.
 AC   Q45955;
 DT   01-FEB-1994  (first entry)
 DE   mRXR-beta.
 KW   Retinoid X receptor; RXR; retinoic acid receptor; RAR;
 KW   thyroid receptor; TR; retinoic acid response elements; RARE;
 KW   thyroid receptor response element; TRE;
```

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 KW   retinoid X receptor response element; RXRE;
 KW   subunit; heterodimer; ss.
 OS   Mus musculus.
 FH   Key                 Location/Qualifiers
 FT   CDS                 76..1422
 FT   /*tag=  a
 FT   /label= RXR-beta
 PN   WO9315216-A.
 PD   05-AUG-1993.
 PF   25-JAN-1993; U00639.
 PR   24-JAN-1992; US-825667.
 PA   (CNRS ) CENT NAT RECH SCI.
 PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
 PA   (SQUI ) SQUIBB & SONS INC E R.
 PA   (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
 PI   Chambon P,  Kastner P,  Leid M;
 DR   WPI; 93-258691/32.
 DR   P-PSDB; R39467.
 PT   Heterodimer comprising retinoic acid or thyroid receptor and
 PT   retinoid X receptor - useful in diagnosis and for generation of
 PT   antibodies
 PS   Claim 26; Page 84-86; 128pp; English.
 CC   Two different types of nuclear receptors, RAR and TR dimerise with
 CC   RXR to form a heterodimer which is capable of binding to RARE, TRE
 CC   or RXRE at physiological conditions.  Sequences encoding 1 isoform
 CC   of mouse RXR-beta, 3 isoforms of human RXR-beta, 1 isoform of mouse
 CC   RXR-alpha and 1 isoform of mouse RXR-gamma are provided (Q45955-60).
 SQ   Sequence   2285 BP;    447 A;    665 C;    681 G;    492 T;

Initial Score    =     113  Optimized Score    =     386  Significance =  6.63
Residue Identity =     49%  Matches            =     471  Mismatches   =   360
Gaps             =     124  Conservative Substitutions                 =     0

              X        10        20        30         40          50
              GTCGACT-GGAACGAGACGACCTGCTCCAGAC-CATTCAGCAATCCTG--CTCTGG----GC
                | | | |||| ||   ||||| |||  | |    | |  ||  |||  |  |||    ||
    TCTTCAAGCGCACCATTCGGAAGGACCTGACCTACTCGTGTCGTGATAACAAAGACTGTACAGTGGACAAGC
         510  X    520       530       540       550       560       570

            60        70         80          90         100           110
    TCC----CAAGGGCTGAGATTACAGGTG-TAACCGAGAT--AAGACC-CTGGC-TG---AGTCA-ACGATGC
     ||     ||  ||||  | ||| |  | || | ||  |    | || ||||| ||   ||  |  || | |
    GCCAGCGGAATCGCTGTCAGTACTGTCGCTATCAGAAGTGCCTGGCCACTGGCATGAAAAGGGAGGCGGTTC
       580       590       600       610       620       630       640

        120       130             140       150       160       170
    ACAAGGCTCGAATCCTAGGGATGG-----GA-GGGGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTT
    |  |||  ||    |  |||| ||     || ||||| ||  |     || ||| |   ||||        |
    AGGAGGAGCGTCAACGGGGGAAGGACAAAGACGGGGATGG--AGATGGGGCTGGGGGAGCCCCTGAGGAGAT
     650       660       670       680         690       700       710

  180       190       200       210        220       230       240       250
    GCCCTTTGCCAGCGAAGGCCCCAGGCGGCTGCCAGC-AGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAG
    |||  | | ||| ||     || || ||| |  |||  ||     |||| || |||| ||    | || |
    GCCTGTGGACAG-GA----TCCTGGAGGCAG--AGCTTGC-----TGTG-GA-GCAGAAGAGTGACCAAGGC
     720        730           740              750         760       770

           260       270       280         290       300       310       320
    CAACAGCTGCCTGGGCCGAGGCTCTGGGAGCT--CCGTGGCTTCTAGGGCTATGGGACTCCTTGGGGGCAGC
        ||   |||||| | |  |   ||| | |  | |  ||    | | |   | ||||       | |||
      GTTGAGGGTCCTGGGGCCA--CCGGGGGTGGTGGCAGCAGCCCAAATGACCCAGTGACTAACATCTGCCAGG
         780       790         800       810       820       830       840

             330       340        350        360       370       380
      AGGGTGGAGGAGTCCGGCTG-GCACTGCACCTCCAG-GCACCGAGAGAAATTCTGGCAGGCCT--TCCCGA-
        | | ||  |   | ||||  |||  | | |  || |  |  |||| |  ||  |||   ||  |||| |
      CAGCT-GACAA--ACAGCTGTTCAC-ACTCGTTGAGTGGGCAAAGAGGA--TCCCGCACTTCTCCTCCCTAC
          850         860        870       880         890       900       910

      390        400       410       420       430       440       450
      TACAGGGC-TTCAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAAT
        | || |  ||||  ||  | |||| | |||||   |    | ||| |     ||   |  ||   |  ||
      CTCTGGACGATCAGGTCATACTGCTGCGGGCAGG---CTGGAACGAGCT-CCTCATTGCGTCCTTCTCCCAT
             920       930       940          950        960       970

     460       470       480       490          500       510       520
      CGCAGACATTCTGGTAGGGGCTGGAAGGTACATG---AGGTGACAAAATGTATCTCGGTGTTGACGTCC--T
      ||    ||||   ||  | | ||| |    | ||   | | | |   ||||  | | |       | ||  |
      CG-GTCCATTGATGTCCGAGATGGCATCCTCCTGGCCACGGGTCTTCATGT-GCACAGAAACTCAGCCCATT
     980        990      1000      1010      1020       1030      1040

        530          540            550       560        570        580
      CCAGAAGCGTTTG---CATCTTAGACC-----CTGCCACAGTCTTCAGT-TGCTCTAT-CCAGCGCTGGGCT
      ||  | ||||  |   |||||| || |     ||| || || ||  ||| | |   || |  |   || |
      CCGCAGGCGTGGGAGCCATCTTTGATCGGGTGCTGACAGAG-CT--AGTGTCCAAAATGCGTGACATGAGGA
    1050      1060      1070      1080       1090        1100      1110

      590       600         610       620        630       640       650
      AGGAAGAGGCTCCACAAGGC--CTTGCAGTGCTTC-TCGTCCTGAAGATTGACGGCCACAGTGACTGGGTAA
       |||  || |    |  |||  | ||| |    || || |  | ||    ||| |||| || | ||    ||
      TGGACAAGACAGAGCTTGGCTGCCTGCGGGCAATCATCATGTTTAATCCAGAC-GCCA-AGGGCCTCTCCAA
     1120      1130      1140      1150      1160      1170        1180

       660       670              680       690       700       710       720
      TCTTTAAGCAGGTGG---TCAGTC----AACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTG
       | |  || ||||||   ||  ||     |   | ||  | |||||    |  |   | | |   ||  ||
      CCCTGGAG-AGGTGGAGATCCTTCGGGAGAAGGTGTACGCCTCACTGGAGACCTATTGCA-AGCAGA-AGTA
     1190       1200      1210      1220      1230      1240       1250

            730        740       750         760       770       780
      GCTGAAGTAACA-GTCAGGTGTCCCCCGCAG--GCAAGGACTCAGCAGCAGCAACAGCAGCAACAG--GGAG
       |   || | || | | ||| | ||  || |  |  | | ||   | ||  |  | ||  || | |    |
      CCCTGAGCAGCAGGGCCGGTTTGCCAAGCTGCTGTTACGTCT-TCCTGC--CCTCCGCTCCATCGGCCTCAA
      1260      1270      1280      1290       1300        1310      1320

     790        800        810       820       830         840         850
      GAATTTGG-GCTCCAG-GCTGGCGCCAGCACTGTCATCTCTGCCGGGGACCCC--TCATGCCT--GTGACAG
      |  | ||| || || |  ||    | |||    ||||   || ||    ||||  | |  |||   | |  |
      GTGTCTGGAGCACCTGTTCTTCTTCAAGC----TCAT---TGGCGACACCCCCATTGACACCTTCCTCATGG
       1330      1340      1350             1360      1370      1380      1390

         860          870         X
      AGCAGGT--CGTCT-CGTTCCAG-TCGAC
      ||  | |   | || |   |||| | | |
      AGATGCTTGAGGCTCCCCACCAGCTAGCCTGAGCCCAGA
            1400      1410      1420


  13. US-08-162-407-1' (1-879)
      Q43031       Collagen-like polymer DCP2-C2(A12)C2 coding sequen
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 ID   Q43031 standard; DNA; 432 BP.
 AC   Q43031;
 DT   07-SEP-1993  (first entry)
 DE   Collagen-like polymer DCP2-C2(A12)C2 coding sequence.
 KW   Recombinant; collagen-like polymer; CLP; tripeptide; helix; membrane;
 KW   fibre; film; coating; triad sequence; collagen; mammalian; moulding;
 KW   hydrogel; interchain linkage; colloid suspension; DCP; antibody; ds.
 OS   Synthetic.
 PN   WO9310154-A.
 PD   27-MAY-1993.
 PF   04-NOV-1992; U09485.
 PR   12-NOV-1991; US-791960.
 PA   (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PI   Cappello J,  Ferrari FA;
 DR   WPI; 93-182496/22.
 DR   P-PSDB; R37737.
 PT   High mol. wt. collagen-like protein polymers - capable of being
 PT   produced in unicellular microorganisms
 PS   Disclosure; Page 38; 82pp; English.
 CC   The sequences given in Q43030-34 encode examples of recombinantly
 CC   produced DCP collagen-like polymers (CLPs) which consist of repeated
 CC   tripeptide sequences selected from a wide range of GXY sequences,
 CC   where X and Y can be any amino acid.  These sequences can be cloned
 CC   into plasmids and used to transform E. coli to produce the DCP
 CC   proteins.  DCP peptides comprise repeated units of; A = GAPGPAGPP,
 CC   B = GSRGDPGPP and/or C = GAHGPAGPK.  These polymers may be used to
 CC   raise anti-DCP antibodies in rabbits.  These polymers have molecular
 CC   weights of >30 kD and are able to form helices due to interchain
 CC   linkages.  These polymers pref. contain a proportion of tripeptide
 CC   triad sequences found in natural collagens, pref. mammalian collagens.
 CC   The CLPs impart unique characteristics to materials such as fibres,
 CC   membranes, films, coatings, hydrogels, colloid suspensions and moulded
 CC   articles.
 SQ   Sequence   432 BP;    54 A;    162 C;    165 G;    51 T;

Initial Score    =    112  Optimized Score   =    204  Significance =  6.56
Residue Identity =    51%  Matches           =    239  Mismatches   =   177
Gaps             =     48  Conservative Substitutions              =     0

       190    X  200       210       220       230       240       250
    TTGCCAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAG
               |  | ||  ||||  |||||||  ||   | | |  |||   ||  |||||||  | | ||
              GGTGCTCA--CGGC--CCAGCAGGTCCGAAGGGCG-CGCA-TGGC-CCAGCAGGCCCGAAAG
              X         10          20        30           40        50

       260         270         280       290          300       310
    CT--GCCTGGGCCG--AGG--CTCTGGGAGCTCCGTGGCTTCTAGG---GCTATGGGACTCCTTGGGGGCAG
     |  |||||| |||   ||  | | ||| |||||| | | |  |||   || | ||  | |||  ||  | |
    GTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTGCAGGCCCGCCA-GGTGCGCCT--GGACCGG
       60        70        80        90       100        110         120

  320       330       340       350       360        370       380       390
    CAGGGTGGAGGAGTCCGGCTGGCACTGCACCTCCAGGCACCGAGA-GAAATTCTGGCAGGCCTTCCCGATAC
    |  |||  |     |||| ||   | | |||| ||||| |||  | |     ||||   | ||   | |
    C-TGGTCCA-----CCGGGTGCTCCGGGACCTGCAGGC-CCGCCAGGTGCGCCTGGACCGGCTGGTCCACCG
        130            140       150        160       170       180

           400       410       420        430         440       450
    AGGGCTTCAGAGCAAGCAGCTGTGTGCAGGTG-TCCTTCAGGAGGTGG--GAGATGTTGGTCTGGACGAATC
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   | ||| | |  |  ||||    |  ||||||  |||  |   | |||   |   | || || ||  ||
  GGTGCTCCGGGACCTGCAGGCCCG-CCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGG--GACCT
190       200       210        220       230       240       250

460       470       480       490       500       510        520       530
  GCAGACATTCTGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTG-ACGTCCTCCAGA
  |||| |   |  |  | | |||||  |    || |   ||    ||  ||  ||   || | | || ||||
  GCAGGCCCGCCAGGTGCGCCTGGACCG--GCTG-GTCCACCGGGTG-CTCCGGGACCTGCAGGCCCGCCAGG
 260       270       280          290       300        310       320

         540       550       560       570       580        590        600
  AGCGTTTGCATCTTAGACCCTGCCACAGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAG-GAAGA-GGCTCC
   |||  || | |   | |    |||| |  | |    |  |  | ||| ||  | |  | |   | ||| |
  TGCGCCTGGACC---GGCTGGTCCACCGGGTGCTCCGGGAC-CTGCAG-GCCCGCCAGGTGCCCATGGCCCA
   330          340       350       360        370        380       390

         610       620       630       640 X     650
  ACAAGGCCTTGCAGTGCTTCTCGTCCTGAAGATTGACGGCCACAGTGACTGG
   || | ||     | |||    |||| | ||   | | |  |
  GCAGGACCGAAAGGAGCTCACGGTCCGGCAG---GTCCGAAA
      400       410       420          430 X

14. US-08-162-407-1' (1-879)
    Q43032        Collagen-like polymer DCP3-C2(AB12)C2 coding seque

 ID   Q43032 standard; DNA; 756 BP.
 AC   Q43032;
 DT   07-SEP-1993  (first entry)
 DE   Collagen-like polymer DCP3-C2(AB12)C2 coding sequence.
 KW   Recombinant; collagen-like polymer; CLP; tripeptide; helix; membrane;
 KW   fibre; film; coating; triad sequence; collagen; mammalian; moulding;
 KW   hydrogel; interchain linkage; colloid suspension; DCP; antibody; ds.
 OS   Synthetic.
 PN   WO9310154-A.
 PD   27-MAY-1993.
 PF   04-NOV-1992; U09485.
 PR   12-NOV-1991; US-791960.
 PA   (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PI   Cappello J,  Ferrari FA;
 DR   WPI; 93-182496/22.
 DR   P-PSDB; R37738.
 PT   High mol. wt. collagen-like protein polymers - capable of being
 PT   produced in unicellular microorganisms
 PS   Disclosure; Page 39; 82pp; English.
 CC   The sequences given in Q43030-34 encode examples of recombinantly
 CC   produced DCP collagen-like polymers (CLPs) which consist of repeated
 CC   tripeptide sequences selected from a wide range of GXY sequences,
 CC   where X and Y can be any amino acid.  These sequences can be cloned
 CC   into plasmids and used to transform E. coli to produce the DCP
 CC   proteins.  DCP peptides comprise repeated units of; A = GAPGPAGPP,
 CC   B = GSRGDPGPP and/or C = GAHGPAGPK.  These polymers may be used to
 CC   raise anti-DCP antibodies in rabbits.  These polymers have molecular
 CC   weights of >30 kD and are able to form helices due to interchain
 CC   linkages.  These polymers pref. contain a proportion of tripeptide
 CC   triad sequences found in natural collagens, pref. mammalian collagens.
 CC   The CLPs impart unique characteristics to materials such as fibres,
 CC   membranes, films, coatings, hydrogels, colloid suspensions and moulded
 CC   articles.
 SQ   Sequence   756 BP;    84 A;    288 C;    291 G;    93 T;
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Initial Score     =    112  Optimized Score  =     315  Significance =  6.56
Residue Identity  =    51%  Matches          =     370  Mismatches   =   272
Gaps              =     74  Conservative Substitutions               =     0

     190    X  200       210       220       230       240       250
  TTGCCAGCGAAGGCCCCAGGCGGCTGCCAGCAGCACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAG
             |  | ||  ||||  |||||||  ||   | | |  |||   ||  |||||||  | | ||
            GGTGCTCA--CGGC--CCAGCAGGTCCGAAGGGCG-CGCA-TGGC-CCAGCAGGCCCGAAAG
            X         10          20        30           40        50

     260         270         280       290          300       310
  CT--GCCTGGGCCG--AGG--CTCTGGGAGCTCCGTGGCTTCTAGG---GCTATGGGACTCCTTGGGGGCAG
   |  |||||| |||   ||  | | ||| |||||| | | |  |||   || | ||  | |||  ||  | |
  GTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTGCAGGCCCGCCA-GGTGCGCCT--GGACCGG
     60        70        80        90        100        110         120

320       330       340       350       360        370       380       390
  CAGGGTGGAGGAGTCCGGCTGGCACTGCACCTCCAGGCACCGAGA-GAAATTCTGGCAGGCCTTCCCGATAC
  |  |||  |     |||| ||   | | |||| ||||| |||  | |     ||||   | ||   | |
  C-TGGTCCA-----CCGGGTGCTCCGGGACCTGCAGGC-CCGCCAGGTGCGCCTGGACCGGCTGGTCCACCG
      130            140       150        160       170       180

         400       410       420        430         440       450
  AGGGCTTCAGAGCAAGCAGCTGTGTGCAGGTG-TCCTTCAGGAGGTGG--GAGATGTTGGTCTGGACGAATC
   | ||| | |  |  ||||    |  ||||||  |||  |   | |||   |   | || || ||  ||
  GGTGCTCCGGGACCTGCAGGCCCG-CCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGG--GACCT
190       200       210        220       230       240       250

460       470       480       490       500       510        520       530
  GCAGACATTCTGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTG-ACGTCCTCCAGA
  |||| |   |  |  | | |||||  |    || |   ||    ||  ||  ||   || | | || ||||
  GCAGGCCCGCCAGGTGCGCCTGGACCG--GCTG-GTCCACCGGGTG-CTCCGGGACCTGCAGGCCCGCCAGG
 260       270       280          290       300        310       320

         540       550          560       570          580       590
  AGCGTTTGCATCTTAGACCCTGCCACAG---TCTTCAGTTGCT-CTATCCAGC--GCTGGGCTAGGAAGAGG
   |||  || | |   | |    |||| |    || | |   || |   || ||  | || ||  || |  ||
  TGCGCCTGGACC---GGCTGGTCCACCGGGTGCTCCGGGACCTGCAGGCCCGCCAGGTGCGCCTGG-ACCGG
   330          340       350       360       370       380        390

   600       610       620       630       640        650         660
  CTCCACAAGGCCTTGCAGTGCTTCTCGTCCTGAAGATTGACGGCCA-CAGTGACTGGGTAATCT--TTAAGC
  ||   | |  ||     ||||| |  | |||| ||   | | ||||   | | ||||     ||  |  | |
  CTGGTCCA--CC---GGGTGCTCCGGGACCTGCAG---GCCCGCCAGGTGCGCCTGGACCGGCTGGTCCACC
     400            410       420          430       440       450

    670       680       690       700       710         720        730
  AGGTGGTCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGG--GACTGTG-GCTGAAGTAACAG
   |||| || |  | ||  |    |  |    ||    ||||   | |||   || | | |||   | | | |
  GGGTGCTCCGGGACCT-GCAGGCCCGCCAGGTGCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTG
 460       470        480       490       500       510       520

     740       750       760       770       780       790       800
  TCAGGTGTCCCCCGCAGGCAAGGACTCAGCAGCAGCAACAGCAGCAACAGGGAGGAATTTGGGCTCCAGGCT
   ||||    ||  |   ||  |||| | || |   || | |  ||  | ||||       |  | ||||| |
  -CAGGCCCGCCAGGTGCGCCTGGAC-CGGCTGGTCCACCGGGTGC-TCCGGGACCTGCAGGCCCGCCAGG-T
 530       540       550        560       570        580       590

   810       820       830       840        850       860        870
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    GGCGCCAGCACTGTCATCTCTGCCGGGGACCCCTCATGCCTG-TGACAGAGCAGGT-CGTCTCGTTC--CAG
    | |||| | || | |   ||  |||||  | ||     ||||  | |    ||||| || || |  |  | |
    G-CGCCTGGACCGGCTGGTCCACCGGGTGCTCC-GGGACCTGCAGGCCCGCCAGGTGCGCCTGGACCGGCTG
     600       610       620        630       640       650       660

         X
    -TCGAC
     || ||
    GTCCACCGGGTGCTCC
    670  X    680


15. US-08-162-407-1' (1-879)
    Q37818        Sequence encoding the alpha 1B-2 human calcium cha

 ID   Q37818 standard; cDNA; 7175 BP.
 AC   Q37818;
 DT   30-JUN-1993  (first entry)
 DE   Sequence encoding the alpha 1B-2 human calcium channel subunit.
 KW   Human calcium channel subunit; diagnosis; agonist; antagonist;
 KW   Lambert Eaton syndrome; ss.
 OS   Homo sapiens.
 FH   Key              Location/Qualifiers
 FT   CDS              144..6857
 FT   /*tag=  a
 PN   WO9304083-A.
 PD   04-MAR-1993.
 PF   14-AUG-1992; U06903.
 PR   15-AUG-1991; US-745206.
 PR   10-APR-1992; US-868354.
 PA   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
 PI   Brenner R,  Ellis SB,  Feldman DH,  Harpold MM,  Mccue AF,
 PI   Williams ME;
 DR   WPI; 93-093936/11.
 DR   P-PSDB; R33550.
 PT   DNA encoding specific human calcium channel sub-units - used for
 PT   identifying calcium channel agonists and antagonists and
 PT   diagnosing Lambert Eaton syndrome
 PS   Disclosure; Page 120-128; 150pp; English.
 CC   DNA encoding the alpha 1B subunit was isolated by screening a
 CC   human basal ganglia cDNA library with  fragments of the rabbit
 CC   skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
 CC   A portion of one of the positive clones was used to screen an IMR32
 CC   cell cDNA library. Clones that hybridized to the basal ganglia
 CC   DNA prove were used to further screen an IMR32 cell cDNA library
 CC   to identify overlapping clones that in turn were used to screen a
 CC   human hippocampus cDNA library. In this way, a sufficient series of
 CC   clones to span nearly the entire length of the nucleotide sequence
 CC   encoding the human alpha 1B subunit was obtained. PCR amplification
 CC   of specific regions of the IMR32 cell alpha 1B mRNA yielded
 CC   additonal segments of the alpha 1B coding sequence. A full-length
 CC   alpha 1B DNA clone was constructed by ligating portions of the
 CC   partial cDNA clones (see Q37817, Q37818). Alpha 1B-1 and alpha
 CC   1B-2 are derived by alternative splicing of the alpha 1B subunit
 CC   transcript.
 SQ   Sequence   7175 BP;    1415 A;    2204 C;    2162 G;    1394 T;

Initial Score     =    112  Optimized Score =    404  Significance =  6.56
Residue Identity  =    51%  Matches         =    488  Mismatches   =   336
Gaps              =    122  Conservative Substitutions           =     0
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              X        10        20        30          40         50
              GTCGA-CTGGAACGAGACGACCTGCTCCAGACCAT-TCAG-CA-ATCCTGCTCTG-GGCTCC
              || ||  ||||  || |||| |  ||    | || |   || || | || |  ||| |||| |
    GCCGCTGGTGGTGGAGCTGGGCCGCGACGGCGCGCGGGGGCCCGTGGGAGGCAAAGCCCGACCTGAGGCTGC
   2590      2600      2610      2620      2630      2640      2650

     60        70        80         90          100       110        120
    CAAGGGCTGAGATTACAGGTGTAACC-GAGATAAG--ACC-CTGGCTGAGTCAACGATGCACAAG-GCTCGA
      ||| |   ||   |  ||  | ||   |   ||  ||| | |||   | | || | | |||||  | |
    GGAGGCCCCCGAGGGC--GTCGACCCTCCGCGCAGGCACCACCGGCACCG-CGAC-AAGGACAAGACCCCCG
 2660      2670        2680      2690      2700       2710       2720

       130          140       150       160       170       180       190
    ATCCTAGGGA-TGGGA--GGGGAGGGGCACCCCAGGGTGGAGCTCCCCCCTCCTTCTTGCCCTTTGCCAGCG
       |  ||||   |||  | | || ||| ||| | || ||||  |      ||    |||||      ||||
    CGGCGGGGGACCAGGACCGAGCAGAGGC-CCCGAAGGCGGAGAGCGGGGAGCC-CGGTGCCCGGGAGGAGCG
   2730      2740      2750       2760      2770       2780      2790

           200       210        220       230       240       250       260
    ---AAGGCCCCAGGCGGCTGCCAGCAGC-ACCAGTGTGAGAGGCAGCAGCAGCAGCAGGAGCAACAGCTGCC
         |||| ||  | || |||| |||| |  ||   | | |||  | | ||  || ||||| |  || |||
    GCCGCGGCCGCA--CCGCAGCCA-CAGCAAGGAGGCCGCGGGGCCCCCGGAGGCGC-GGAGCGAGCGCGGCC
   2800        2810       2820      2830      2840      2850       2860

          270       280         290       300       310         320
    TGGGCCGAGGCTCTGGGAGC-TCCG-TGGCTTCTAGGGCTATGGGACTCCTTG--GGGGCAGCAGGGTGGAG
      |||| |||| | | | ||  |||  |||  |   |||   | | ||||  |  || || ||   | |  |
    GAGGCCCAGGCCCCGAGGGCGGCCGGCGGCACCACCGGC---GCGGCTCCCCGCAGGAGCCGC-CCGAGCGG
     2870      2880      2890      2900         2910      2920       2930

  330       340       350       360       370        380        390
    GAGTCCGGCTGGCACTGCACCTCCAGGCACCGAGAGAAATTCTGGC-AGGCCTTC-CCGATAC--AGGGCTT
    ||| || |  | ||| || |   | |||||| || |  || |  || |||  | | |||   |  |||||
    GAGCCCCGACGCCACCGCGCGCACCGGCACC-AG-G--ATCCGAGCAAGGAGTGCGCCGGCGCCAAGGGC--
       2940      2950      2960          2970      2980      2990

    400       410       420       430       440       450       460
    CAGAGCAAGCAGCTGTGTGCAGGTGTCCTTCAGGAGGTGGGAGATGTTGGTCTGGACGAATCGCAGACATTC
    ||| |   |  || |      || | ||  |  |||  |||    |   | | ||| ||  ||  ||    |
    CAGCGGCGGGCGCGGCACCGCGGCGGCC--CCCGAGCGGGGCCCCGGGAGGC-GGA-GA-GCGGGGAGGAGC
 3000      3010      3020        3030      3040       3050        3060

  470       480       490       500       510       520       530       540
    TGGTAGGGGCTGGAAGGTACATGAGGTGACAAAATGTATCTCGGTGTTGACGTCCTCCAGAAGCGTTTGCAT
     ||  | ||| | |  |  |     |  ||||   | | |  | |   || |   |  ||||| |    ||
    CGG-CGCGGCGGCACCGGGC---CCGGCACAAGGCGCAGCCTGCTCACGAGGCTGTGGAGAAG-GAGACCA-
     3070      3080         3090      3100      3110      3120       3130

           550         560       570       580       590               600
    CTTAG-ACCCTGCCAC--AGTCTTCAGTTGCTCTATCCAGCGCTGGGCTAGGAAGAG--GCT------CCAC
    |  || |    |||||  ||      | ||   ||      ||  | | ||||| ||  |||      ||||
    CGGAGAAGGAGGCCACGGAGAAGGAGGCTGAGATAGTGGAAGC-CGACAAGGAAAAGGAGCTCCGGAACCAC
        3140      3150      3160      3170       3180      3190      3200

         610       620        630       640         650       660       670
    AAGGCCTTGCAGTGCTTCT-CGTCCTGAAGATTGACGGCCACAGTGAC--TGGGTAATCTTTAAGCAGGTGG
     || ||  | ||     ||  | |||| |||   |  |  || |||||  |||||    |  |  ||  ||
    CAGCCCCGGGAGCCACACTGTGACCTGGAGA-CCAGTGGGACTGTGACTGTGGGTCCCATGCACACA-CTGC
       3210      3220      3230       3240      3250      3260       3270
```

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        680       690       700       710       720       730
  TCAGTCAACTCTCTAAACTTCACTTTGAAGTTGGAGGAGATGGGACTGTGGCTGAAGTAACAGTCAG----G
   ||| || || |||  |         |||| |||||  ||   | | | || || ||  ||| ||||
  CCAG-CACCTGTCTCCA---------GAAGGTGGAG--GAACAGCCAGAGGATGCAG--ACAATCAGCGGAA
      3280               3290        3300      3310        3320      3330

740       750            760       770         780             790
  TGTCCCCCGCA--GGCA---AGGACTCAGCAGCAGCAACAGCA--GCA------ACAGGGAGGAATTTGGGC
   ||| | ||||  ||||   ||  | ||| | | | ||||  |  | |       ||| || |     ||||
  CGTCACTCGCATGGGCAGTCAGCCCCCAG-ACCCG-AACACTATTGTACATATCCCAGTGATGCTGACGGGC
       3340      3350      3360        3370      3380      3390      3400

 800       810        820             830       840       850
  TCCAGGCTGGCGCCAG-CACTGTC-ATCTCTG-----CCGGGGACCCCTCATGCCTGTGACAG----AGCAG
   |    || | |  || ||| |||  || | |      || |||||    | |||    | ||    || ||
  CC---TCTTGGGGAAGCCACGGTCGTTCCCAGTGGTAACGTGGACCTGGAAAGCCAAGCAGAGGGGAAGAAG
          3410      3420      3430      3440      3450      3460      3470

860       870        X
  GTCGTCTCGTTCCAGTCGAC
  |  |  | |   | |  |||
  GAGG--TGGAAGCGGATGACGTGATGAGGA
          3480      3490
```

maryh@stic **stdin**

NeWSprinter20
Thu Apr 06 10:12:42 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

Spector 243545

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> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq5.res made by  on Wed 5 Apr 95 18:23:51-PDT.

Query sequence being compared:US-08-162-407-5 (1-988)
Number of sequences searched:             313646
Number of scores above cutoff:              3864

    Results of the initial comparison of US-08-162-407-5 (1-988) with:
  Data bank : EMBL-NEW 1, all entries
  Data bank : GenBank 86, all entries
  Data bank : GenBank-NEW 1, all entries
  Data bank : UEMBL 41_86, all entries

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N      -
U00000-
M      -
B      -
E      -
R      -
       -*
O      -
F00000- *
       -
S      -
E50000-
Q      -
U      *  *
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N      -
C      -
E      -
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  5000-
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       -
       -
       -
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   50-     *
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    -
    -
    -      *
    -
   10-
    -        *
    -
    5-      **
    -
    -
    -
    -
    -
    -              * *              *         *
    0------------------------------------------------------------------
      ||  |||||||  |    |    |    |    |    |    |    |
SCORE 0|  |108||| 216  324  432  540  648  756  864  972
STDEV -1      9

                          PARAMETERS

Similarity matrix      Unitary     K-tuple                 4
Mismatch penalty             1     Joining penalty        30
Gap penalty               1.00     Window size            32
Gap size penalty          0.33
Cutoff score                 2
Randomization group          0

Initial scores to save      45     Alignments to save     15
Optimized scores to save     0     Display context        10

                          SEARCH STATISTICS

Scores:                 Mean       Median      Standard Deviation
                          31           30        13.95

Times:                  CPU                    Total Elapsed
                      00:42:44.01              00:42:48.00

Number of residues:          288682119
Number of sequences searched:   313646
Number of scores above cutoff:    3864

Cut-off raised to 22.
Cut-off raised to 27.
Cut-off raised to 30.
Cut-off raised to 33.
Cut-off raised to 36.
Cut-off raised to 39.
Cut-off raised to 42.
Cut-off raised to 45.
Cut-off raised to 49.
Cut-off raised to 52.
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Cut-off raised to 56.
Cut-off raised to 59.
Cut-off raised to 62.
Cut-off raised to 66.
Cut-off raised to 70.
Cut-off raised to 74.
Cut-off raised to 78.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                     Init. Opt.
Sequence Name      Description                 Length Score Score  Sig. Frame
-----------------------------------------------------------------------------
                       **** 67 standard deviations above mean ****
   1. HSU03858      Human flt3 ligand mRNA, compl   1080   972   979  67.45   0
                       **** 51 standard deviations above mean ****
   2. HSU04806      Human FLT3/FLK2 ligand mRNA,     859   747   767  51.32   0
                       **** 26 standard deviations above mean ****
   3. MMU04807      Mus musculus FLT3/FLK2 ligand   1152   400   611  26.45   0
                       **** 24 standard deviations above mean ****
   4. MUSLIGAND     Mouse flt3 ligand mRNA, compl    829   378   580  24.87   0
                       **** 13 standard deviations above mean ****
   5. S65267        drebrin A {alternatively spli   1919   221   404  13.62   0
   6. CHKDEBPDA     Chicken drebrin mRNA.           2102   221   448  13.62   0
   7. HSELASRNA     H.sapiens RNA for dermal fibr   2241   218   405  13.40   0
   8. HSELASRNA     H.sapiens RNA for dermal fibr   2241   218   405  13.40   0
   9. HSELASRNA     H.sapiens RNA for dermal fibr   2241   218   405  13.40   0
  10. HUMELASF      Human elastin mRNA, complete    2242   218   405  13.40   0
  11. HSELASF       Human elastin mRNA, complete    2242   218   405  13.40   0
                       **** 11 standard deviations above mean ****
  12. HSOXYTOC      H.sapiens gene for oxytocin r   3617   193   461  11.61   0
  13. HSOXYTOC      H.sapiens gene for oxytocin r   3617   193   461  11.61   0
  14. HSMRNAOXY     H.sapiens mRNA for oxytocin r   4103   193   456  11.61   0
  15. TCU17917      Thermomonospora curvata alpha   2093   185   450  11.04   0
  16. TC17917       Thermomonospora curvata alpha   2093   185   450  11.04   0
                       **** 10 standard deviations above mean ****
  17. GGGFBPA       G.gallus gammaFBP-A mRNA.       3597   178   454  10.54   0
  18. STMPGLYZ      Streptomyces coelicolor bacte   9461   176   419  10.39   0
  19. SCPGLYZ       Streptomyces coelicolor bacte   9461   176   419  10.39   0
  20. DMHSP82       Drosophila melanogaster gene    5024   173   437  10.18   0
                       ****  9 standard deviations above mean ****
  21. PAXCPSP       P.aeruginosa genes xcpR, xcpS   5940   168   452   9.82   0
  22. AZSNIFA       A.lipoferum gene for NifA pro   2820   167   454   9.75   0
  23. SGSTR         Streptomyces griseus genes st  10653   166   457   9.68   0
  24. PMPEMA62A     Peromyscus maniculatus clone    1573   165   403   9.60   0
  25. MMRNAMHA      M.musculus mRNA for mouse hai   1591   164   436   9.53   0
  26. RABBCCBIII    Rabbit mRNA for rabbit brain    7713   163   437   9.46   0
  27. MZEKINAA      Z.mays protein cdc2 kinase mR   1325   162   436   9.39   0
  28. GGGFBPC       G.gallus gammaFBP-C mRNA.       3411   160   454   9.25   0
  29. GGGFBPB       G.gallus gammaFBP-B mRNA.       3551   160   454   9.25   0
  30. S45791        band 3-related protein=renal    3964   160   451   9.25   0
  31. BOVA1ADRE     Cow A1 adenosine receptor mRN   1977   159   444   9.17   0
  32. HSU11690      Human faciogenital dysplasia    4266   158   452   9.10   0
  33. HS11690       Human faciogenital dysplasia    4266   158   452   9.10   0
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  34. HUMOP2A       Homo sapiens osteogenic prote   1842   157   438   9.03   0
  35. HUMOP2A       Homo sapiens osteogenic prote   1842   157   438   9.03   0
                       ****  8 standard deviations above mean ****
  36. SCU03771      Streptomyces coelicolor A3(2)   6630   156   459   8.96   0
  37. HUMPDEAA      Human cyclic AMP (cAMP)-speci   2619   155   456   8.89   0
  38. HSGAA01       Human acid alpha-glucosidase    3441   155   452   8.89   0
  39. PIGI2AA       Porcine G protein gene, exon     983   152   388   8.67   0
  40. OAMGF         O.aries MGF mRNA for mammary    2820   150   448   8.53   0
  41. OAMGF         O.aries MGF mRNA for mammary    2820   150   448   8.53   0
  42. RATBCCA1S     Rat calcium channel alpha-1 s   6639   150   438   8.53   0
  43. AVIHUPZ       Azotobacter chroococcum hydro   5400   148   456   8.39   0
  44. RNDES         R.norvegicus gene for desmin.   2285   147   435   8.31   0
  45. ECPIFC        E. coli miniF plasmid gene pi   1710   146   439   8.24   0


1. US-08-162-407-5 (1-988)
   HSU03858     Human flt3 ligand mRNA, complete cds.

LOCUS       HSU03858      1080 bp    mRNA            PRI       19-JUL-1994
DEFINITION  Human flt3 ligand mRNA, complete cds.
ACCESSION   U03858
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1080)
  AUTHORS   Lyman,S.D., James,L., Johnson,L., Brasel,K., de Vries,P.,
            Escobar,S.S., Downey,H., Splett,R.R., Beckmann,M.P. and
            McKenna,H.J.
  TITLE     Cloning of the human homologue of the murine flt3 ligand: a growth
            factor for early hematopoietic progenitor cells
  JOURNAL   Blood 83, 2795-2801 (1994)
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 1080)
  AUTHORS   Lyman,S.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1993) Stewart D. Lyman, Immunex Research and
            Development Corporation, 51, University St., Seattle, WA 98101, USA
  STANDARD  full automatic
COMMENT     NCBI gi: 494978
FEATURES             Location/Qualifiers
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     CDS             84..791
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                     cells"
                     /product="flt3 ligand"
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                     TEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
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     misc_feature    630..698
                     /note="transmembrane domain"
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     3'UTR           792..1080
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     polyA_signal    1059..1064
     polyA_site      1080
                     /note="32 A residues"
BASE COUNT      204 a    384 c    290 g    202 t
ORIGIN

Initial Score    =    972  Optimized Score  =    979  Significance = 67.45
Residue Identity =    98%  Matches          =    980  Mismatches   =     8
Gaps             =      2  Conservative Substitutions            =     0

                    X        10        20        30        40        50        60
                    CGGCCGGA--ATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAA
                    || | |||    |  |||||||||||||||||||||||||||||||||||||||||||||||
          CAAGACCCGGCGACAGGAGGCATGAGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAA
                50  X     60        70        80        90       100       110

                 70        80        90       100       110       120       130
          CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGGACCCAGGACTGCTCCTTCCAACACA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGGACCCAGGACTGCTCCTTCCAACACA
             120       130       140       150       160       170       180

               140       150       160       170       180       190       200
          GCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCA
           190       200       210       220       230       240       250

             210       220       230       240       250       260       270
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGA
         260       270       280       290       300       310       320       330

           280       290       300       310       320       330       340
          TGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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                 340       350       360       370       380       390       400

         350       360       370       380       390       400       410       420
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TTGTCACCAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCC
               410       420       430       440       450       460       470

                 430       440       450       460       470       480       490
          TGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGG
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       480       490       500       510       520       530       540

            500       510       520       530       540       550       560
          AGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          AGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCC
           550       560       570       580       590       600       610

          570       580       590       600       610       620       630
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CGACAGCCCCGCAGCCCCCTCTGCTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCT
         620       630       640       650       660       670       680       690

          640       650       660       670       680       690       700
          GGTGCCTGCACTGGCAGAGGACGCGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GGTGCCTGCACTGGCAGAGGACGCGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTC
                 700       710       720       730       740       750       760

         710       720       730       740       750       760       770       780
          CCCAGGACCTGCTGCTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CCCAGGACCTGCTGCTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTG
              770       780       790       800       810       820       830

                 790       800       810       820       830       840       850
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          AGACAGACATCTATCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGG
             840       850       860       870       880       890       900

              860       870       880       890       900       910       920
          ATGTATAGCCTGGACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCATTCCCTCCCC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ATGTATAGCCTGGACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCATTCCCTCCCC
           910       920       930       940       950       960       970

            930       940       950       960       970       980      X
          AGAATGGAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
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          AA


2. US-08-162-407-5 (1-988)
   HSU04806      Human FLT3/FLK2 ligand mRNA, complete cds.

LOCUS       HSU04806       859 bp    mRNA            PRI       11-MAY-1994
DEFINITION  Human FLT3/FLK2 ligand mRNA, complete cds.
ACCESSION   U04806
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 798)
```

```
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 859)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483844
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 ORIGIN

Initial Score    =    747  Optimized Score =    767  Significance = 51.32
Residue Identity =    96%  Matches         =    771  Mismatches   =    25
Gaps             =      5  Conservative Substitutions              =     0

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              || | |||    |  |||||||||||||||||||||||||||||||||||||||||||||||
    CCTGACCCGGCGACAGGAGGCATGAGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAA
           60 X      70        80        90       100       110       120

            70        80        90       100       110       120       130
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    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGACCCAGGACTGCTCCTTCCAACACA
        130       140       150       160       170       180       190

         140       150       160       170       180       190       200
    GCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCA
      200       210       220       230       240       250       260

       210       220       230       240       250       260       270
    CCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGA
    |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
    CCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCGCTCTGGCGGCTGGTCCTGGCACAGCGCTGGA
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    270       280       290       300       310       320       330

     280       290       300       310       320       330       340
    TGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACT
  340       350       360       370       380       390       400       410

   350       360       370       380       390       400       410       420
    TTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCC
          420       430       440       450       460       470       480

           430       440       450       460       470       480       490
    TGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGG
        490       500       510       520       530       540       550

         500       510       520       530       540       550       560
    AGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCC
      560       570       580       590       600       610       620

       570       580       590       600       610       620       630
    CGACAGCCCCGCAGCCCCCTCTGCTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CGACAGCCCCGCAGCCCCCTCTGCTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCT
    630       640       650       660       670       680       690

     640       650       660       670       680       690       700
    GGTGCCTGCACTGGCAGAGGACGCGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GGTGCCTGCACTGGCAGAGGACGCGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTC
  700       710       720       730       740       750       760       770

   710       720       730       740       750       760       770       780
    CCCAGGACCTGCTGCTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTG
    |||||||||||||||||||||||||||||||||||||||||||||||||| ||||  |  |   | |||
    CCCAGGACCTGCTGCTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGGGGAGGAT--ACGTAGGCACAC
          780       790       800       810       820         830       840

           790       800
    AGACAGACATCTATCATCCCATTTTACAG
    |||  |   || | || ||
    AGAGGGAGTC-ACCAGCC
          850         X


3. US-08-162-407-5 (1-988)
   MMU04807      Mus musculus FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS        MMU04807     1152 bp    mRNA             ROD        11-MAY-1994
 DEFINITION   Mus musculus FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION    U04807
 KEYWORDS     .
 SOURCE       mouse.
   ORGANISM   Mus musculus
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            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Rodentia; Myomorpha; Muridae; Mus.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
            Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
            Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
            Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
            Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
  TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
            haematopoietic stem cells and is encoded by variant RNAs
  JOURNAL   Nature 368, 643-648 (1994)
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 1152)
  AUTHORS   Culpepper,J.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
            Institute, 901 California Avenue, Palo Alto, CA 94304, USA
  STANDARD  full automatic
COMMENT     NCBI gi: 483846
FEATURES             Location/Qualifiers
     source          1..1152
                     /clone="mouse Flt3/Flk2 ligand T110"
                     /clone_lib="TA4 cDNA"
                     /organism="Mus musculus"
                     /cell_line="TA4 stroma"
     CDS             256..954
                     /note="NCBI gi: 483847"
                     /codon_start=1
                     /product="FLT3/FLK2 ligand"
                     /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                     KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                     NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQ
                     CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARR
                     RGELHPGVPLPSHP"
BASE COUNT      238 a    346 c    324 g    244 t
ORIGIN

Initial Score    =    400  Optimized Score =     611  Significance = 26.45
Residue Identity =    67%  Matches         =     646  Mismatches   =   258
Gaps             =     57  Conservative Substitutions          =     0

           X          10        20        30        40        50
           CGG---CCGGAATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCA
           | |   | || | |  |||| ||||||| || ||||||||||||||||||||||||||||||
 TTCCAAGAACCTGTCACAGGCA-TGAGGGGTCCCCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCA
    220    X  230        240       250       260       270       280

60           70        80        90        100       110       120
 ACAACCTATC---TCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGACCCAGGACTGCTCCTTCCAA
 |   |||  |   | || ||| |||||||||||||  |  | ||  | |||| |  ||||| | ||||
 AATTCCTCCCTGTTGCTGCTGTTGCTGCTGCTGAGTCCTTGCCTGCGGGGACACCTGACTGTTACTTCAGC
  290       300       310       320       330       340       350

130       140       150       160       170       180       190       200
 CACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCA
 ||||| |||||||||||| |||||   || ||  |  | ||| || ||||| |||||||| |||||||||||
 CACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCA
 360       370       380       390       400       410       420

         210       220       230       240       250       260       270
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  GTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGC
  ||||| ||||||  ||| || ||||||||| ||| ||||  || | | ||| | ||  |||| || ||||||
  GTCACTGTGGCCGTCAATCTTCAGGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGC
430       440       450       460       470       480       490       500

       280       290       300       310        320       330       340
  TGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGC-AAGGCTTGCTGGAGCGCGTGAACACGGAGAT
  ||||| ||||  || |||||||| || ||||| ||||||| || |||| ||||||  ||| ||||| |||||
  TGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAACGCTT-CTGGAGGACGTCAACACCGAGAT
        510       520       530       540        550       560       570

      350       360       370       380       390       400       410
  ACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCG
  ||| |||||||||  |||| |||| |||||||  ||    ||||| || ||||||||||||||||||||||
  ACATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCA
       580       590       600       610       620       630       640

    420       430       440       450       460             470       480
  CCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATC----ACTC--GCCAGAACTTCTC
  ||||||| |||| |||| |   |||||| | |  ||||||||||| |||    |  |  ||||||| |||||
  CCTCCTGAAGGACACCTGCACACAGCTGCTTGGTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTC
     650       660       670       680       690       700       710

        490       500       510       520       530       540       550
  CCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGA
   |||||||||||| ||||||| ||||| |||||||| |||||||  |||||| ||||||||    |||| ||
  TCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGA
   720       730       740       750       760       770       780

        560       570         580        590       600          610
  GGCCAC--AGCCCCGACAGCCCCG---CAGCCCCCT-CTGCTCCTCCTACTGCTGCTGC--CC-GTGGGCCT
   |||||  ||| || | |||| ||   ||| |  ||  ||||||| || ||||||||||  ||  |    ||
  AGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCTGCCTCTCACACT
790       800       810       820       830       840       850       860

    620       630       640       650       660       670        680
  CCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCGGAGGACACCCCGCC-CTGGGGAGC
    |||||||||| || |||||| |||| | |||||| ||| |  |  |||||      | || |   ||
  GGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGG---
         870       880       890       900       910       920

  690       700       710       720       730       740       750
  AGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGC
   |||||||| |  | ||  |||| ||||   |   |||||| | |  ||||   |||| || || |||  |
  -GGTGCCCCTCCCCTCCCATCCCTAGGATGCGAGCCTTGTGCATCGTTGACTCAGCCAGGGTCTTATCTCGA
930       940       950       960       970       980       990      1000

760       770       780       790       800       810       820       830
  GGAGCCTTAAACAACGCAGTGAGACAGACATCTATCATCCCATTTTACAGGGGAGGATACTGAGGCACACAG
   |||   | || |        | || ||| |  |  | | |  |       | |   | |||   |||| |
  TGAGGTCTCAATATGTTGCCCAAACTGACTTTGAAAACCTCGAT-------GCACCTTCCTGCCCCACAAAC
       1010      1020      1030      1040              1050      1060

        840       850       860       870       880       890       900
  AGGGGAGTCACCAGCCAGAGGATGTATAGCCTGGACACAGAGGAAGTTGGCTAGAGGCCGGTC-CCTTCCTT
       |   || || | | || | ||  | |  |  | | |  ||   ||||     |   ||  ||| |||
  TTCCAA---AC-AG-CTG-GGCT-TACGGGCATGCTATATA-CAACAAGGCT---TTCTTTTCTTCTTTCTT
  1070           1080       1090       1100         1110      1120

       910       920       930       940
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GGGCCCCTCTCATTCCCTCCCCAGAATGGAGGCAACGCCAGAATC
||    ||    ||         |||   |  |||
GG--TGCTAGAGTT-------GGGAACCAAAACAA
  1130             1140      1150 X


4. US-08-162-407-5 (1-988)
  MUSLIGAND    Mouse flt3 ligand mRNA, complete cds.

 LOCUS       MUSLIGAND     829 bp ss-mRNA            ROD       04-JAN-1994
 DEFINITION  Mouse flt3 ligand mRNA, complete cds.
 ACCESSION   L23636
 KEYWORDS    ligand.
 SOURCE      Mus musculus (strain SJL/J) cDNA to mRNA.
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 829)
   AUTHORS   Lyman,S.D., James,L., VandenBos,T., deVries,P., Brasel,K.,
             Gliniak,B., Hollingsworth,L., Picha,K.S., McKenna,H.J.,
             Splett,R.R., Fletcher,F.A., Maraskovsky,E., Farrah,T.,
             Foxworthe,D., Williams,D.E. and Beckmann,M.P.
   TITLE     Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
             receptor -- a proliferative factor for primitive hematopoietic
             cells
   JOURNAL   Cell 75, 1157-1167 (1993)
   STANDARD  full automatic
 COMMENT     NCBI gi: 439441
 FEATURES             Location/Qualifiers
      source          1..829
                      /organism="Mus musculus"
                      /strain="SJL/J"
                      /sequenced_mol="cDNA to mRNA"
      sig_peptide     32..109
                      /codon_start=1
      CDS             32..727
                      /note="NCBI gi: 439442"
                      /codon_start=1
                      /product="flt3 ligand"
                      /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                      KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                      NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQ
                      CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR
                      GELHPGVPLPSHP"
      mat_peptide     110..724
                      /codon_start=1
 BASE COUNT      163 a    265 c    221 g    180 t
 ORIGIN

Initial Score     =    378  Optimized Score  =    580  Significance = 24.87
Residue Identity  =    71%  Matches          =    612  Mismatches   =   193
Gaps              =     55  Conservative Substitutions             =     0

    X          10        20        30        40        50        60
    CGG---CCGGAATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAACAACCTATC
    | |   | || | |  |||| ||||||| || |||||||||||||||||||||||||||||||   |||  |
    CTGTCACAGGCA-TGAGGGGTCCCCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCC
    X       10        20        30        40        50        60        70

      70        80        90       100       110       120       130
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 ---TCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGACCCAGGACTGCTCCTTCCAACACAGCCCCA
    | || ||| |||||||||||||  |  | ||  | ||||| |  ||||| | ||||  ||||| ||||
 TGTTGCTGCTGTTGCTGCTGCTGAGTCCTTGCCTGCGGGGACACCTGACTGTTACTTCAGCCACAGTCCCA
        80        90       100       110       120       130       140

140       150       160       170       180       190       200       210
 TCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGG
 |||||||| |||||   || ||  |  | ||| || ||||| |||||||| |||||||||||||||| ||||
 TCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGG
     150       160       170       180       190       200       210

        220       230       240       250       260       270       280
 CCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGC
 ||  ||| || ||||||||| ||| ||||  || | | ||| | ||  |||| || ||||||||||| ||||
 CCGTCAATCTTCAGGACGAGAAGCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGC
   220       230       240       250       260       270       280

       290       300       310       320       330       340       350
 GGCTCAAGACTGTCGCTGGGTCCAAGATGC-AAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTC
   || |||||||| || ||||| ||||||| || |||| ||||||  ||| ||||| |||||||| ||||||
 AACTGAAGACTGTGGCAGGGTCTAAGATGCAAACGCTT-CTGGAGGACGTCAACACCGAGATACATTTTGTC
 290       300       310       320       330       340       350

      360       370       380       390       400       410       420
 ACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAG
 |||  |||| |||| |||||||  ||    ||||| || |||||||||||||||||||||| ||||||| ||
 ACCTCATGTACCTTCCAGCCCCTACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAG
360       370       380       390       400       410       420       430

   430       440       450       460                 470       480       490
 GAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATC----ACTC--GCCAGAACTTCTCCCGGTGCCTG
 || |||| |   |||||| | || ||||||||||| |||    |  |  ||||||| ||||| |||||||||
 GACACCTGCACACAGCTGCTTGCTCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTG
        440       450       460       470       480       490       500

       500       510       520       530       540       550         560
 GAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCAC--AG
 ||| ||||||| ||||| |||||||| |||||||  |||||| ||||||||    |||| || |||||  ||
 GAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAG
      510       520       530       540       550       560       570

       570          580        590       600       610       620
 CCCCGACAGCCCCG---CAGCCCCCT-CTGCTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCC
 | || | |||| ||   ||| |  ||  ||||||| || |||||||||||  |    ||  ||||||||||
 CTCCCAGAGCCTCGGCCCAGGCAGCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCA
    580       590       600       610       620       630       640

630       640       650       660         670        680       690
 GCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCGGA--GGACACC-CCGCCCTGGGGAGCAGGTGCCCCCC
 || |||||| |||| | |||||| ||| |  |  |||  ||  | | || |||||||| ||     || |||
 GCCGCCTGGGGCCTTCGCTGGCAAAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGC----CCCTCCC
   650       660       670       680       690       700          710

700       710       720       730       740       750       760       770
 GTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAA
  ||||   |||| ||||   |   |||||| | |  ||||   |||| || || |||   |||    ||| |
 CTCCC--ATCCCTAGGATTCGAGCCTTGTGCATCGTTGACTCAGCCAGGGTCTTATC--TCGG----TTACA
      720       730       740       750       760       770

            780        790       800       810        820       830     X 840
    CAACGCAGTGA-GACAGACATCTATCATCCCATTTTACAGGGGAGGA-TACTGAGGCACACAGAGGGGAGTC
    |    | || |   ||| | | |   | ||       ||| | |||| | ||||     |  |   ||
    C----CTGTAATCTCAGCCCT-TGGGAGCC-------CAGAGCAGGATTGCTGA-----ATGGTCTGG
        780       790        800              810       820           X


    ACCAGC


5. US-08-162-407-5 (1-988)
   S65267       drebrin A {alternatively spliced, clone Dcb21} [ch

 LOCUS       S65267       1919 bp    mRNA            VRT       01-NOV-1993
 DEFINITION  drebrin A {alternatively spliced, clone Dcb21} [chickens, postnatal
             1-day old, mRNA Partial, 1919 nt].
 ACCESSION   S65267
 KEYWORDS    .
 SOURCE      chickens postnatal 1-day old.
   ORGANISM  Gallus sp.
             Unclassified.
 REFERENCE   1  (bases 1 to 1919)
   AUTHORS   Kojima,N., Shirao,T. and Obata,K.
   TITLE     Molecular cloning of a developmentally regulated brain protein,
             chicken drebrin A and its expression by alternative splicing of the
             drebrin gene
   JOURNAL   Brain Res. Mol. Brain Res. 19, 101-114 (1993)
   STANDARD  full automatic
 COMMENT     GenBank staff at the National Library of Medicine created this
             entry [NCBI gibbsq 137017] from the original journal article.

             This sequence comes from Fig. 3b.

             NCBI gi: 410593
 FEATURES             Location/Qualifiers
      source          1..1919
                      /organism="Gallus sp."
                      /note="chickens"
       CDS            1..1565
                      /partial
                      /note="Authors give incomplete codon for residue number
                      20;  Method: conceptual translation supplied by author.
                      This sequence comes from Fig. 3b.  Author-given protein
                      sequence is in conflict with the conceptual translation.
                      NCBI gi: 410594"
                      /codon_start=1
                      /product="drebrin A"
                      /translation="LSNGLARVSSPVLHRLRLREDENAEPVGTTYQKTDATVEMKRLN
                      REQFWEQAKKEEELRKEEERKKALDARLRFEQERMEQERLEQEERERRYREREEQIEE
                      HRRKQQSMEAEEARQRLKEQSIFGEQQEEDDRQQLRKSESEVEEAAAIIAQRPDNPRE
                      FFKQQERVASGSGDAISPGSHRTGRLHCPFIKTADSGPPSSSSSSSSPPRTPFPYITC
                      HRTPNLSSFFPCSQSDYRKVSAAGCSPCESSPASTPLGEQRTRAPAEETPATPKDSPS
                      PSTQVAEPAATEQHWPFPGPEDKAAEPPGDEPDPDPRPAWTAGADVLGDLVTLEPSEP
                      SPAPAASEPQPVETPGVAEPLIELWQSDGAAPAATSTWPLPDTPAGPPVPPEEGTLLG
                      LDELPEPPATFCDAEQHEEVEEEEEEEEEATAGEPHPTGLGYQEGYQEGPEVPPITNG
                      EMGPKDGTAGRGEQASEGYFSQSQEEEAPPPEEPSAKAPQPVFYNKPPEIDITCWDTD
                      PLPEEEESFGGGL"
 BASE COUNT      358 a    678 c    644 g    239 t
 ORIGIN

Initial Score    =     221  Optimized Score  =     404  Significance = 13.62
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Residue Identity =    49%  Matches           =   471  Mismatches    =   376
Gaps             =    100  Conservative Substitutions               =     0

     90       100        110       120       130        140       150
    TGAGCTCGGGACT-CAGTGGGACCCAGGACTGCTCCTTCCAACAC--AGCCCCATCTCCTCCGACTTC--GC
               || ||  |||   | ||   ||  | |||| | |   ||  || | ||| || || |  |
              TCTCCAACGGG---CTGGCGCGCGTC-TCCAGCCCCGTGCTGCACCGCCTGCGGCTGCGTGA
              X        10          20         30        40       50

        160        170        180       190       200        210        220
    TGTC-AAAAT-CCGTGAGCTGTCTG-ACTACCTGCTTCAAGATTACCCA-GTCACCGTGGCCTCCAACCTGC
     | | | ||| ||| |  | ||  | || |||| |  || ||  ||| | | ||||||||     || | ||
    GGACGAGAATGCCGAG-CCCGTGGGCACGACCTAC--CA-GAAAACCGACGCCACCGTGGAGATGAAGCGGC
    60        70         80        90          100       110       120

         230       240       250       260       270       280       290
    AGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG
       ||  |||||  | | |||  |       |   |    ||    ||||  |  ||||  |   || |  |
    TCAACCGGGAGCAGTTCTGGGAACAAGCCAAGAAAGAGGAGGAGTTGCGCAAGGAGGAGGAGAGGAA-AAAG
     130       140       150       160       170       180       190

       300        310       320       330       340       350       360
    TCGCTGGGT-CCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCC
     || ||| | |   | |||    |  || ||||||| || |   ||||   |    ||   |   | | ||
    GCGTTGGATGCGCGGCTGCGGTTCGAGCAGGAGCGCATGGAGCAGGAGCGGC----TGGAGCAGGAGGAGCG
    200       210       220       230       240           250       260

      370       380       390       400       410       420       430
    TTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAG
        || | |  ||     |    |||   |  |||| | |      | |      |||| ||| |   |||
    CGAGAGGCGCTACC-----GGGAGCGCGAGGAGCAGATCGAGGAGCACAGGAGGAAGCAGCAGAGCATGGAG
      270           280       290       300       310       320       330

    440       450        460       470       480       490       500
    CAGCTGGTGGCGCTGAAGC-CCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAG--TGTCAG
      |  || ||| | | ||| |||| |  |   || ||  | |||   ||   | | |   | ||   | |||
    GCGGAGGAGGCCCGGCAGCGCCTGAAGGA---GC-AGTCCATCTTTGGGGAGCAGCAAGAGGAGGACGACAG
         340       350       360           370       380       390       400

       510       520       530          540       550       560       570
    CC--CGACTCCTCAACCCTGCCACCCCCAT---GGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCC
     |  |  ||||  ||  | |   |     |   |||| || | |||      | |||  | || |||| |||
    GCAGCAGCTCCGGAAATCAGAGTCAGAGGTGGAGGAGGCCGCTGCCATCATTGCCCAGCGACCTGACAACCC
           410       420       430       440       450       460       470

          580       590       600           610        620         630
    C--GCAGCCCCCTCTGCTCCTCCTACTGCTG----CTGCCCGTGG-GCCTCCTGCT-GC-TGGCCGC----T
    |  | ||  |     ||  |     | | ||    | | | | || | | ||  || ||  ||| ||
    CCGGGAGTTCTTCAAGCAGCAGGAGCGGGTGGCATCGGGCAGCGGCGACGCCATCTCGCCGGGCAGCCATAG
         480       490       500       510       520       530       540

          640       650           660       670       680       690
    GCCTGGT-GCCTGCACTGGC---AGAGGACG-CGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCG
    | | ||| | |||||||| |     |  | | | || ||       ||||| |      |   | | || |
    GACAGGTCGTCTGCACTGTCCTTTCATAAAGACAGCTGACAGTGGGCCGCCTTCTTCTTC--TTCCTCCTCC
       550       560       570       580       590       600         610

  700       710       720       730        740       750        760
    TCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCA-CTGACCTGGCCAAGGCCTCATC-CTGCGGAGCCTTAA
    ||| |   |||  |||||   | |   |  | || ||| |   ||  |  ||  ||| || |     |||
    TCCTCCCCCCCGCGGACCCCTTTCCCCTATATCACCTGCCACCGC--ACCCCAAATCTCTCCTCTTTCTT--
       620       630       640       650         660       670       680

  770       780       790        800        810          820       830
    ACAACGCAGTGAGACAGACATCTATC-ATCCCATTTTACAG-GGGAGG-ATA--CTGAGGCACACAGAGGGG
     | | ||||  || | ||   ||| | |     ||   ||| |||  | |    ||| |   | |||   ||
    CCCATGCAGCCAGTCCGA---CTACCGAAAGGTTTCGGCAGCGGGCTGCAGCCCCTGCGAGTC-CAGCCCGG
         690       700          710       720       730       740        750

      840        850         860       870       880       890       900
    AGT-CAC-CAGCCAGAGGA--TGTATAGCCTGGACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGG
      | ||| | ||  |  ||   |   | ||  | | | |  ||||      ||| |||||   |  ||   |
    CCTCCACGCCGCTGGGCGAGCAGCGCACCCGCGCCCCGGCCGAAG------AGACGCCGGCAACGCCCAAAG
           760       770       780       790             800       810

       910         920            930       940       950       960
    GCCCCTCTCATTCCC--TCCCCAG-----AATGGAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCA
     | || | ||  |||    |||||     |  |  |||| || | ||   |||||| |||||   || ||
    ACTCC-CCCAGCCCCAGCACCCAGGTGGCAGAGCCGGCAGCGACTGA--GCAGCACTGGCCC---TTCCCTG
     820        830       840       850       860         870          880

  970         980       X
    ACTCTGA--ACAAAGCCCCCG
       ||||  |||||||  | |
    GGCCTGAAGACAAAGCTGCAGAGCCGCCGGG
         890       900  X    910


 6. US-08-162-407-5 (1-988)
    CHKDEBPDA    Chicken drebrin mRNA.

  LOCUS       CHKDEBPDA    2102 bp ss-mRNA            VRT       27-JUL-1990
  DEFINITION  Chicken drebrin mRNA.
  ACCESSION   M36961
  KEYWORDS    drebrin.
  SOURCE      Chicken brain cDNA to mRNA, clone pDcw17.
    ORGANISM  Gallus gallus
              Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
              Neognathae; Galliformes; Phasianidae.
  REFERENCE   1  (bases 1 to 2102)
    AUTHORS   Kojima,N., Kato,Y., Shirao,T. and Obata,K.
    TITLE     Nucleotide sequences of two embryonic drebrins, developmentally
              regulated brain proteins, and developmental change in their mRNAs
    JOURNAL   Mol. Brain Res. 4, 207-215 (1988)
    STANDARD  full automatic
  COMMENT     NCBI gi: 211725
  FEATURES             Location/Qualifiers
       source          1..2102
                       /organism="Gallus gallus"
       CDS             60..1883
                       /note="drebrin;  NCBI gi: 211726"
                       /codon_start=1
                       /translation="MAGVGFAAHRLELLASYQDVIGEDSPTDWALYTYEDGSDDLKLA
                       ASGGGGLLELSGHFEIQKVMYGFCSVKEPQAVLPKYVLVNWVGEDVPDARKCACASHV
                       AKIAEFFQGVDVIVNASSVEDIDPGAIGQRLSNGLARVSSPVLHRLRLREDENAEPVG
                       TTYQKTDATVEMKRLNREQFWEQAKKEEELRKEEERKKALDARLRFEQERMEQERLEQ
                       EERERRYREREEQIEEHRRKQQSMEAEEARQRLKEQSIFGEQQEEDDRQQLRKSESEV
                       EEAAAIIAQRPDNPREFFKQQERVASGSGDAISPGSHRTGSQSDYRKVSAAGCSPCES
                       SPASTPLGEQRTRAPAEETPATPKDSPSPSTQVAEPAATEQHWPFPGPEDKAAEPPGD
                       EPDPDPRPAWTAGADVLGDLVTLEPSEPSPAPAASEPQPVETPGVAEPLIELWQSDGA
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                       APAATSTWPLPDTPAGPPVPPEEGTLLGLDELPEPPATFCDAEQHEEVEEEEEEEEA
                       TAGEPHPTGLGYQEGYQEGPEVPPITNGEMGPKDGTAGRGEQASEGYFSQSQEEAPP
                       PEEPSAKAPQPVFYNKPPEIDITCWDTDPLPEEEESFGGGL"
 BASE COUNT       399 a    707 c    742 g    254 t
 ORIGIN

Initial Score     =    221  Optimized Score   =    448  Significance = 13.62
Residue Identity  =    50%  Matches           =    536  Mismatches   =   400
Gaps              =    126  Conservative Substitutions                  =     0

              X          10           20          30         40         50
              CGGCC---GGAATTC-CGGGGCC--CCCGGCCGA--AATGACAGTG-CTGG-CGCCAGCCTG
                |||   |  |  | || ||||      || ||    |  ||| |  |||  |  | | |
    GCCCGCAAATGTGCCTGTGCCAGCCACGTGGCCAAGATCGCAGAGTTCTTCCAGGGTGTGGATGTTATCGTC
      340     X 350       360       370       380       390       400

          60          70        80        90       100        110
    GAGCCCAACAACCT--ATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGGAC-CCA--GGACT--
     |  ||| || | |  |   | |  ||   | | ||     |||||   ||| ||  | |||  || ||
    AATGCCAGCAGCGTGGAGGACAT--TGACCCGGGGGC---CATCGGG---CAGCGGCTCTCCAACGGGCTGG
    410       420       430         440             450       460       470

     120        130         140       150          160        170        180
    -GCTCCT-TCCAACAC--AGCCCCATCTCCTCCGACTTC--GCTGTC-AAAAT-CCGTGAGCTGTCTG-ACT
     || | | |||| | |   ||  || | ||| || || |  |  | | | ||| ||| |  | ||  | ||
    CGCGCGTCTCCAGCCCCGTGCTGCACCGCCTGCGGCTGCGTGAGGACGAGAATGCCGAG-CCCGTGGGCACG
              480       490       500       510       520       530        540

           190       200        210       220       230       240       250
    ACCTGCTTCAAGATTACCCA-GTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGG
    |||| |  || ||  ||| | | ||||||||     || | ||   ||  |||||  | | |||  |
    ACCTAC--CA-GAAAACCGACGCCACCGTGGAGATGAAGCGGCTCAACCGGGAGCAGTTCTGGGAACAAGCC
           550        560       570       580       590       600       610

          260       270       280       290       300        310       320
    CGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGT-CCAAGATGCAAGGCTTGCT
      |   |    ||    ||||  |  ||||  |   || |  | || ||| | |   | |||    |  ||
    AAGAAAGAGGAGGAGTTGCGCAAGGAGGAGGAGAGGAA-AAAGGCGTTGGATGCGCGGCTGCGGTTCGAGCA
          620       630       640        650       660       670       680

         330       340       350       360       370       380       390
    GGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTT
    ||||||| || |   ||||   |    ||   |   | | ||     || | |  ||     |    |||
    GGAGCGCATGGAGCAGGAGCGGC----TGGAGCAGGAGGAGCGCGAGAGGCGCTACC-----GGGAGCGCGA
         690       700           710       720       730            740

       400       410       420       430       440       450        460
    CGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGC-CCTGGATCA
     |  |||| | |      | |      |||| ||| |   |||  |  || ||| | | ||| |||| |  |
    GGAGCAGATCGAGGAGCACAGGAGGAAGCAGCAGAGCATGGAGGCGGAGGAGGCCCGGCAGCGCCTGAAGGA
      750       760       770       780       790       800       810

      470       480       490       500           510       520       530
    CTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAG--TGTCAGCC--CGACTCCTCAACCCTGCCACCCCCA
       || ||  | |||   ||   | | |   | ||   | ||| |  |  ||||  ||  | |   |
    ---GC-AGTCCATCTTTGGGGAGCAGCAAGAGGAGGACGACAGGCAGCAGCTCCGGAAATCAGAGTCAGAGG
        820       830       840       850       860       870       880

        540       550        560       570        580        590       600
    TGGAGTCCCCGGCCCCTGGAGGCCA-CAGCCCCGACAGCCCCG-CAGCCCCC-TCTGCTCCTCCTACTGCTG
    |||||     |||| ||    |||| ||   || |  | || | || |||||    | || ||   | || |
    TGGAG---GAGGCCGCT----GCCATCATTGCCCAGCGACCTGACAACCCCCGGGAGTTCTTCAAGCAGCAG
      890              900       910       920       930       940       950

         610       620       630       640       650         660         670
    CTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGAC--GCGGC--GGAGGAC
      ||  || ||| ||  || || ||| |  |||   |  | |  | | || |||||  || ||  |   |||
    GAGCGGGT-GGCATCGGGCAGC-GGC-GACGCCATCTCGCCGGGCAGCCATAGGACAGGCAGCCAGTCCGAC
            960       970         980       990      1000      1010

              680       690        700         710           720       730
    -ACC--CCGCCCTGGGGAGCAGG-TGCCCCCCGTCCCCAGTCC--CCAGGACCT----GCTGCTTGTGGAGC
     |||    |   | || ||| || |||  ||| |  | |||||  || || |||    || ||| |  ||||
    TACCGAAAGGTTTCGGCAGCGGGCTGCAGCCCCT-GCGAGTCCAGCCCGG-CCTCCACGCCGCTGGGCGAGC
 1020      1030      1040      1050       1060       1070      1080

          740        750       760       770       780         790       800
    A-CTGACCTG-GCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACA--TCTATCATCCC
    | |  ||| | |||  ||||  |    | |  |||   |||  | ||  ||  |   ||   | | || |||
    AGCGCACCCGCGCCCCGGCCGAA----GAGACGCCGGCAAC-GCCCAAAGACTCCCCCAGCCCCAGCA-CCC
 1090      1100      1110          1120       1130      1140      1150

              810       820       830       840        850       860
    ATTTTACAG---GGGAGGATACTGAGGCACACAGAGGGGAGTCAC-CAGCCAGAGGATGTATAGCCTGGACA
    |  |  |||    ||  |  ||||| |||  ||  ||    || |   ||| || ||   | || |||  ||
    AGGTGGCAGAGCCGGCAGCGACTGA-GCA-GCACTGGCCCTTCCCTGGGCCTGAAGA--CAAAG-CTG--CA
     1160      1170      1180        1190      1200      1210           1220

   870       880       890       900        910       920        930
    CAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCC-CCTCTCATTCCCTCCCCAGA-ATG--GAGGCA
     ||  |  |  ||   ||| |||  |||  ||   ||||  |    |   |     | ||  ||  | || |
    GAGCCGCCG-GGGGACGAGCCCGACCCCGACCCCAGGCCGGCGTGGACAGCGGGGGCTGACGTGCTGGGGGA
           1230      1240      1250      1260      1270      1280      1290

           940          950       960        970         980         X
    AC------GCCAGAATC---CAGCACCGGCCCCATTTACC-CAAC-TCTGAA-CAAAGCCCCCG
     |       || | | |   | |  ||  |||||    || |  | || ||| |  |||||  |
    CCTGGTGACCCTGGAGCCCTCCGAGCCATCCCCAGCGCCCGCTGCGTCCGAACCCCAGCCCGTGGAGACACC
         1300      1310      1320      1330      1340      1350    X 1360

    CG


7. US-08-162-407-5 (1-988)
 HSELASRNA     H.sapiens RNA for dermal fibroblast elastin.

 LOCUS       HSELASRNA    2241 bp  RNA               PRI       16-DEC-1994
 DEFINITION  H.sapiens RNA for dermal fibroblast elastin.
 ACCESSION   X52896
 KEYWORDS    elastin.
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2241)
   AUTHORS   Fazio,M.J., Olsen,D.R., Kauh,E.A., Baldwin,C.T., Indik,Z.,
             Ornstein-Goldstein,N., Yeh,H., Rosenbloom,J. and Uitto,J.
   TITLE     Cloning of full-length elastin cDNAs from a human skin fibroblast
             recombinant cDNA library: further elucidation of alternative
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             splicing utilizing exon-specific oligonucleotides
 JOURNAL     J. Invest. Dermatol. 91, 458-464 (1988)
   STANDARD  full automatic
 COMMENT     NCBI gi: 31133
 FEATURES             Location/Qualifiers
      source          1..2241
                      /organism="Homo sapiens"
 BASE COUNT      333 a    597 c    840 g    471 t
 ORIGIN

Initial Score     =     218   Optimized Score    =     405   Significance = 13.40
Residue Identity  =     49%   Matches            =     478   Mismatches   =   374
Gaps              =     113   Conservative Substitutions                  =     0

              X            10                 20        30         40
              CG--GCCGGA---ATTCCGG-----GGC----CCCCGGCCGAAATGACAG-TGCTGGCGCC-
              ||  | ||||    | ||||     |||    |||| |  |    | |||  |||| ||||
    GAGGTGTTCCCGGAGTCGGAGGTGTCCCGGGAGTTGGCATTTCCCCCGAAGCTCAGGCAGCAGCTGCCGCCA
  1320      1330      1340      1350      1360      1370      1380      1390

      50        60              70        80         90        100       110
    AGCCTGGAGCCCAACAACCTA------TCTCCTCCTGCTGCTGCTGCT-GAGCTCGGGACTCAGTGGGACCC
    || |||    ||||  ||  |       | ||  | ||||| ||||||  |||    | |  ||  |  |||
    AGGCTG----CCAAGTACGGAGTGGGGACCCCAGCAGCTGCAGCTGCTAAAGCAGCCGCCAAAGCCG--CCC
              1400      1410      1420      1430      1440      1450

          120          130       140       150       160       170
    AGGACTGCTCCTTCCAA---CACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTC-TGAC
    | |  ||||| |  |||     |||    |  ||||  |   |||  ||     |||  ||| || | || |
    A-GTTTGCTCTTCTCAATCTTGCAGGGTTAGTTCCT--GGTGTCGGCGT--GGCTCCTGGAGTTGGCGTGGC
     1460      1470      1480      1490        1500        1510      1520

  180       190       200       210       220       230              240
    TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC-------TGCGGGGG
    | |||| |    |  |  |   |     |||| |    |||| ||   | |  ||||       ||  | ||
    T-CCTGGTGTCGGTGTGGCTCCTGGAGTTGGCTTGGCTCCTGGAGTTGGCGTGGCTCCTGGAGTTGGTGTGG
        1530      1540      1550      1560      1570      1580      1590

       250            260        270       280       290       300       310
    CCTCTGGC---GGC-TGG-TCCTGGCA-CAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGAT
    |  |||||   ||| ||| ||| ||||   || |||| |||||  ||   || |||  ||    |||  | |
    CTCCTGGCGTTGGCGTGGCTCCCGGCATTGGCCCTGG-TGGAGTTGC---AG-CTGCAGCAAAATCC--GCT
      1600      1610      1620      1630       1640          1650

           320        330       340       350       360       370       380
    GCAAGGCTTGCTG-GAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCA
    || | | | ||||  |  ||   | | | ||| | ||  | | |       ||| ||  || |||    |
    GCCAAGGTGGCTGCCAAAGC-CCAGCTCCGAGCTGCAGCTGGGC----TTGGTG-CTGGCATCCCTGGACTT
 1660      1670       1680      1690      1700           1710      1720

          390       400       410       420       430       440       450
    GCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGA
    |  |  || |  ||| |  | ||     ||      |  ||| || |  |   ||   |  | ||| ||||
    G--GAGTTGGTGTCGGC--GTCCCTGGACTTGGAGTTGGTGCTGGTGTTCCTGGACTTGGAGTTGGTGCTGG
       1730      1740        1750      1760      1770      1780      1790

         460       470       480       490       500         510       520
    AG-CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCC--CGACTCCTCAACCC
     |  ||||| |  |  | ||| || |    |  || |||  |||  ||   |||||    |     || |
    TGTTCCTGGCT-TCGGGGCAGTACCTGGAGCCCTGGCTGCCGCTAAAG---CAGCCAAATATGGAGCAGCAG
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     1800       1810      1820      1830      1840         1850      1860

         530        540       550           560       570       580
  TGCC--ACCCCCATGGA-GTCCCCGGCCCCT----GGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTG
  ||||      || |||| | | | || | ||    ||||    || ||| | | |    |  |   |  | |
  TGCCTGGGGTCCTTGGAGGGCTCGGGGCTCTCGGTGGAGTAGGCATCCCAGGCGGTGTGGTGGGAGC--CGG
       1870      1880      1890      1900      1910      1920        1930

  590       600       610       620         630         640       650
  CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGC--TGGCCGCTGCCTGGT--GCCTGCACTGGCAGAG
    || ||  | || ||||||   |      |||||||    |||||  || | |  ||||  | ||| ||
  ACCCGCC-GCCGCCGCTGCCGCAGCCAAAGCTGCTGCCAAAGCCGC--CCAGTTTGGCCT--AGTGGGAGCC
        1940      1950      1960      1970        1980        1990

    660        670       680        690       700       710          720
  GACGCG-GCGGAGGACACCCCGCCCTGGGGAGC-AGGTGCCCCCCGTCCCCAGTCCCCAGGACCT---GCTG
  |  | |  |||||||| |   | |  || | ||  || |  ||  ||     |  ||  |||  |    ||
  GCTGGGCTCGGAGGACTCGGAGTC--GGAGGGCTTGGAGTTCCAGGTGTTGGGGGCCTTGGAGGTATACCTC
2000      2010      2020        2030      2040      2050      2060

       730        740       750       760       770       780       790
  CTTGTGGAG-CACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATCTA
  |   || || | || |    || ||   |   | |||| | |||||  |     |   | |   | |    |
  CAGCTGCAGCCGCTAAAGCAGCTAAATAC-GGTGCTGCTG-GCCTTGGAGGTGTCCTAGGGGGTGCCGGGCA
2070      2080      2090       2100       2110      2120      2130

      800       810       820       830       840       850       860
  TCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGG
     |||||  ||  ||| | ||   |     |   |   ||   ||| ||         | ||   |||||
  -GTTCCCA-CTTGGAGGAGTGGCAGCAAGACCTGGCTTCGGATTGTCTCCCATTTTCCCAGGTGGGGCCTG-
 2140       2150      2160      2170      2180      2190      2200

    870       880       890       900   X   910
  ACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCA
     | | ||||    ||| | ||||||         ||
  --CCTGGGGAA---AGCTTGTGGCCGGAAGAGAAAATGA
   2210         2220      2230      2240
```

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8. US-08-162-407-5 (1-988)
   HSELASRNA    H.sapiens RNA for dermal fibroblast elastin.

 LOCUS       HSELASRNA    2241 bp    RNA             PRI       23-NOV-1994
 DEFINITION  H.sapiens RNA for dermal fibroblast elastin.
 ACCESSION   X52896
 KEYWORDS    elastin.
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2241)
   AUTHORS   Fazio,M.J., Olsen,D.R., Kauh,E.A., Baldwin,C.T., Indik,Z.,
             Ornstein-Goldstein,N., Yeh,H., Rosenbloom,J. and Uitto,J.
   TITLE     Cloning of full-length elastin cDNAs from a human skin fibroblast
             recombinant cDNA library: further elucidation of alternative
             splicing utilizing exon-specific oligonucleotides
   JOURNAL   J. Invest. Dermatol. 91, 458-464 (1988)
   STANDARD  full automatic
 COMMENT     NCBI gi: 31133
 FEATURES             Location/Qualifiers
```

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      source          1..2241
                      /organism="Homo sapiens"
 BASE COUNT      333 a    597 c    840 g    471 t
 ORIGIN

Initial Score    =    218  Optimized Score =    405  Significance = 13.40
Residue Identity =    49%  Matches         =    478  Mismatches   =   374
Gaps             =    113  Conservative Substitutions         =     0

             X            10                 20        30         40
             CG--GCCGGA---ATTCCGG-----GGC----CCCCGGCCGAAATGACAG-TGCTGGCGCC-
             ||  | ||||    | ||||     |||    |||| |  |    | |||  |||| ||||
   GAGGTGTTCCCGGAGTCGGAGGTGTCCCGGGAGTTGGCATTTCCCCCGAAGCTCAGGCAGCAGCTGCCGCCA
 1320      1330      1340      1350      1360      1370      1380      1390

     50        60              70        80         90      100       110
   AGCCTGGAGCCCAACAACCTA------TCTCCTCCTGCTGCTGCTGCT-GAGCTCGGGACTCAGTGGGACCC
   || |||    ||||  ||  |       | ||  | ||||| ||||||  |||    | |  ||  |  |||
   AGGCTG----CCAAGTACGGAGTGGGGACCCCAGCAGCTGCAGCTGCTAAAGCAGCCGCCAAAGCCG--CCC
             1400      1410      1420      1430      1440      1450

         120          130       140       150       160       170
   AGGACTGCTCCTTCCAA---CACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTC-TGAC
   | |  ||||| |  |||     |||    |  ||||  |   |||  ||     |||  ||| || | || |
   A-GTTTGCTCTTCTCAATCTTGCAGGGTTAGTTCCT--GGTGTCGGCGT--GGCTCCTGGAGTTGGCGTGGC
    1460      1470      1480      1490        1500        1510      1520

 180       190       200       210       220       230              240
   TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC-------TGCGGGGG
   | |||| |    |  |  |   |     |||| |    |||| ||   | |  ||||       ||  | ||
   T-CCTGGTGTCGGTGTGGCTCCTGGAGTTGGCTTGGCTCCTGGAGTTGGCGTGGCTCCTGGAGTTGGTGTGG
       1530      1540      1550      1560      1570      1580      1590

      250            260        270       280       290       300       310
   CCTCTGGC---GGC-TGG-TCCTGGCA-CAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGAT
   |  |||||   ||| ||| ||| ||||   || |||| |||||  ||   || |||  ||    |||  | |
   CTCCTGGCGTTGGCGTGGCTCCCGGCATTGGCCCTGG-TGGAGTTGC---AG-CTGCAGCAAAATCC--GCT
     1600      1610      1620      1630       1640          1650

          320        330       340       350       360       370       380
   GCAAGGCTTGCTG-GAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCA
   || | | | ||||  |  ||   | | | ||| | || |       ||| ||  || |||    |
   GCCAAGGTGGCTGCCAAAGC-CCAGCTCCGAGCTGCAGCTGGGC----TTGGTG-CTGGCATCCCTGGACTT
1660      1670       1680      1690      1700           1710      1720

         390       400       410       420       430       440       450
   GCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGA
   |  |  || |  ||| |  | ||     ||      |  ||| || |  |   ||   |  | ||| ||||
   G--GAGTTGGTGTCGGC--GTCCCTGGACTTGGAGTTGGTGCTGGTGTTCCTGGACTTGGAGTTGGTGCTGG
      1730      1740        1750      1760      1770      1780      1790

        460       470       480       490       500         510       520
   AG-CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCC--CGACTCCTCAACCC
    |  ||||| |  |  | ||| || |    |  || |||  |||  ||   |||||    |     || |
   TGTTCCTGGCT-TCGGGGCAGTACCTGGAGCCCTGGCTGCCGCTAAAG---CAGCCAAATATGGAGCAGCAG
      1800       1810      1820      1830      1840         1850      1860

          530        540       550           560       570       580
   TGCC--ACCCCCATGGA-GTCCCCGGCCCCT----GGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTG
   ||||      || |||| | | | || | ||    ||||    || ||| | | |    |  |   |  | |
    TGCCTGGGGTCCTTGGAGGGCTCGGGGCTCTCGGTGGAGTAGGCATCCCAGGCGGTGTGGTGGGAGC--CGG
         1870      1880      1890      1900      1910      1920        1930

    590       600       610       620         630         640       650
    CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGC--TGGCCGCTGCCTGGT--GCCTGCACTGGCAGAG
      || ||  | || ||||||   |      |||||||    |||||  || | |  ||||  | ||| ||
    ACCCGCC-GCCGCCGCTGCCGCAGCCAAAGCTGCTGCCAAAGCCGC--CCAGTTTGGCCT--AGTGGGAGCC
          1940      1950      1960      1970        1980        1990

      660        670       680        690       700       710          720
    GACGCG-GCGGAGGACACCCCGCCCTGGGGAGC-AGGTGCCCCCCGTCCCCAGTCCCCAGGACCT---GCTG
    |  | |  |||||||| |   | |  || | ||  || |  ||  ||     |  ||  |||  |    ||
    GCTGGGCTCGGAGGACTCGGAGTC--GGAGGGCTTGGAGTTCCAGGTGTTGGGGGCCTTGGAGGTATACCTC
  2000      2010      2020        2030      2040      2050      2060

         730        740       750       760       770       780       790
    CTTGTGGAG-CACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATCTA
    |   || || | || |    || ||   |   | |||| | |||||  |     |   | |   | |     |
    CAGCTGCAGCCGCTAAAGCAGCTAAATAC-GGTGCTGCTG-GCCTTGGAGGTGTCCTAGGGGGTGCCGGGCA
  2070      2080      2090       2100       2110      2120      2130

        800       810       820       830       840       850       860
    TCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGG
       |||||  ||  ||| | ||   |     |   |   ||   ||| ||         | ||   |||||
    -GTTCCCA-CTTGGAGGAGTGGCAGCAAGACCTGGCTTCGGATTGTCTCCCATTTTCCCAGGTGGGGCCTG-
   2140       2150      2160      2170      2180      2190      2200

      870       880       890       900   X   910
    ACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCA
       | | ||||    ||| | ||||||         ||
    --CCTGGGGAA---AGCTTGTGGCCGGAAGAGAAAATGA
     2210         2220      2230      2240

 9. US-08-162-407-5 (1-988)
    HSELASRNA    H.sapiens RNA for dermal fibroblast elastin

 ID   HSELASRNA  standard; RNA; PRI; 2241 BP.
 XX
 AC   X52896;
 XX
 DT   18-FEB-1992 (Rel. 31, Created)
 DT   16-DEC-1994 (Rel. 42, Last updated, Version 5)
 XX
 DE   H.sapiens RNA for dermal fibroblast elastin
 XX
 KW   elastin.
 XX
 OS   Homo sapiens (human)
 OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC   Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 XX
 RN   [1]
 RP   1-2241
 RA   Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
 RA   Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
 RT   "Cloning of full-length elastin cDNAs from a human skin fibroblast
 RT   recombinant cDNA library: further elucidation of alternative
 RT   splicing utilizing exon-specific oligonucleotides";
 RL   J. Invest. Dermatol. 91:458-464(1988).
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XX
FH   Key             Location/Qualifiers
FH
FT   source          1..2241
FT                   /organism="Homo sapiens"
XX
SQ   Sequence 2241 BP; 333 A; 597 C; 840 G; 471 T; 0 other;

Initial Score    =    218  Optimized Score   =    405  Significance = 13.40
Residue Identity =    49%  Matches           =    478  Mismatches   =   374
Gaps             =    113  Conservative Substitutions          =     0

              X            10                  20        30          40
              CG--GCCGGA---ATTCCGG-----GGC----CCCCGGCCGAAATGACAG-TGCTGGCGCC-
              ||  | ||||    | ||||     |||    |||| |  |    | |||  |||| ||||
    GAGGTGTTCCCGGAGTCGGAGGTGTCCCGGGAGTTGGCATTTCCCCCGAAGCTCAGGCAGCAGCTGCCGCCA
  1320      1330      1340      1350      1360      1370      1380      1390

      50        60              70        80         90       100       110
    AGCCTGGAGCCCAACAACCTA------TCTCCTCCTGCTGCTGCTGCT-GAGCTCGGGACTCAGTGGGACCC
    || |||    ||||  ||  |       | ||  | |||| | ||||||  |||    | |  ||  |  |||
    AGGCTG----CCAAGTACGGAGTGGGGACCCCAGCAGCTGCAGCTGCTAAAGCAGCCGCCAAAGCCG--CCC
              1400      1410      1420      1430      1440      1450

          120          130       140       150       160       170
    AGGACTGCTCCTTCCAA---CACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTC-TGAC
    | |  ||||| |  |||     |||    |  ||||  |   |||  ||     |||  ||| || | || |
    A-GTTTGCTCTTCTCAATCTTGCAGGGTTAGTTCCT--GGTGTCGGCGT--GGCTCCTGGAGTTGGCGTGGC
     1460      1470      1480      1490        1500        1510      1520

  180       190       200       210       220       230              240
    TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC-------TGCGGGGG
    | |||| |    |  |  |   |     |||| |    |||| ||   | |  ||||       ||  | ||
    T-CCTGGTGTCGGTGTGGCTCCTGGAGTTGGCTTGGCTCCTGGAGTTGGCGTGGCTCCTGGAGTTGGTGTGG
       1530      1540      1550      1560      1570      1580      1590

      250            260        270       280       290       300       310
    CCTCTGGC---GGC-TGG-TCCTGGCA-CAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGAT
    |  |||||   ||| ||| ||| ||||   || |||| |||||  ||   || |||  ||    |||  | |
    CTCCTGGCGTTGGCGTGGCTCCCGGCATTGGCCCTGG-TGGAGTTGC---AG-CTGCAGCAAAATCC--GCT
     1600      1610      1620      1630       1640          1650

          320        330       340       350       360       370       380
    GCAAGGCTTGCTG-GAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCA
    || | | | ||||  |  ||   | | | ||| | ||  | | |        ||| ||  || |||    |
    GCCAAGGTGGCTGCCAAAGC-CCAGCTCCGAGCTGCAGCTGGGC----TTGGTG-CTGGCATCCCTGGACTT
 1660      1670       1680      1690      1700           1710      1720

         390       400       410       420       430       440       450
    GCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGA
    |  |  || |  ||| |  | ||     ||      |  ||| || |  |   ||   |  | ||| ||||
    G--GAGTTGGTGTCGGC--GTCCCTGGACTTGGAGTTGGTGCTGGTGTTCCTGGACTTGGAGTTGGTGCTGG
      1730      1740        1750      1760      1770      1780      1790

        460       470       480       490       500         510       520
    AG-CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCC--CGACTCCTCAACCC
     |  ||||| |  |  | ||| || |    |  || |||  |||  ||   |||||    |     || |
    TGTTCCTGGCT-TCGGGGCAGTACCTGGAGCCCTGGCTGCCGCTAAAG---CAGCCAAATATGGAGCAGCAG
      1800       1810      1820      1830      1840        1850      1860
```

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         530        540       550           560       570       580
  TGCC--ACCCCCATGGA-GTCCCCGGCCCCT----GGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTG
  ||||      || |||| | | | || | ||    ||||    || ||| | | |    |  |   |  | |
  TGCCTGGGGTCCTTGGAGGGCTCGGGGCTCTCGGTGGAGTAGGCATCCCAGGCGGTGTGGTGGGAGC--CGG
       1870      1880      1890      1900      1910      1920        1930

  590       600       610       620         630         640       650
  CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGC--TGGCCGCTGCCTGGT--GCCTGCACTGGCAGAG
    || ||  | || ||||||   |      |||||||    |||||  || | |  ||||  | ||| ||
  ACCCGCC-GCCGCCGCTGCCGCAGCCAAAGCTGCTGCCAAAGCCGC--CCAGTTTGGCCT--AGTGGAGCC
        1940      1950      1960      1970        1980        1990

    660        670        680        690        700        710          720
  GACGCG-GCGGAGGACACCCCGCCCTGGGGAGC-AGGTGCCCCCCGTCCCCAGTCCCCAGGACCT---GCTG
  |  | |  |||||||| |   | |  || | ||  || |  ||  ||     |  ||  |||  |    ||
  GCTGGGCTCGGAGGACTCGGAGTC--GGAGGGCTTGGAGTTCCAGGTGTTGGGGGCCTTGGAGGTATACCTC
2000      2010      2020        2030      2040      2050      2060

       730         740       750       760       770       780       790
  CTTGTGGAG-CACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATCTA
  |   || || | || |    || ||   |   | |||| | |||||  |     |   | |   | |    |
  CAGCTGCAGCCGCTAAAGCAGCTAAATAC-GGTGCTGCTG-GCCTTGGAGGTGTCCTAGGGGGTGCCGGGCA
2070      2080      2090       2100       2110      2120      2130

      800        810       820       830       840       850       860
  TCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGG
     |||||  ||  ||| | ||   |     |   |   ||   ||| ||         | ||   |||||
  -GTTCCCA-CTTGGAGGAGTGGCAGCAAGACCTGGCTTCGGATTGTCTCCCATTTTCCCAGGTGGGCCTG-
 2140       2150      2160      2170      2180      2190      2200

    870       880       890       900    X    910
  ACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCA
     | | ||||    ||| | ||||||         ||
  --CCTGGGGAA---AGCTTGTGGCCGGAAGAGAAAATGA
   2210         2220      2230      2240


10. US-08-162-407-5 (1-988)
    HUMELASF      Human elastin mRNA, complete cds.

 LOCUS       HUMELASF      2242 bp ss-mRNA           PRI       07-NOV-1994
 DEFINITION  Human elastin mRNA, complete cds.
 ACCESSION   M36860
 KEYWORDS    elastin.
 SOURCE      Human skin fibroblast, cDNA to mRNA.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2242)
   AUTHORS   Fazio,M.J., Olsen,D.R., Kauh,E.A., Baldwin,C.T., Indik,Z.,
             Ornstein-Goldstein,N., Yeh,H., Rosenbloom,J. and Uitto,J.
   TITLE     Cloning of full-length elastin cDNAs from a human skin fibroblast
             recombinant cDNA library: further elucidation of alternative
             splicing utilizing exon-specific oligonucleotides
   JOURNAL   J. Invest. Dermatol. 91, 458-464 (1988)
   STANDARD  full automatic
 COMMENT     NCBI gi: 182061
 FEATURES             Location/Qualifiers
      source          1..2242
                      /organism="Homo sapiens"
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                      /note="elastin signal peptide"
                      /codon_start=1
      CDS             50..2242
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                      /map="7cen-q21.1"
                      /note="elastin precursor;  NCBI gi: 182062"
                      /codon_start=1
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                      PGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYG
                      LPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAAGVLPG
                      VGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGGPGFGPGVV
                      GVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGARPGVGVG
                      GIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAAKAA
                      KYGVGTPAAAAAKAAAKAAQFALLNLAGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVG
                      VAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVP
                      GLGVGAGVPGLGVGAGVPGFGAVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGV
                      VGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAK
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      mat_peptide     128..2239
                      /note="elastin"
                      /codon_start=1
 BASE COUNT      333 a    598 c    840 g    471 t
 ORIGIN

Initial Score     =    218  Optimized Score  =     405  Significance = 13.40
Residue Identity  =    49%  Matches          =     478  Mismatches   =   374
Gaps              =    113  Conservative Substitutions                =     0

             X            10                 20        30         40
             CG--GCCGGA---ATTCCGG-----GGC----CCCCGGCCGAAATGACAG-TGCTGGCGCC-
             ||  | ||||    | ||||     |||    |||| |  |    | |||  |||| ||||
   GAGGTGTTCCCGGAGTCGGAGGTGTCCCGGGAGTTGGCATTTCCCCCGAAGCTCAGGCAGCAGCTGCCGCCA
1320      1330      1340      1350      1360      1370      1380      1390

     50        60              70        80          90       100       110
   AGCCTGGAGCCCAACAACCTA------TCTCCTCCTGCTGCTGCTGCT-GAGCTCGGGACTCAGTGGACCC
   || |||    ||||  ||  |       | ||  | ||||| ||||||  |||    | |  ||  |  |||
   AGGCTG----CCAAGTACGGAGTGGGGACCCCAGCAGCTGCAGCTGCTAAAGCAGCCGCCAAAGCCG--CCC
            1400      1410      1420      1430      1440      1450

         120          130       140       150       160       170
   AGGACTGCTCCTTCCAA---CACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTC-TGAC
   | |  ||||| |  |||     |||    |  ||||  |   |||  ||     |||  ||| || | || |
   A-GTTTGCTCTTCTCAATCTTGCAGGGTTAGTTCCT--GGTGTCGGCGT--GGCTCCTGGAGTTGGCGTGGC
   1460      1470      1480      1490        1500        1510      1520

 180       190       200       210       220       230              240
   TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC-------TGCGGGGG
   | |||| |    |  |  |   |     |||| |    |||| ||   | |  ||||       ||  | ||
   T-CCTGGTGTCGGTGTGGCTCCTGGAGTTGGCTTGGCTCCTGGAGTTGGCGTGGCTCCTGGAGTTGGTGTGG
      1530      1540      1550      1560      1570      1580      1590

      250            260         270       280       290       300       310
   CCTCTGGC---GGC-TGG-TCCTGGCA-CAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGAT
   |  |||||   ||| ||| ||| ||||   || |||| |||||  ||   || |||  ||    |||  | |
   CTCCTGGCGTTGGCGTGGCTCCCGGCATTGGCCCTGG-TGGAGTTGC---AG-CTGCAGCAAAATCC--GCT
```

```
    1600      1610      1620      1630       1640          1650        1660

          320        330       340       350       360       370       380
   GCAAGGCTTGCTG-GAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCA
   || | | | ||||  |  ||   | | | ||| | ||  | | |       ||| ||  || |||    |
   GCCAAGGTGGCTGCCAAAGC-CCAGCTCCGAGCTGCAGCTGGGC----TTGGTG-CTGGCATCCCTGGACTT
         1670      1680       1690      1700           1710      1720

         390       400       410       420       430       440       450
   GCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGA
   |  |  || |  ||| |  | ||     ||      |  ||| || |  |   ||   |  | ||| ||||
   G--GAGTTGGTGTCGGC--GTCCCTGGACTTGGAGTTGGTGCTGGTGTTCCTGGACTTGGAGTTGGTGCTGG
     1730      1740        1750      1760      1770      1780      1790

        460       470       480       490       500         510       520
   AG-CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCC--CGACTCCTCAACCC
    |  ||||| |  |  | ||| || |    |  || |||  |||  ||   |||||    |     || |
   TGTTCCTGGCT-TCGGGGCAGTACCTGGAGCCCTGGCTGCCGCTAAAG---CAGCCAAATATGGAGCAGCAG
     1800       1810      1820      1830      1840         1850      1860

          530        540       550           560       570       580
   TGCC--ACCCCCATGGA-GTCCCCGGCCCCT----GGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTG
   ||||      || |||| | | | || | ||    ||||    || ||| | | |    |  |   |  | |
   TGCCTGGGGTCCTTGGAGGGCTCGGGGCTCTCGGTGGAGTAGGCATCCCAGGCGGTGTGGTGGGAGC--CGG
       1870      1880      1890      1900      1910      1920        1930

   590       600       610       620         630         640       650
   CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGC--TGGCCGCTGCCTGGT--GCCTGCACTGGCAGAG
     || ||  | || ||||||   |      |||||||    |||||  || | |  ||||  | ||| ||
   ACCCGCC-GCCGCCGCTGCCGCAGCCAAAGCTGCTGCCAAAGCCGC--CCAGTTTGGCCT--AGTGGGAGCC
        1940      1950      1960      1970        1980        1990

     660        670       680        690       700       710          720
   GACGCG-GCGGAGGACACCCCGCCCTGGGGAGC-AGGTGCCCCCCGTCCCCAGTCCCCAGGACCT---GCTG
   |  | |  |||||||| |   | |  || | ||  || |  ||  ||     |  ||  |||  |    ||
   GCTGGGCTCGGAGGACTCGGAGTC--GGAGGGCTTGGAGTTCCAGGTGTTGGGGGCCTTGGAGGTATACCTC
2000      2010      2020        2030      2040      2050      2060

        730        740       750       760       770       780       790
   CTTGTGGAG-CACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATCTA
   |   || || | || |    || ||   |   | |||| | |||||  |     |   | |   | |    |
   CAGCTGCAGCCGCTAAAGCAGCTAAATAC-GGTGCTGCTG-GCCTTGGAGGTGTCCTAGGGGGTGCCGGGCA
2070      2080      2090       2100       2110      2120      2130

       800       810       820       830       840       850       860
   TCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGG
      |||||  ||  ||| | ||   |     |   |   ||   ||| ||         | ||   |||||
   -GTTCCCA-CTTGGAGGAGTGGCAGCAAGACCTGGCTTCGGATTGTCTCCCATTTTCCCAGGTGGGGCCTG-
 2140       2150      2160      2170      2180      2190      2200

     870       880       890       900   X   910
   ACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCA
      | | ||||    ||| | ||||||         ||
   --CCTGGGGAA---AGCTTGTGGCCGGAAGAGAAAATGA
   2210         2220      2230      2240 X


11. US-08-162-407-5 (1-988)
    HSELASF      Human elastin mRNA, complete cds.
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ID   HSELASF    standard; RNA; PRI; 2242 BP.
XX
AC   M36860;
XX
DT   05-SEP-1990 (Rel. 25, Created)
DT   16-DEC-1994 (Rel. 42, Last updated, Version 5)
XX
DE   Human elastin mRNA, complete cds.
XX
KW   elastin.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC   Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
XX
RN   [1]
RP   1-2242
RA   Fazio M.J., Olsen D.R., Kauh E.A., Baldwin C.T., Indik Z.,
RA   Ornstein-Goldstein N., Yeh H., Rosenbloom J., Uitto J.;
RT   "Cloning of full-length elastin cDNAs from a human skin fibroblast
RT   recombinant cDNA library: further elucidation of alternative
RT   splicing utilizing exon-specific oligonucleotides";
RL   J. Invest. Dermatol. 91:458-464(1988).
XX
DR   SWISS-PROT; P15502; ELS_HUMAN.
XX
CC   NCBI gi: 182061
XX
FH   Key             Location/Qualifiers
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FT   source          1..2242
FT                   /organism="Homo sapiens"
FT   sig_peptide     50..127
FT                   /note="elastin signal peptide"
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FT                   /gdb_xref="G00-119-107"
FT   mat_peptide     128..2239
FT                   /note="elastin"
FT                   /codon_start=1
XX
SQ   Sequence 2242 BP; 333 A; 598 C; 840 G; 471 T; 0 other;

Initial Score    =    218  Optimized Score  =    405  Significance = 13.40
Residue Identity =    49%  Matches          =    478  Mismatches   =   374
Gaps             =    113  Conservative Substitutions              =     0

              X            10                 20        30         40
              CG--GCCGGA---ATTCCGG-----GGC----CCCCGGCCGAAATGACAG-TGCTGGCGCC-
              ||  | ||||    | ||||     |||    |||| |  |    | |||  |||| ||||
    GAGGTGTTCCCGGAGTCGGAGGTGTCCCGGGAGTTGGCATTTCCCCCGAAGCTCAGGCAGCAGCTGCCGCCA
 1320      1330      1340      1350      1360      1370      1380      1390

      50        60              70        80         90       100       110
    AGCCTGGAGCCCAACAACCTA-------TCTCCTCCTGCTGCTGCTGCT-GAGCTCGGGACTCAGTGGACCC
    || |||    ||||  ||  |       | ||  | ||||| ||||||  |||    | |  ||  |  |||
  AGGCTG----CCAAGTACGGAGTGGGACCCCAGCAGCTGCAGCTGCTAAAGCAGCCGCCAAAGCCG--CCC
           1400      1410      1420      1430      1440      1450

        120          130       140       150       160       170
  AGGACTGCTCCTTCCAA---CACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTC-TGAC
  | |  ||||| |  |||     |||    |  ||||  |   |||  ||     |||  ||| || | || |
  A-GTTTGCTCTTCTCAATCTTGCAGGGTTAGTTCCT--GGTGTCGGCGT--GGCTCCTGGAGTTGGCGTGGC
  1460      1470      1480      1490        1500        1510      1520

180       190       200       210       220       230              240
  TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC-------TGCGGGGG
  | |||| |    |  |  |   |     |||| |    |||| ||   | |  ||||       ||  | ||
  T-CCTGGTGTCGGTGTGGCTCCTGGAGTTGGCTTGGCTCCTGGAGTTGGCGTGGCTCCTGGAGTTGGTGTGG
     1530      1540      1550      1560      1570      1580      1590

     250            260       270       280       290       300        310
  CCTCTGGC---GGC-TGG-TCCTGGCA-CAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGAT
  |  |||||   ||| ||| ||| ||||   || |||| |||||  ||   || |||  ||    |||  | |
  CTCCTGGCGTTGGCGTGGCTCCCGGCATTGGCCCTGG-TGGAGTTGC---AG-CTGCAGCAAAATCC--GCT
   1600      1610      1620      1630       1640          1650        1660

         320       330       340       350       360       370        380
  GCAAGGCTTGCTG-GAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCA
  || | | | ||||  |  ||   | | | ||| | ||  | | |       ||| ||  || |||    |
  GCCAAGGTGGCTGCCAAAGC-CCAGCTCCGAGCTGCAGCTGGGC----TTGGTG-CTGGCATCCCTGGACTT
        1670      1680       1690      1700           1710      1720

        390       400       410       420       430       440       450
  GCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGA
  |  |  || |  ||| |  | ||     ||      |  ||| || |  |   ||   |  | ||| ||||
  G--GAGTTGGTGTCGGC--GTCCCTGGACTTGGAGTTGGTGCTGGTGTTCCTGGACTTGGAGTTGGTGCTGG
    1730      1740        1750      1760      1770      1780      1790

       460       470       480       490       500         510       520
  AG-CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCC--CGACTCCTCAACCC
   |  ||||| |  |  | ||| || |    |  || |||  |||  ||   |||||    |     || |
  TGTTCCTGGCT-TCGGGGCAGTACCTGGAGCCCTGGCTGCCGCTAAAG---CAGCCAAATATGGAGCAGCAG
    1800       1810      1820      1830      1840           1850    1860

         530        540       550           560       570       580
  TGCC--ACCCCCATGGA-GTCCCCGGCCCCT----GGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTG
  ||||      || |||| | | | || | ||    ||||    || ||| | | |    |  |   |  | |
  TGCCTGGGGTCCTTGGAGGGCTCGGGGCTCTCGGTGGAGTAGGCATCCCAGGCGGTGTGGTGGGAGC--CGG
      1870      1880      1890      1900      1910      1920        1930

  590       600       610       620         630         640       650
  CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGC--TGGCCGCTGCCTGGT--GCCTGCACTGGCAGAG
    || ||  | || ||||||   |      |||||||    |||||  || | |  ||||  | ||| ||
  ACCCGCC-GCCGCCGCTGCCGCAGCCAAAGCTGCTGCCAAAGCCGC--CCAGTTTGGCCT--AGTGGGAGCC
       1940      1950      1960      1970        1980        1990

    660        670       680       690       700       710           720
  GACGCG-GCGGAGGACACCCCGCCCTGGGGAGC-AGGTGCCCCCCGTCCCCAGTCCCCAGGACCT---GCTG
  |  | |  ||||||| |   | |  || | ||  || |  ||  ||     |  ||  |||  |    ||
  GCTGGGCTCGGAGGACTCGGAGTC--GGAGGGCTTGGAGTTCCAGGTGTTGGGGGCCTTGGAGGTATACCTC
2000     2010      2020        2030      2040      2050      2060

       730        740       750       760       770       780       790
  CTTGTGGAG-CACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATCTA
  |   || || | || |    || ||   |   | |||| | |||||  |     |   | |   | |    |
```

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    CAGCTGCAGCCGCTAAAGCAGCTAAATAC-GGTGCTGCTG-GCCTTGGAGGTGTCCTAGGGGGTGCCGGGCA
 2070      2080      2090       2100      2110       2120      2130

        800       810       820       830       840       850       860
    TCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGG
       |||||  ||  ||| | ||   |     |   |   ||   ||| ||         | ||   |||||
    -GTTCCCA-CTTGGAGGAGTGGCAGCAAGACCTGGCTTCGGATTGTCTCCCATTTTCCCAGGTGGGGCCTG-
  2140      2150      2160      2170      2180      2190       2200

      870       880       890       900   X   910
    ACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCA
       | | ||||    ||| | ||||||         ||
    --CCTGGGGAA---AGCTTGTGGCCGGAAGAGAAAATGA
    2210        2220      2230      2240  X


12. US-08-162-407-5 (1-988)
    HSOXYTOC      H.sapiens gene for oxytocin receptor.

 LOCUS       HSOXYTOC     3617 bp    DNA              PRI       01-JAN-1995
 DEFINITION  H.sapiens gene for oxytocin receptor.
 ACCESSION   X80282
 KEYWORDS    oxytocin receptor.
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 3617)
   AUTHORS   Inoue,T., Kimura,T., Azuma,C., Inazawa,J. and Takemura,M.
   TITLE     Structural Organization of the Human Oxytocin Receptor Gene
   JOURNAL   Unpublished
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 3617)
   AUTHORS   Kimura,T.
   TITLE     Direct Submission
   JOURNAL   Submitted (13-JUL-1994) to the EMBL/GenBank/DDBJ databases. T.
             Kimura, Dept of Obstetrics, and Gynaecology, Osaka University Med
             School, 2-2 Yamadaoka suita City, Osaka 565, JAPAN
   STANDARD  full automatic
 COMMENT     NCBI gi: 609014
 FEATURES             Location/Qualifiers
      source          1..3617
                      /organism="Homo sapiens"
                      /chromosome="3p 26.2"
      exon            1063..1445
      exon            2085..2180
      exon            2347..3412
      CDS             2489..>3412
                      /note="NCBI gi: 609015"
                      /codon_start=1
                      /product="oxytocin receptor"
                      /translation="MEGALAANWSAEAANASAAPPGAEGNRTAGPPRRNEXLARVEVA
                      VLCLILLLALSGNACVLLALRTTRQKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDIT
                      FRFYGPDLLCRLVKYLQVVGMFASTYLLLLMSLDRCLAICQPLRSLRRRTDRLAVLAT
                      WLGCLVASAPQVHIFSLREVADGVFDCWAVFIQPWGPKAYITWITLAVYIVPVIVLAA
                      CYGLISFKIWQNLRLKTAAAAAAEAPEGAAAGDGGRVALARVSSVKLISKAKIRTVKM
                      TFIIVLAFIVCWTPFFFVQMWSVWDANAPKEG"
 BASE COUNT      735 a    992 c   1099 g    790 t      1 others
 ORIGIN
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Initial Score     =    193  Optimized Score  =     461  Significance = 11.61
Residue Identity  =    52%  Matches          =     561  Mismatches   =   361
Gaps              =    141  Conservative Substitutions              =     0

              X       10        20        30        40        50        60
              CGGCCGGAATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAG--CCCAA
              |  ||| |   ||||  ||||  | || || ||  |  |||||||  || |||||    |
    GGGCCGAGGGCAACCGCACCGCCGGACCCCCGCGGCGCAACGA-GGSCCTGGCGC--GCGTGGAGGTGGCGG
        2560  X   2570      2580      2590       2600        2610      2620

            70        80        90       100       110         120
    CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGGACC--CAGG-ACTGCTCCTTCCAAC
         | |||| ||||||| |||  ||||||  ||||| |  ||| |  |  | ||  |||| |    ||
    TGCTGTGTCTCATCCTGCTCCTGGCGCTGAG--CGGGAATGCGTGTGTGCTGCTGGCGCTGCGCACCACACG
         2630      2640      2650        2660      2670      2680      2690

  130       140       150        160        170               180
    ACAGCCCCATCTCCTCCGACTTCGCTGTCA-AAATC-CGTGAGC-TGTCTGAC-------TACC--TGCTTC
     |||   || |||   |  ||||    |||  || | | | ||| |  | |||       |  |  || |||
    CCAGAAGCA-CTCGCGCCTCTTCTTCTTCATGAAGCACCTAAGCATCGCCGACCTGGTGGTGGCAGTGTTTC
         2700       2710      2720      2730      2740      2750      2760

  190         200       210         220        230       240       250
    AAG-ATTACC-CAGTCACCGTGG--CCTCCAACCTGCAG-GACGAGGAGCTCTGCGGGGGCCTCTGGCGGCT
    | |   | || ||||  | ||||  | ||  |||| | |   | | | || |  |  |   || || || ||
    AGGTGCTGCCGCAGTTGCTGTGGGACATC--ACCTTCCGCTTCTACGGGCCCGACCTG---CTGTGCCGCCT
        2770      2780      2790        2800      2810         2820

     260       270       280       290       300       310       320
    GGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTG---CTGGA
    ||| |  ||   || || ||| | |||  | |   | | |    | |  | |||    | ||   |||||
    GGT-CAAGTAC-TTGCAGG-TGGTG-GGC--ATGTTCGCCTCCACCTACCTGCTGCTGCTCATGTCCCTGGA
 2830        2840       2850         2860      2870      2880      2890

      330       340       350       360       370       380       390
    GCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGT
     ||| ||  |  ||  ||   ||  | || |   || | ||  | || || || || | | |  ||| | |
    CCGC-TG--CCTGGCCAT---CT--GCCAGCCGCTGCG-CTCGCTGCGCCGCCGCA-CCGAC--CGCCTGG-
      2900        2910           2920       2930      2940         2950

    400       410         420        430       440       450       460
    CCAGACCAACATCTCCCGCCTC--CTG-CAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCAC
     |||  |  |  | |  | |||  ||| | || | ||  || || || ||| || |   | |      || |
    -CAGTGC-TCGCCACGTGGCTCGGCTGCCTGGTGGCCAGCGCGCCGCAGGT-GCAC---ATC-----TTCTC
       2960       2970      2980      2990      3000          3010

      470        480       490       500       510         520       530
    TC-GCCAGAACT-TCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGAC-TCCTC-AACCCTGCCACCCCCAT
    || ||  ||  |  ||  ||| | ||    |||| |     | ||| | || || | |||||     ||||
    TCTGCGCGAGGTGGCTGACGGCGTCTTCGACTGCTG-----GGCCGTCTTCATCCAGCCCTG-GGGACCCAA
     3020      3030      3040      3050           3060      3070       3080

       540       550        560          570         580        590
    GGAGTCCCCGGCCCCTGGAGGCCAC-AGC-CCCGACA--GCCCCG--CAGCCCCCTCTGCT-CCTCCTACTG
    ||  |   |  | | ||||   | | |||   | ||| |  |||  || |   ||| ||| ||| |||| |
    GGCCT--ACATCACATGGATCACGCTAGCTGTCTACATCGTGCCGGTCATCGTGCTC-GCTGCCTGCTACGG
           3090      3100      3110      3120      3130       3140      3150

   600       610       620         630       640       650       660
    -CTGCTGCCCGTGGGCCTCCTGCTG--CTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCG---G
```

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   ||  |   | |     ||  || |  || || ||| |  |    |||||  ||| | || || ||||   |
  CCTTATCAGCTTCAAGATCTGGCAGAACTTGCGGCT-CAAGACCGCTGCAGCGGCGGCGGCCGAGGCGCCAG
        3160      3170      3180       3190      3200      3210      3220

    670       680       690       700       710       720       730
  AGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCAC-TG
  ||| | |  ||  |||| ||   || || |   |  ||| | | |  |   | || ||  ||  ||| | |
  AGGGCGCGGCG-GCTGGCGATGGGGGGCGCGTGG--CCCTGGCGC--GTGTCAGCAGC--GTCAAGCTCATC
       3230       3240      3250        3260        3270        3280

    740        750          760       770       780       790
  ACC-TGGCCAAG-GCCTCA---TCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATC-TATCAT---CC
   ||  |||||||  || ||   ||  |  || | || | || ||   || | |   |||| | |  |   ||
  TCCAAGGCCAAGATCCGCACGGTCAAGATGA-CTTTCATCATCGTGCTG-GCC-TTCATCGTGTGCTGGACC
  3290      3300      3310       3320      3330        3340      3350

800         810       820       830       840       850       860
  CATTT-TAC-AGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGGAC--
  | ||| | |   | |  |||   |||   |   || |  |   ||  |||  |||| |  ||||| || |
  CCTTTCTTCTTCGTGCAGATGTGGAGCGTCTGGGATGCCA---ACGCGCCCAAGGAAG-GTAGCCAGGGCTG
   3360      3370      3380      3390         3400      3410       3420

  870       880       890       900       910       920       930
  ACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCATTCCCTCCCCAGAATG--GAGGCAA
    |||   ||  ||   ||| | |||  ||       |||| | || || |  || |||||||   |||
  GGAGACCCAGGAGGAGGGAGCCTGGTGGCTGGGGGAAGCCCTTATC-TTGCTGCCTCAGAATGTCCAGGGGT
     3430      3440      3450      3460       3470      3480      3490

  940        950          960             970           980         X
  CGCCAGA-ATCCAG---CACCGGCCCCATTTA---CCCA---ACT--CTGAAC--AAAGCCCCCG
  |    ||  ||| |    |   ||    || |   ||||   | |  |||  |    | |||  |
  CTGTGGACTTCCTGGGGGATAAGCGGGTTTGAAATCCCACAGAGTCACTGCTCTGTCATCCCTTGACCAAGT
    3500      3510      3520      3530      3540      3550      3560

  GAC
```

```
13. US-08-162-407-5 (1-988)
    HSOXYTOC      H.sapiens gene for oxytocin receptor

 ID   HSOXYTOC   standard; DNA; PRI; 3617 BP.
 XX
 AC   X80282;
 XX
 DT   01-JAN-1995 (Rel. 42, Created)
 DT   01-JAN-1995 (Rel. 42, Last updated, Version 2)
 XX
 DE   H.sapiens gene for oxytocin receptor
 XX
 KW   oxytocin receptor.
 XX
 OS   Homo sapiens (human)
 OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC   Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 XX
 RN   [1]
 RA   Inoue T., Kimura T., Azuma C., Inazawa J., Takemura M.;
 RT   "Structural Organization of the Human Oxytocin Receptor Gene";
 RL   Unpublished.
```

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XX
RN   [2]
RP   1-3617
RA   Kimura T.;
RT   ;
RL   Submitted (13-JUL-1994) to the EMBL/GenBank/DDBJ databases.
RL   T. Kimura, Dept of Obstetrics, and Gynaecology, Osaka University
RL   Med School, 2-2 Yamadaoka suita City, Osaka 565, JAPAN
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..3617
FT                   /organism="Homo sapiens"
FT                   /chromosome="3p 26.2"
FT   CDS             2489..>3412
FT                   /partial
FT                   /product="oxytocin receptor"
FT   exon            1063..1445
FT   exon            2085..2180
FT   exon            2347..3412
XX
SQ   Sequence 3617 BP; 735 A; 992 C; 1099 G; 790 T; 1 other;

Initial Score    =    193  Optimized Score  =    461  Significance = 11.61
Residue Identity =    52%  Matches          =    561  Mismatches   =   361
Gaps             =    141  Conservative Substitutions           =     0

             X       10        20        30        40        50          60
             CGGCCGGAATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAG--CCCAA
             |  ||| |   ||||  ||||  | || || ||  |  |||||||  || |||||    |
   GGGCCGAGGGCAACCGCACCGCCGGACCCCCGCGGCGCAACGA-GGSCCTGGCGC--GCGTGGAGGTGGCGG
       2560  X   2570      2580      2590       2600        2610      2620

           70        80        90       100       110          120
   CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGGACC--CAGG-ACTGCTCCTTCCAAC
        | |||| ||||||| |||  ||||||  ||||| |  ||| |  |  | ||  |||| |    ||
   TGCTGTGTCTCATCCTGCTCCTGGCGCTGAG--CGGGAATGCGTGTGTGCTGCTGGCGCTGCGCACCACACG
        2630      2640      2650        2660      2670      2680      2690

 130       140       150        160        170               180
   ACAGCCCCATCTCCTCCGACTTCGCTGTCA-AAATC-CGTGAGC-TGTCTGAC-------TACC--TGCTTC
    |||   || |||   |  ||||    |||  || | | | ||| |  | |||       |  |  || |||
   CCAGAAGCA-CTCGCGCCTCTTCTTCTTCATGAAGCACCTAAGCATCGCCGACCTGGTGGTGGCAGTGTTTC
        2700       2710      2720      2730      2740      2750      2760

 190         200       210         220        230        240        250
   AAG-ATTACC-CAGTCACCGTGG--CCTCCAACCTGCAG-GACGAGGAGCTCTGCGGGGGCCTCTGGCGGCT
   | |   | || ||||  | ||||  | ||  |||| | |   | | | || |  |  |   || || || ||
   AGGTGCTGCCGCAGTTGCTGTGGGACATC--ACCTTCCGCTTCTACGGGCCCGACCTG---CTGTGCCGCCT
       2770      2780      2790        2800      2810         2820

    260       270       280       290       300       310       320
   GGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTG---CTGGA
   ||| |  | ||   || || ||| | |||  | |   | | |    | |  | |||    | ||   |||||
   GGT-CAAGTAC-TTGCAGG-TGGTG-GGC--ATGTTCGCCTCCACCTACCTGCTGCTGCTCATGTCCCTGGA
2830        2840       2850         2860      2870      2880      2890

     330       340       350       360       370        380      390
   GCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGT
    ||| ||  |  ||  ||   ||  | || |   || | ||  | || || || || | | |  ||| | |
```

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  CCGC-TG--CCTGGCCAT---CT--GCCAGCCGCTGCG-CTCGCTGCGCCGCCGCA-CCGAC--CGCCTGG-
    2900        2910           2920       2930      2940         2950

  400       410         420        430       440       450       460
  CCAGACCAACATCTCCCGCCTC--CTG-CAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCAC
   |||  |  |  | |  | |||  ||| | || | ||  || || || ||| || |   | |      || |
  -CAGTGC-TCGCCACGTGGCTCGGCTGCCTGGTGGCCAGCGCGCCGCAGGT-GCAC---ATC-----TTCTC
     2960       2970      2980      2990      3000          3010

    470        480       490       500       510         520       530
  TC-GCCAGAACT-TCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGAC-TCCTC-AACCCTGCCACCCCCAT
  || ||  ||  |  ||  ||| | ||    |||| |     | ||| | || || | |||||     ||||
  TCTGCGCGAGGTGGCTGACGGCGTCTTCGACTGCTG-----GGCCGTCTTCATCCAGCCCTG-GGGACCCAA
   3020      3030      3040      3050           3060      3070       3080

     540       550        560          570          580       590
  GGAGTCCCCGGCCCCTGGAGGCCAC-AGC-CCCGACA--GCCCCG--CAGCCCCCTCTGCT-CCTCCTACTG
  ||  |   |  | | ||||   | | |||   | |||  |  |||  || |   ||| ||| ||| |||| |
  GGCCT--ACATCACATGGATCACGCTAGCTGTCTACATCGTGCCGGTCATCGTGCTC-GCTGCCTGCTACGG
         3090      3100      3110      3120      3130       3140      3150

 600       610       620         630       640       650       660
  -CTGCTGCCCGTGGGCCTCCTGCTG--CTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCG---G
   ||  |   | |     ||  || |  || || ||| |  |    |||||  ||| | || || ||||   |
  CCTTATCAGCTTCAAGATCTGGCAGAACTTGCGGCT-CAAGACCGCTGCAGCGGCGGCGGCCGAGGCGCCAG
        3160      3170      3180       3190      3200      3210      3220

    670       680       690       700       710       720       730
  AGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCAC-TG
  ||| | |  ||  |||| ||   || || |   |  ||| | | |  |   | || ||  ||  ||| | |
  AGGGCGCGGCG-GCTGGCGATGGGGGGCGCGTGG--CCCTGGCGC--GTGTCAGCAGC--GTCAAGCTCATC
       3230       3240      3250        3260        3270        3280

    740        750          760       770       780       790
  ACC-TGGCCAAG-GCCTCA---TCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATC-TATCAT---CC
   ||  |||||||  || ||   ||  |  || | || | || ||   || | |   |||| | |  |   ||
  TCCAAGGCCAAGATCCGCACGGTCAAGATGA-CTTTCATCATCGTGCTG-GCC-TTCATCGTGTGCTGGACC
  3290      3300      3310       3320      3330        3340      3350

800         810       820       830       840       850       860
  CATTT-TAC-AGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTGGAC--
  | ||| | |   | |  |||   |||   |   || |  |   ||  |||  |||| |  ||||| || |
  CCTTTCTTCTTCGTGCAGATGTGGAGCGTCTGGGATGCCA---ACGCGCCCAAGGAAG-GTAGCCAGGGCTG
   3360      3370      3380      3390         3400      3410       3420

  870       880       890       900       910       920       930
  ACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCATTCCCTCCCCAGAATG--GAGGCAA
    |||   ||  ||   ||| | |||  ||       |||| | || || |  || |||||||   |||
  GGAGACCCAGGAGGAGGGAGCCTGGTGGCTGGGGGAAGCCCTTATC-TTGCTGCCTCAGAATGTCCAGGGGT
     3430      3440      3450      3460       3470      3480      3490

  940        950          960             970           980       X
  CGCCAGA-ATCCAG---CACCGGCCCCATTTA---CCCA---ACT--CTGAAC--AAAGCCCCCG
  |    ||  ||| |    |   ||    || |   ||||   | |  |||  |    | |||  |
  CTGTGGACTTCCTGGGGGATAAGCGGGTTTGAAATCCCACAGAGTCACTGCTCTGTCATCCCTTGACCAAGT
    3500      3510      3520      3530      3540      3550      3560

  GAC
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14. US-08-162-407-5 (1-988)
    HSMRNAOXY     H.sapiens mRNA for oxytocin receptor.

 LOCUS       HSMRNAOXY    4103 bp    RNA             PRI       10-NOV-1993
 DEFINITION  H.sapiens mRNA for oxytocin receptor.
 ACCESSION   X64878
 KEYWORDS    hormone receptor; oxytocin receptor.
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 4103)
   AUTHORS   Kimura,T.
   TITLE     Direct Submission
   JOURNAL   Submitted (28-FEB-1992) to the EMBL/GenBank/DDBJ databases. T.
             Kimura, Dept of Obstetrics and Gynecology, Osaka University Medical
             School, 2-2 Yamadaoka, Suita-shi, Osaka 565, JAPAN
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 4100)
   AUTHORS   Kimura,T., Tanizawa,O., Mori,K., Brownstein,M.J. and Okayama,H.
   TITLE     Structure and expression of a human oxytocin receptor [published
             erratum appears in Nature 1992 May 14;357(6374):176]
   JOURNAL   Nature 356, 526-529 (1992)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 4103)
   AUTHORS   Kimura,T.
   TITLE     Direct Submission
   JOURNAL   Submitted (28-APR-1992) to the EMBL/GenBank/DDBJ databases. Kimura
             T., same adress
   STANDARD  full automatic
 COMMENT     NCBI gi: 34764
 FEATURES             Location/Qualifiers
      source          1..4103
                      /organism="Homo sapiens"
                      /tissue_type="uterus"
      CDS             368..1537
                      /note="NCBI gi: 34765"
                      /codon_start=1
                      /product="oxytocin receptor"
                      /translation="MEGALAANWSAEAANASAAPPGAEGNRTAGPPRRNEALARVEVA
                      VLCLILLLALSGNACVLLALRTTRQKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDIT
                      FRFYGPDLLCRLVKYLQVVGMFASTYLLLLMSLDRCLAICQPLRSLRRRTDRLAVLAT
                      WLGCLVASAPQVHIFSLREVADGVFDCWAVFIQPWGPKAYITWITLAVYIVPVIVLAT
                      CYGLISFKIWQNLRLKTAAAAAAEAPEGAAAGDGGRVALARVSSVKLISKAKIRTVKM
                      TFIIVLAFIVCWTPFFFVQMWSVWDANAPKEASAFIIVMLLASLNSCCNPWIYMLFTG
                      HLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLSHRSSSQRSCSQPSTA"
 BASE COUNT     1171 a    966 c   1035 g    931 t
 ORIGIN

Initial Score     =     193  Optimized Score  =     456  Significance = 11.61
Residue Identity  =     52%  Matches          =     552  Mismatches   =   373
Gaps              =     136  Conservative Substitutions               =     0

          X       10        20        30        40        50          60
          CGGCCGGAATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAG--CCCAA
          |  ||| |   ||||  ||||  | || || ||  |  |||||||  || |||||    |
GGGCCGAGGGCAACCGCACCGCCGGACCCCCGCGGCGCAACGA-GGCCCTGGCGC--GCGTGGAGGTGGCGG
      440 X     450       460       470        480         490       500
```

```
          70        80        90       100        110        120       130
  CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTC-AGTGGGACCCAGG-ACTGCTCCTTCCAACA
       | |||| ||||||| |||  |||||||  || || |  ||| |   | ||  |||| |    ||
  TGCTGTGTCTCATCCTGCTCCTGGCGCTGAGC-GGGAACGCGTGTGTGCTGCTGGCGCTGCGCACCACACGC
         510       520       530        540       550       560       570

         140       150        160        170               180         190
  CAGCCCCATCTCCTCCGACTTCGCTGTCA-AAATC-CGTGAGC-TGTCTGAC-------TACC--TGCTTCA
  |||   || |||   |  ||||    |||  || | | | ||| |  | |||       |  |  || ||||
  CAGAAGCA-CTCGCGCCTCTTCTTCTTCATGAAGCACCTAAGCATCGCCGACCTGGTGGTGGCAGTGTTTCA
         580       590       600       610       620       630       640

           200       210         220        230       240       250
  AG-ATTACC-CAGTCACCGTGG--CCTCCAACCTGCAG-GACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTG
   |   | || ||||  | ||||  | ||  |||| | |   | | | || |  |  |   || || || |||
  GGTGCTGCCGCAGTTGCTGTGGGACATC--ACCTTCCGCTTCTACGGGCCCGACCTG---CTGTGCCGCCTG
       650       660       670         680       690          700

  260       270       280       290       300       310       320
  GTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTG---CTGGAG
  || |  | ||   || || ||| | |||  | |   | | |    | |  | |||    | ||   |||||
  GT-CAAGTAC-TTGCAGG-TGGTG-GGC--ATGTTCGCCTCCACCTACCTGCTGCTGCTCATGTCCCTGGAC
710         720        730          740       750       760       770

   330       340       350       360       370       380       390
  CGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTC
  ||| ||  |  ||  ||   ||  | || |   || | ||  | || || || || | | |  ||| | |
  CGC-TG--CCTGGCCAT---CT--GCCAGCCGCTGCG-CTCGCTGCGCCGCCGCA-CCGAC--CGCCTGG--
     780            790         800        810       820          830

 400       410         420        430       440       450       460
  CAGACCAACATCTCCCGCCTC--CTG-CAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACT
  |||  |  |  | |  | |||  ||| |  | | ||  || || || ||| || |   | |      || ||
  CAGTGC-TCGCCACGTGGCTCGGCTGCCTGGTGGCCAGCGCGCCGCAGGT-GCAC---ATC-----TTCTCT
       840       850       860       870       880                890

   470        480       490       500       510         520       530
  C-GCCAGAACT-TCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGAC-TCCTC-AACCCTGCCACCCCCATG
  | ||  ||  |  ||  ||| | ||    |||| |     | ||| | || || | |||||     |||| |
  CTGCGCGAGGTGGCTGACGGCGTCTTCGACTGCTG-----GGCCGTCTTCATCCAGCCCTG-GGGACCCAAG
    900       910       920       930            940       950        960

    540       550        560          570         580        590
  GAGTCCCCGGCCCCTGGAGGCCAC-AGC-CCCGACA--GCCCCG--CAGCCCCCTCTGCT-CCTCCTACTG-
  |  |   |  | | ||||   | | |||   | |||  |  |||  || |   ||| ||| ||| |||| |
  GCCT--ACATCACATGGATCACGCTAGCTGTCTACATCGTGCCGGTCATCGTGCTC-GCTACCTGCTACGGC
          970       980       990      1000      1010       1020      1030

600       610       620         630       640       650       660
  CTGCTGCCCGTGGGCCTCCTGCTG--CTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCG---GA
  ||  |   | |     ||  || |  || || ||| |  |    |||||  ||| | || || ||||   ||
  CTTATCAGCTTCAAGATCTGGCAGAACTTGCGGCT-CAAGACCGCTGCAGCGGCGGCGGCCGAGGCGCCAGA
        1040      1050      1060       1070      1080      1090      1100

   670            680       690       700       710        720       730
  GGACAC-----CCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAG-GACCTGCTGCTTGTGGA--
  || | |     |  ||  ||||| ||  |||  ||| | | |  |||  ||| | |  ||| | | |  |
  GGGCGCGGCGGCTGGCGATGGGGGGCGCGTG-GCCCTGGCGCGTGTCAGCAGCGTCAAGCT-CATCTCCAAG
       1110      1120      1130       1140      1150      1160       1170
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               740         750            760       770        780       790
    GCACTGA----CCTGGCCAAG--GCC-----TCATCCTGCGGAGCCTTAAAC-AACGCAGTGAGACAGACAT
    ||   ||    |  || ||||  | |     ||||| ||| | ||||| | |    || |   | |   | |
    GCCAAGATCCGCACGGTCAAGATGACTTTCATCATCGTGCTG-GCCTTCATCGTGTGCTGGACGCCTTTCTT
         1180      1190      1200      1210       1220      1230      1240

           800       810         820       830       840       850
    CTATCATCCCATTTTACAGGG--GAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGAT-GT-AT
    || || | |   | |  || |    |||| |  | || | || || | || | |   |   |  || || ||
    CT-TCGTGCAGATGTGGAGCGTCTGGGATGCCAACGCGCCCA-AG-GAAGCCTCGGCCTTCATCATCGTCAT
         1250      1260      1270      1280        1290      1300      1310

    860        870       880       890       900        910       920
    -AGCCTGGACA-CAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCT-TGGGCCCCTCTCATTCCCTCCCCAGA
       ||||| || |      || ||     |  || |   || | |   |  | |   |   | || ||  ||
    GCTCCTGGCCAGCCTCAACAGCTGCTGCAACCCCTGGATCTACATGCTGTTCACGGGCCACCTCTTCCACGA
         1320      1330      1340      1350      1360      1370      1380

    930       940         950       960       970       980       X
    ATGGAGGCAACGCCAGAATCC--AGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
    |     ||| |||     |||   ||  |  | |||  ||||  |    |  || |  ||  |
    ACTCGTGCAGCGC----TTCCTGTGCTGCTCCGCCAGCTACCTGA---AGGGCAGACGCCTGGGAGAGACGA
       1390          1400      1410      1420         1430      1440

    G


15. US-08-162-407-5 (1-988)
    TCU17917     Thermomonospora curvata alpha-glucosidase (aglA) g

 LOCUS        TCU17917     2093 bp ds-DNA              BCT       19-DEC-1994
 DEFINITION   Thermomonospora curvata alpha-glucosidase (aglA) gene, complete
              cds.
 ACCESSION    U17917
 KEYWORDS     .
 SOURCE       Thermomonospora curvata.
   ORGANISM   Thermomonospora curvata
              Eubacteria; Firmicutes; Actinomycetes; Thermomonospora group;
              Thermomonospora.
 REFERENCE    1  (bases 1 to 2093)
   AUTHORS    Janda,L., Tichy,P. and Petricek,M.
   TITLE      Thermomonospora curvata aglA gene encoding alpha-glucosidase
   JOURNAL    Unpublished
   STANDARD   full automatic
 REFERENCE    2  (bases 1 to 2093)
   AUTHORS    Petricek,M.
   TITLE      Direct Submission
   JOURNAL    Submitted (01-DEC-1994) Miroslav Petricek, Institute of
              Microbiology, ASCR, Biogenesis & Biotechnol. of Natur. Prod.,
              Videnska 1083, Prague 4, 142 20, Czech Republic
   STANDARD   full automatic
 COMMENT      NCBI gi: 603047
 FEATURES               Location/Qualifiers
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      CDS               109..1743
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                        /EC_number="3.2.1.20"
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                         /codon_start=1
                         /product="alpha-glucosidase"
                         /translation="MQQVPDSVHLTAPTAHTHWWRHAVIYQIYVRSFADSNGDGEGDL
                         NGIRERLPALVSLGVDAIWLTPFYVSPLADGGYDVADYRDVDPRFGTLADFDALLATA
                         HDLGLRVIIDIVPNHTSSAHRWFRDALAAGPGSPERDRYVFRPGRGENGELPPNNWQS
                         IFGGPAWTRVTEPDGTPGEWYLHLFDVEQPDLNWENPEVRAEFADILRFWLDRGVDGF
                         RIDVAHGMIKDPALPDIAEGQKADMLDGHTRLPYFDQDGVHEIYREWRAIVDSYPGER
                         ALVAEAWVENAERVARYLRPDELHQAFNFEYLTADWDAATLRAVVDRSLAANNAVGAP
                         TTWVLSNHDVTRHVTRFGGGAQGLARARAALLLMLALPGSVYLYQGEELGLPEVTDLP
                         EEALQDPTWKRSGYTERGRDGCRVPLPWEGDEPPFGFGCSAERSWLPVPAEWRSLTRE
                         VQERDPDSTLSLYKKALRLRRELLLPAEDALHWADAPQNVLAFRREPGFTCAVNFGAD
                         PVTLPFEGEVVLSSGPVEQDGTHLVLPGDTAVWLRQ"
 BASE COUNT        342 a    725 c    703 g    323 t
 ORIGIN

Initial Score      =    185  Optimized Score  =    450  Significance = 11.04
Residue Identity =    50%  Matches            =    541  Mismatches   =   391
Gaps               =    130  Conservative Substitutions          =     0

              X       10        20                30        40         50
              CGGCCGGAATTCCGGGGCCCCC--------GGCCGAAATGACAGTGCTG-GCGCCAGCCTGG
              || | |  |  ||||||  | |        ||||||   |   |||  |  |||    |  |
    GCGCCATCGTCGACAGCTACCCCGGGGAGCGCGCGCTGGTGGCCGAGGCGTGGGTGGAGAACGCGGAACGCG
       910    X  920       930       940       950       960       970

         60        70        80        90       100           110        120
    AGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACT--CAGT--GGGACCCAGGACT-GCT
     | ||  | ||||  | || |     |||||  | | ||     |||   |||     |||   |||| |
    TGGCCCGCTACCT-CCGCCCCGACGAGCTGCACCAG-GCGTTCAACTTCGAGTACCTCACCGCAGACTGGGA
     980        990      1000      1010       1020      1030      1040

           130          140         150       160         170       180
    CCTTCCAACAC--AGCCCCAT-CTCCTCCG--ACTTCGCTGTCAA-AATCCG-TGAGCTGTCTGACTACCTG
    |  | |||| |   || || |  |   |||   | | || |  || ||  || || |    | ||| || ||
    CGCTGCAACGCTGCGCGCCGTGGTGGACCGCTCCCTGGCCGCGAACAACGCGGTGGGGGCGCCGACCACATG
    1050      1060      1070      1080      1090      1100      1110

      190       200       210       220       230       240        250
    CTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGC-CTCTGGCGGCT
      |   | |   |||  |||   | | | || || ||| | |     | || |||||||| | |  | ||||
    GGT---GCT-CTCCAACCAC---GACGT-CACCCGGCACGTCACCCGGTTCGGCGGGGGCGCGCAAG-GGCT
  1120          1130          1140      1150      1160      1170       1180

     260       270       280       290       300       310       320
    GGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGC-
    ||  | ||||| |||| |   |   | ||| | | ||| | |||   ||  |||    | ||  ||  | |
    GGCGCGGGCAC-GCGCCG--CGCTCCTGCTGATG-CTGGCCCTG---CCGGGAT--CGGTCTACCTCTACCA
         1190         1200      1210       1220           1230      1240

    330        340        350       360        370             380       390
    GCGTGAACA-CGGAGA-TACACTTTGTCACCAAATGTGCC-TTTCAGCCCC------CCCCCAGCTGTCTTC
    | ||||  | | | || | | |   ||||||  || ||||     || |||       |||||  ||    |
    GGGTGAGGAGCTGGGACTTCCCGAGGTCACC-GATCTGCCGGAGGAGGCCCTGCAGGACCCCACGTGGAAGC
      1250      1260      1270       1280      1290      1300      1310

           400        410        420       430       440       450       460
    GCTTCGTCCAGACC-AACATCTCC-CGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTG
    ||| ||   | |||  | |    || || |   ||| ||   || | |  |    |  ||||  | |||||
    GCTCCGGATACACCGAGCGGGGCCGCGACGGATGCCGGGTGCCGCTG-CCTTGGGAAGGCGACG-AGCCCCC
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     1320      1330      1340      1350       1360       1370      1380

           470       480         490       500         510       520
    GATCACTCGCCAGAACTTCTC-CCGGTGC-CTG-GAGCTG-CAGTGTCAGCCCGACTCCTCAACCCTGCCAC
    | ||   |  | |  || |||  ||| || | |   |||| | ||| | | | || |      | |||  ||
    GTTC-GGCTTCGG--CTGCTCGGCGGAGCGCAGTTGGCTGCCGGTGCCCG-CGGAGTGGCGGTCGCTG--AC
      1390        1400      1410      1420      1430       1440        1450

   530        540       550      560       570            580       590
    CCCCATGGAGTCCCCG--GCCCCTGGAGGCCACAGCCCCGACAGC----CCCGCAGCCCCCTCTGCTCCTCC
    ||    ||||  || |  || |     || | |  ||| | | ||    |  | || | |  | ||||| ||
    CC---GGGAGGTCCAGGAGCGCGACCCGGACTCGACCCTGTC-GCTGTACAAGAAGGCGCTGCGGCTCCGCC
            1460      1470      1480      1490       1500      1510

          600         610        620       630       640       650       660
    ---TACTGCTGCTGCCCG--TGGGCCTC-CTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGC
        ||||||||| ||||    || | | ||||    ||| |  |||  |   | | ||  || |      |
    GCGAACTGCTGCTCCCCGCAGAGGACGCGCTGCACTGGGCGGACGCCCCG---CAGAACGTGCTGGCTTTCC
 1520      1530      1540      1550      1560         1570      1580

           670        680       690       700       710       720       730
    GGCGGAGGACACCCCG-CCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAG
    | ||  ||| |||  |   |    | || ||||  |  ||  | | | |||  || |  |||||   | |||
    GCCG--GGA-ACCGGGTTTCACCTGCGC-GGTGAACTTCG-GCGCTGACCC--GGTCACGCTGCCGTTCGAG
  1590         1600      1610       1620       1630        1640      1650

          740       750         760       770        780       790
    CACTGACCTGGCCAAGGCC--TCATCCTGCGGAGCCTTAAACAACGCA-GTGAGACAGACATCTATCATC-C
      | ||  |||    | ||     ||| | |||||   |    |||||  |    | | |      || | |
    GGC-GAAGTGGTGCTGTCCAGCGGTCCGGTGGAGCAGGACGGCACGCACCTCGTGCTGCCTGGGGACACCGC
        1660      1670      1680      1690      1700      1710      1720

  800       810          820          830       840       850       860
    CATTTTACAG-GGGAGGA---TACTGA---GGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTG
      | |  | | || || |      |||   ||| |   | | |  | |||| | ||||||  ||   | ||
    GGTGTGGCTGCGGCAGTAGCGGGGTGAGTCGGCGCGTGGCGCGCTGACACC-GACAGAGG-GGTCCGGACTT
      1730      1740      1750      1760      1770       1780       1790

       870       880                890        900       910       920
    GACACAGAGGAAGTTGG-----CTAGAGG----CCGGTCCCTTC-CTTGGGCCCCTCTCATTCCCTCCCCAG
      |   | ||  ||| |     ||  | |    ||||    ||| |||||      |||||| | |  | ||
    TTC---GGGGGCGTTCGGACCCCTCTATGTCAACCGGAGATTTCACTTGG--ATTACTCATTTCGTTGCAAG
         1800      1810      1820      1830      1840        1850      1860

     930       940       950       960       970         980       X
    AATGGAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAAC-TC-TGAACAAAGCCCCCG
    ||  |||  ||| |     |||| |    ||   |  |  | ||| ||     ||  || ||||
    AA-AGAGAAAACTC----TTCCAACTTTTGCAAAAAGTTGCTAACGTCCACGCCACCGCACCCGGAAGCCGC
          1870          1880      1890      1900      1910      1920

    GC
  1930
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq5inv.res made by  on Wed 5 Apr 95 20:39:41-PDT.
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Query sequence being compared:US-08-162-407-5’ (1-988)
Number of sequences searched:               313646
Number of scores above cutoff:                4688

      Results of the initial comparison of US-08-162-407-5’ (1-988) with:
   Data bank : EMBL-NEW 1, all entries
   Data bank : GenBank 86, all entries
   Data bank : GenBank-NEW 1, all entries
   Data bank : UEMBL 41_86, all entries

100000-
      -
N     -
U50000-
M     -       **
B     -         *
E     -     *     **
R     -      *   *  *
      -    *
O     -               *
F10000-   *          * *
      -
S     -                  *
E 5000- *               * *
Q     -  *                 *
U     -
E     -                      *
N     -                     * *
C     -*                       *
E     -
S 1000-                          *
      -                         * *
      -                            *
   500-
      -
      -                              **
      -                             *
      -                                  *
      -
      -                                 * **
   100-
      -                                     **
      -                                          *
    50-                                        *
      -                                       *   *
      -
      -                                            *
      -                                         *
      *                                             *** *
      -                                                  *
    10-                                                *  *          *
      -
      -
     5-                                                    *
      -
      -
      -                                                     ** * *
      -
      -
      -                                                 *   * * *
     0---------------------------------------------------------------------
      |   | |  |   |   | |  |   |   | |  |   ||   ||   | |      |
SCORE 0   | 19 |  39   | 58 |  78   |97  | 117|  136   |156   175
STDEV    -1    0   1   2    3   4   5    6    7   8    9

                            PARAMETERS

Similarity matrix       Unitary     K-tuple                  4
Mismatch penalty              1     Joining penalty         30
Gap penalty                1.00     Window size             32
Gap size penalty           0.33
Cutoff score                  2
Randomization group           0

Initial scores to save       45     Alignments to save      15
Optimized scores to save      0     Display context         10

                            SEARCH STATISTICS

Scores:                   Mean         Median      Standard Deviation
                           30            30          13.31

Times:                     CPU                     Total Elapsed
                       00:42:31.05                 00:42:38.00

Number of residues:                288682119
Number of sequences searched:         313646
Number of scores above cutoff:          4688

Cut-off raised to 23.
Cut-off raised to 27.
Cut-off raised to 30.
Cut-off raised to 33.
Cut-off raised to 36.
Cut-off raised to 39.
Cut-off raised to 42.
Cut-off raised to 45.
Cut-off raised to 49.
Cut-off raised to 52.
Cut-off raised to 55.
Cut-off raised to 58.
Cut-off raised to 61.
Cut-off raised to 65.
Cut-off raised to 68.
Cut-off raised to 71.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                    Init. Opt.
Sequence Name     Description                Length Score Score  Sig. Frame
-----------------------------------------------------------------------------
```

```
                           **** 10 standard deviations above mean ****
  1. GORINVOLUC    Gorilla gorilla involucrin ge    1488   175   463  10.89   0
  2. HUMPKNB       Human mRNA for PKN.              2968   171   350  10.59   0
  3. HS4ULIR3      epstein-barr virus simple rep    1150   170   454  10.52   0
  4. U02454        Cloning vector pCMVEBNA, comp    5452   170   454  10.52   0
  5. U02428        Cloning vector pDR2, complete   10737   170   454  10.52   0
  6. U02455        Cloning vector rpDR2, complet   10850   170   454  10.52   0
  7. EBV           Epstein-Barr virus (EBV) geno  172281   170   454  10.52   0
  8. HS4B958RAJ    Epstein-Barr virus, artifactu  184113   170   454  10.52   0
  9. HS4B958RAJ    Epstein-Barr virus, artifactu  184113   170   454  10.52   0
 10. EBV           Epstein-Barr virus (EBV) geno  172281   170   454  10.52   0
 11. EBV           Epstein-Barr virus (EBV) geno  172281   170   454  10.52   0
 12. HUMLSPRO      Human lymphocyte surface prot    2622   167   464  10.29   0
 13. STMCARA       Streptomyces thermotolerans c    2393   164   448  10.07   0
                           ****  9 standard deviations above mean ****
 14. GORINVOLUB    Gorilla gorilla involucrin ge    1818   160   462   9.76   0
 15. GORINVOLUA    Gorilla gorilla involucrin ge    1908   160   462   9.76   0
 16. PPU12557      Pseudomonas putida PRS1 catBC    3686   155   452   9.39   0
 17. PP12557       Pseudomonas putida PRS1 catBC    3686   155   452   9.39   0
 18. STMCARB       Streptomyces thermotolerans g    2749   153   456   9.24   0
                           ****  8 standard deviations above mean ****
 19. SSRYR1B       S.scrofa RYR1 gene for ryanod    1546   148   418   8.86   0
 20. SCHCOADH      S.coelicolor genes for hydrox    5670   148   383   8.86   0
 21. ORAINVOL      Orang-utan involucrin gene, c    2508   147   460   8.79   0
 22. MASHCA        Mesocricetus auratus alpha-ca   32415   146   431   8.71   0
 23. HUMMMDBC      Human DNA from cosmid DNA MMD   68505   144   438   8.56   0
 24. HUMCACHNT     Human N-type calcium channel     7364   143   442   8.49   0
 25. HSCACHNT      Human N-type calcium channel     7364   143   442   8.49   0
 26. DROSEV3       D.virilis sevenless gene, exo    8779   143   451   8.49   0
 27. MUS5SRR5      Mouse gene for 5S rRNA.          1452   142   360   8.41   0
 28. MUS5SRR6      Mouse gene for 5S rRNA.          1476   142   359   8.41   0
 29. MMCRKING      M.musculus gene for mitochond    6031   142   400   8.41   0
 30. RNMTP1        R.norvegicus mtp1 mRNA.          2674   141   445   8.34   0
 31. HUMBCL2A      Human B-cell leukemia/lymphom    5086   140   320   8.26   0
 32. HSBCL2A       Human B-cell leukemia/lymphom    5086   140   320   8.26   0
 33. I08038        Sequence 1 from patent EP 025    5105   140   320   8.26   0
 34. HSREP10       Human beta-tubulin gene (5-be    8874   140   444   8.26   0
 35. CFCALCPH      Dog mRNA for calcyphosin.        1300   139   328   8.19   0
 36. CFCPHOS       Canis familiaris mRNA for cal    1304   139   327   8.19   0
 37. XELFIMC1X     Frog integumentary mucin (FIM    2161   139   317   8.19   0
 38. RATPKNA       Rat mRNA for PKN.                3035   139   386   8.19   0
 39. HUMIR3EB1     Human DNA with homology to EB    1400   138   349   8.11   0
 40. ECU08369      Escherichia coli phosphogluco    3176   138   433   8.11   0
 41. ECU08369      Escherichia coli K12 phosphog    3176   138   433   8.11   0
 42. EC08369       Escherichia coli phosphogluco    3176   138   433   8.11   0
 43. DSANTPE1      D.subobscura antennapedia hom    2016   137   422   8.04   0
 44. HUMGFB        Human basic fibroblast growth    6757   137   381   8.04   0
 45. HSGFB         Human basic fibroblast growth    6757   137   381   8.04   0


1. US-08-162-407-5' (1-988)
   GORINVOLUC   Gorilla gorilla involucrin gene small allele, comp

 LOCUS       GORINVOLUC    1488 bp ds-DNA            PRI       07-SEP-1994
 DEFINITION  Gorilla gorilla involucrin gene small allele, complete cds.
 ACCESSION   M23605 J04499
 KEYWORDS    epidermal protein; involucrin.
 SOURCE      Gorilla gorilla (individual_isolate Gorilla K) vagina DNA.
   ORGANISM  Gorilla gorilla
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
```

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            Eutheria; Primates; Haplorhini; Catarrhini; Pongidae.
REFERENCE   1  (bases 1 to 1488)
  AUTHORS   Teumer,J. and Green,H.
  TITLE     Divergent evolution of part of the involucrin gene in the
            hominoids: Unique intragenic duplications in the gorilla and human
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 1283-1286 (1989)
  STANDARD  full automatic
COMMENT     Draft entry and computer readable copy of sequence [1] kindly
            provided by J.K. Teumer (03-31-89).

            NCBI gi: 340979
FEATURES             Location/Qualifiers
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                     /codon_start=1
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                     /translation="MSLQHTLPVTLSPALSQELLKTVPPPVNTQQEQMKPPTPLPPPC
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                     NPEQQLKQEKAQRDQQLNKQLEEEKKLLDQQLDQELVKRDEQLGMKKEQLLELPEQRE
                     GELKHLEQQKGQLELPEQQEGQLELPEQQEGQLKHLEQQEGQLELPEQQEGQLELPEQ
                     QEGQLKHLEQQEGQLELPEQQEGQLKHLEQQEGQLELPEQQEGQLELPEQQEGQLKHL
                     EQQEGQLELPEQQEGQLKHLEQQKGQLELPEQQEGQLEHLVQQEGQLEQQEGQVEHLE
                     QQVGQLKHLEEQEGQLKHLEQQQGQLGVPEQQVGQPNNLEQEEKQLELPEQQEGQLKH
                     LEKQEAQLELPEQQVGQPKHLEQQEKQLEHPEQQDGQLKHLEQQEGQLKDLEQQKGQL
                     EQPVFAPAPGQVQDIQPALPTKGELLLPVEHQQQKQEVQWPPKHK"
BASE COUNT      445 a    383 c    515 g    145 t
ORIGIN

Initial Score     =    175  Optimized Score  =    463  Significance = 10.89
Residue Identity =    52%  Matches          =    556  Mismatches   =   366
Gaps              =    141  Conservative Substitutions          =     0

           X        10        20        30        40          50
           CGGGGGCT-TTGTTCAGAGTTGGGTAAATGGGGCCGGTGCTGGA--TTCTGGCGTTGCCTCC
           |  | |||  |    |||| || | || ||||   |  |   ||    |||  |  ||  ||
 GCAACTGGATCAAGAGCTAGTCAAGAGAGATGAGCAACTGGGAATGAAGAAAGAGCAACTGTTGGAGCTCCC
   400     X 410       420       430       440       450       460

60          70         80        90           100       110       120
 A-TTCTG-GGGAGGGAATGAG-AGGGGCCCAAGGA--AG--GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
 |   | | ||||||||  |||  |  || |  |||  ||  | |  |||  || |  | || ||   |
 AGAGCAGCGGGAGGGA--GAGCTGAAGCACCTGGAGCAGCAGAAGGGGCAGCTGG--AGCTCCCAGAG-CAG
 470       480         490       500       510       520         530

    130       140       150         160         170       180       190
 CAGGCTATACATCCTCTGGCTGGTGACTCCC--CTCTG--TGTGCCTCAGTATCCTCCCCTGTAAAATGGGA
 ||||     ||       ||||| | |||||    | |   | |   |||      | |||| |  |  | |
 CAGGAGGGGCA-------GCTGGAG-CTCCCAGAGCAGCAGGAGGGACAGCTGAAGCACCTGGAGCA--GCA
    540              550        560       570       580       590

      200         210       220       230       240       250       260
 TGATAGATGTCTG--TCTCACTGCGTTGTTTAAGGCTCCGCAGGATGAGGCCTTGGCCAGGTCAGTGCTCCA
  ||  |    |||   ||| | | |  |    |||  | || ||| |   ||  |  |||  ||| |    |
```

```
   GGAGGGGCAGCTGGAGCTCCCAGAGCAGCAGGAGGGGCAGCTGGA-GCTCCC-AGAGCAG--CAG-GAGGGA
    600       610       620       630       640         650          660

        270       280       290       300       310           320       330
   CAAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGGGC----GGGGTGTCCTCCGCCGC
   | ||| | ||  ||| | |     ||| |||  ||    ||| ||||| ||    || | | |  | |  ||
   C-AGCTGAAGCACCTAGAGCAGCAGGAGGGGCAGCTGGAGCT-CCCAGAGCAGCAGGAGGGACAGCTGAAGC
        670       680       690       700        710       720       730

            340       350       360         370       380             390
   GTCCTCTGC--CAGTGCAGGCACCAGGCAGCGGCC--AGCAGCAGGAGGCCCACGGGCAGC------AGCAG
     |    ||  |||    |||| | || |||  ||  ||||||||||||  ||   | |||      |||||
   ACCTGGAGCAGCAGGAGGGGCAGCTGG-AGCTCCCAGAGCAGCAGGAGGGGCAGCTGGAGCTCCCAGAGCAG
       740       750       760        770       780       790       800

           400       410        420       430       440       450       460
   TAGGAGG---AGCAGAGGGGGCT-GCGGGGCTGTCGGGGCTGTGGCCTCCAGGGGCCGGGGACTCCATGGGG
    ||||||   ||| || |   || | |  || |  ||||| |    ||  ||   || | | |  ||  ||
   CAGGAGGGACAGCTGAAGCACCTAGAGCAGCAGGAGGGGCAG----CTGGAGCTCCCAGAG-CAGCA--GGA
      810       820       830       840           850       860

          470       480           490       500       510       520
   GTGGCAGGGTTGAGGAGTCGG----GCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
   | | || | |  || |   ||    || ||    ||||||  | || ||  ||| ||  | || | |  | |
   GGGACA-GCTGAAGCACCTGGAGCAGCAGAAGGGGCAGCTGGA-GCTCCCAGAGCAG--CAGGAGGGGCAGC
 870        880       890       900       910        920         930

  530       540       550       560       570       580       590       600
   CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
     | || || |   || |||      |  || |  ||| || | || ||||  |  ||  ||||  |   |
   TGGAGCATCTGGTGCAGCAG------GAGGGGCAGCTGGAGCA-GCAGGAGGGGCAGG--TGGAGCACCTGG
   940       950             960       970        980         990      1000

          610        620       630         640       650       660
   AGACAGCTGG-GGGGGGGCTGAAAGGCACAT-TTGGTG-ACAAAGTGTATCTCCGTGTTCACGCGCTCCAGC
   || |||| || ||||  ||||||  |||| |   || | |  | | | | ||      ||  | ||  ||||
   AG-CAGCAGGTGGGGCAGCTGAA--GCACCTAGAGGAGCAGGAGGGGCAACTGAAGCATCTGGAGCAGCAGC
          1010      1020        1030      1040      1050      1060

 670         680       690       700        710       720         730
   AAGCCTTGCA--TCTTGGACCCAGCGACAGTCTTGAGCCGC-TCCATCCAGCGCTGTGC--CAGGACCAGCC
   | |    |||  |   || ||||| | ||| |  | |  ||  |||  || |   | ||   ||||  |||
   AGG---GGCAGTTGGGGGTCCCAGAG-CAG-CAGGTGGGGCAGCCAAACAACCTGGAGCAGGAGGAGAAGCA
1070         1080      1090        1100      1110      1120      1130

    740         750           760             770         780       790
   GCCAGAGGCCCC--CGCA----GAGCTCCTCGT------CCTGCAG--GTTGGAGGCCACGGTGACTGGGTA
   ||  |||  |||   |||    |||  ||   |      |||| ||  |  ||||| ||| |   ||||
   GCTGGAGCTCCCAGAGCAGCAAGAGGGCCAGCTGAAGCACCTGGAGAAGCAGGAGG-CACAG---CTGGAGC
   1140      1150      1160      1170      1180      1190          1200

      800         810       820       830        840       850       860
   ATCTTGA--AGCAGGTAGTCAGACAGCTCACGGATTTTGA-CAGCGAAGTCGGAGGAGATGGGGCTGTGTTG
     |  ||  |||||||||   ||||||  | | |  | || ||||  ||    || || | | ||
   TCCCAGAGCAGCAGGTAG---GACAGCCAAAGCACCTGGAGCAGC--AGGAAAAGCAGCTAGAGC--ACCCA
     1210      1220         1230      1240        1250      1260

       870       880       890        900       910       920        930
   GAAGGAGCAGTCCTGGGTCCCACTGAGTCCCGAGC-TCAGCAGCAGCAGCAGGAGGAGATAG-GTTGTTG-G
   || | |||||  | |    | |     ||  ||||  ||| ||  ||||| | ||||  | | |  |  |
   GA-GCAGCAGGACGGACAACTAAAACATCTGGAGCAGCAGGAGGGGCAGCTGAAGGACCTGGAGCAGCAGAA
1270       1280      1290      1300      1310      1320      1330      1340

        940       950       960               970        980       X
   GCTCCAGGCTGGCGCCAGCACTGTCATTTC-----GGCCGGG---GGCCCCGGA-ATTCCGGCCG
   |   || ||||| | |||| ||||  || |       || ||   || ||  || ||||   | |
   GGGGCA-GCTGGAG-CAGC-CTGTGTTTGCCCCAGCTCCAGGCCAGGTCCAAGACATTCAACCAGCCCTGCC
          1350        1360      1370      1380      1390      1400 X

   CAC
1410


2. US-08-162-407-5' (1-988)
   HUMPKNB      Human mRNA for PKN.

LOCUS       HUMPKNB      2968 bp ss-mRNA            PRI       12-MAY-1994
DEFINITION  Human mRNA for PKN.
ACCESSION   D26181
KEYWORDS    PKN.
SOURCE      Homo sapiens (library: lambda ZAPII) hippocampus cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE   1  (bases 1 to 2968)
  AUTHORS   Ono,Y. and Mukai,H.
  TITLE     A novel protein kinase with leucine zipper-like sequences: Its
            catalytic domain is highly homologous to that of protein kinase C
  JOURNAL   Biochem. Biophys. Res. Commun. 199, 897-904 (1994)
  STANDARD  full automatic
COMMENT     Submitted (22-Dec-1993) to DDBJ by: Yoshitaka Ono
            Dept. of Biochemistry
            Faculty of Science
            Kobe University
            1-1 Rokkodai-cho, Nada-ku
            Kobe 657
            Japan
            Phone: 078-881-1212 x4450
            Email: yono@niguts.nig.ac.jp
            Fax:   078-801-1740.

            NCBI gi: 473712
FEATURES             Location/Qualifiers
     source          1..2968
                     /organism="Homo sapiens"
                     /sequenced_mol="cDNA to mRNA"
                     /tissue_type="hippocampus"
                     /clone_lib="lambda ZAPII"
BASE COUNT     587 a    928 c    961 g    492 t
ORIGIN

Initial Score     =    171  Optimized Score  =    350  Significance = 10.59
Residue Identity  =    52%  Matches          =    416  Mismatches   =   271
Gaps              =     99  Conservative Substitutions              =     0

      250    X  260       270       280        290       300       310
   GGCCAGGTCAGTGCTCCACAAGCAGCAGGTCCTGGGGACTGG-GGACGGGGGGCACCTGCTCCCCAGGGCGG
             |   ||| |  ||||    ||| ||   | ||  |||  ||    || ||  | | | || |
             GAATTCC-CGCGCAGAGACTCCAGGTCGCAGGTCGACATGG----CCAGCGACGCCGTGCAG
             X        10        20        30        40            50
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   320       330         340         350       360       370       380
  GGTGTCCTCCGCCGC--GTCCTCTGCCAGTGCAG--GCACCAGGCAGCGGCCAGCAGCAGGAGGCCCACGGG
   |||  |  ||| ||  |||| |||| || ||||  |  || ||| | || ||| | | || ||||| ||||
  AGTGAGCCTCGCAGCTGGTCC-CTGCTAGAGCAGCTGGGCCTGGCCG-GGGCAG-ACCTGGCGGCCCCCGGG
   60        70         80        90       100         110       120

     390       400       410       420       430       440       450
  CAGCAGCAGTAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGGGGCTGTGGCCTCCAGGGGCCGGGGACTCCA
     |||||| ||  ||||| |  | ||  | | ||||| ||| |      || | ||| || |  | ||  |
  GTACAGCAGCAGCTGGAGCTGGAGCGG--GAGCGGCTG-CGGCGGGAAATCCGCAAGGAGCTGAAG-CTGAA
   130       140       150         160        170       180        190

   460       470       480       490               500       510
  TGGGGGTGGCAGGGTTGAGGAGTCGGGCTGACACT-------GCAGC-TCCAGGCACCGGGAGAAGTTCTG-
   | |||| || | |     | | |||||   ||||       || ||  || ||  || | |||  | |||
  GGAGGGT-GCTGAGAACCTGCGGCGGGCCACCACTGACCTGGGCCGCAGCCTGGGCCCCGTAGAGCTGCTGC
     200        210       220       230       240       250       260

  520       530       540       550       560       570         580
  -GCGAGTGATCCAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAG--GC-GGGAGATGTTGG
   ||| | | |||   ||  |  | | ||| ||||| |  ||  |  ||||||||||  ||  |   | || |
  TGCG-GGGCTCC-TCGCGCCGCCTCGACCTGCTGCAC-CAG--CAGCTGCAGGAGCTGCACGCCCACGTGGT
     270       280       290       300           310       320       330

   590       600       610       620       630       640        650
  TCTGGACGAAGCGAAGACAGCTGGGGGGGGGCTGAAAGGCACATTTGGTGACAAAGTGTATCTCCGTGTTCA
   ||   |||  ||  | |  |     |  |||    || | |   |||||     | ||  | ||   | |
  GCTTCCCGACCCGGCGGCCAC-CCACGATGGCCCCCAGTCCC--CTGGTG----CGGGTGGCCCCACCTGCT
       340       350       360       370            380       390

 660       670       680       690               700       710       720
  CGCGCTCCAGC--AAGCCTTGCATCTTGGACCCAGCGA--CAGT-----CTTGAGCCGCTCCATCCAGCGCT
  ||  | ||| |   ||||  || |   || ||  | ||  ||||      |||||| |     |  |||
  CGGCCACCAACCTGAGCC--GCGTGGCGGGCCTGGAGAAGCAGTTGGCCATTGAGCTG-AAGGTGAAGCAGG
  400       410         420       430       440       450        460

        730       740       750           760       770       780
  GTGCCAGGACCAGCCGCCAGAGGCCCCCGCA----GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGACT
  | ||   || ||    |||||  |  | |||     ||| ||  |  | | | | ||  |   ||   | |
  GGGCGGAGAACATGATCCAGA-CCTACAGCAATGGCAGCACCAAGGACCGGAAGCTGCTGCTGAC--AGCCC
   470       480        490       500       510       520       530

790       800       810       820       830       840       850
  GGGTAATCTTGAAGCAGGTAGTCAGACAGCTCACGGATTTTGACAGCGAAGTCGGAGGAGA-----TGGGGC
   |   || ||| ||  |  ||| ||||    ||  |||  ||||| |  |  || | |  |       ||||
  AGCAGATGTTGCAG--GACAGTAAGAC----CA-AGAT--TGACATC--ATCCGCATGCAACTCCGCCGGGC
    540         550       560              570         580       590

   860       870       880       890         900       910            920
  TGTGTTGGAAGGAGCAGTCCTGG-GTCCCACTGAGTCCC-GAGCTCAGCAGCAGCAG-CAGGA----GGAGA
    ||  ||  ||  |||  |||| |  |||   || ||| ||   || |    | || |  ||     || |
  GCTGCAGGCCGG-CCAG--CTGGAGAACCAGGCAGCCCCGGATGACACCCAAGGGAGTCCTGACCTGGGGGC
   600       610        620       630        640       650       660

      930            940       950        960         970       980
  TAGGTTGTTGGGC-TCCA--GGCTGGCGCCAGCACTGTC-ATTTCGGC---CGGGGGCCCCGGAATTCC--G
  |  |  | || || || |   ||| ||| || ||||  | | |   ||   ||| ||||  ||  | ||  |
  TGTGGAGCTGCGCATCGAAGAGCT-GCGGCACCACTTCCGAGTGGAGCACGCGGTGGCCGAGG-GTGCCAAG
    670       680        690       700       710       720       730
```

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       X
    GCCG
      ||
    AACGTACTGCGCCT
      740

3. US-08-162-407-5' (1-988)
   HS4ULIR3     epstein-barr virus simple repeat array (ir3).

 LOCUS       HS4ULIR3     1150 bp ds-DNA            VRL       15-JUN-1990
 DEFINITION  epstein-barr virus simple repeat array (ir3).
 ACCESSION   J02079
 KEYWORDS    repeat region.
 SOURCE      ebv (epstein barr virus) from human.
   ORGANISM  Epstein-Barr virus
             Viridae; ds-DNA enveloped viruses; Herpesviridae;
             Gammaherpesvirinae.
 REFERENCE   1  (bases 1 to 1150)
   AUTHORS   Heller,M., van Santen,V.L. and Keiff,E.
   TITLE     simple repeat sequence in epstein-barr virus dna is transcribed in
             latent and productive infections
   JOURNAL   J. Virol. 44, 311-320 (1982)
   STANDARD  full automatic
 COMMENT     NCBI gi: 330445
 FEATURES             Location/Qualifiers
      source          1..1150
                      /organism="Epstein-Barr virus"
 BASE COUNT      302 a    169 c     633 g    46 t
 ORIGIN

Initial Score    =    170  Optimized Score  =    454  Significance = 10.52
Residue Identity =    50%  Matches          =    529  Mismatches   =   418
Gaps             =    105  Conservative Substitutions             =     0

              X       10           20        30        40        50
              CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
              ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
    CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
           80 X      90       100       110       120       130       140

    60        70          80        90           100       110       120
    CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
     |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
    GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
        150       160       170       180       190       200        210

       130       140       150       160       170       180        190
    CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
    | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
    CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
          220        230       240         250       260       270       280

       200       210       220          230        240       250         260
    -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
      ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
    GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
           290         300       310       320       330       340       350
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         270         280           290       300       310       320
  CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
   |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
  GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
         360       370       380       390            400        410

   330       340       350       360       370          380       390
  CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
    ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| ||||| ||
  GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
   420       430        440         450       460       470       480

    400        410       420        430       440        450         460
  GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
  |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
  GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
    490       500       510       520         530       540       550

         470          480        490       500       510       520
  GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
   | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
  AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
    560       570       580       590       600       610       620

 530       540       550       560       570       580       590       600
  CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
    ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
  AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
  630       640       650          660       670       680       690

         610         620           630       640       650       660
  AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
  || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
  AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
    700       710       720       730         740       750       760

   670       680        690         700       710       720       730
  AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
  |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
  AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
    770       780       790       800       810       820       830

       740       750        760       770       780           790
  AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
  ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
  AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
  840        850       860       870        880         890       900

800       810         820       830        840       850       860
  GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
  || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
  GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
      910       920        930         940       950       960       970

 870       880       890       900       910       920        930
  AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
  |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
  AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
       980        990        1000      1010      1020       1030
 940       950       960           970        980       X
   GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
   | | | |   | | ||  |   || | |||    || |  | ||   || |  |
   GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGAAGTCGT
1040      1050      1060      1070      1080      1090  X    1100
```

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4. US-08-162-407-5' (1-988)
   U02454       Cloning vector pCMVEBNA, complete sequence.

 LOCUS       U02454       5452 bp    DNA   circular  SYN      08-NOV-1993
 DEFINITION  Cloning vector pCMVEBNA, complete sequence.
 ACCESSION   U02454
 KEYWORDS    .
 SOURCE      Cloning vector pCMVEBNA.
   ORGANISM  Cloning vector pCMVEBNA
             Artificial sequences; Cloning vector.
 REFERENCE   1  (bases 1 to 5452)
   AUTHORS   Kitts,P.A.
   TITLE     CLONTECH Vectors On Disc version 1.1
   JOURNAL   Unpublished
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 5452)
   AUTHORS   Swirski,R.A., Van Den Berg,D., Murphy,A.J., Lambert,C.M.,
             Friedberg,E.C. and Schimke,R.T.
   TITLE     Improvements in the Epstein-Barr-based shuttle vector system for
             direct cloning in human tissue culture cells
   JOURNAL   Methods: A Companion to Methods in Enzymology 4, 133-142 (1992)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 5452)
   AUTHORS   Kitts,P.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
             4030 Fabian Way, Palo Alto, CA 94303, USA
   STANDARD  full automatic
 COMMENT     This vector can be obtained from CLONTECH Laboratories, Inc., 4030
             Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415)
             424-8222 or (800) 662-2566, extension 1. International customers,
             please contact your local distributor.  For technical information,
             call (415) 424- 8222 or (800) 662-2566, extension 3.
             This sequence has been compiled from information in the sequence
             databases, published literature and other sources; this vector has
             not been completely sequenced. If you suspect there is an error in
             this sequence, please contact CLONTECH's Technical Service
             Department at (415) 424-8222 or (800) 662-2566, extension 3 or
             E-mail CLONTECH@BIOTECHNET.COM.

             NCBI gi: 413820
 FEATURES             Location/Qualifiers
      source          1..5452
                      /organism="Cloning vector pCMVEBNA"
 BASE COUNT     1362 a   1246 c   1736 g   1108 t
 ORIGIN

Initial Score    =    170  Optimized Score  =    454  Significance = 10.52
Residue Identity =    50%  Matches          =    529  Mismatches   =   418
Gaps             =    105  Conservative Substitutions             =     0

              X       10          20         30        40        50
              CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
```

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             ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
   CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
      870    X  880       890      900        910       920       930

   60        70        80        90         100       110       120
   CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
    |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
   GAGGACGAGGAGGCGGAAGACCAGGAGCCCCCGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
    940       950       960       970       980       990      1000

      130       140       150       160       170       180       190
   CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
   | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
   CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
  1010          1020      1030       1040      1050      1060      1070

      200       210       220          230       240       250         260
   -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
     ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
   GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
      1080      1090       1100      1110      1120      1130      1140

          270       280           290       300       310       320
   CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
    |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
      1150      1160      1170      1180      1190           1200

    330       340       350       360       370          380       390
   CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
     ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| ||||| ||
   GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
1210      1220      1230        1240       1250      1260      1270

     400        410       420        430       440        450         460
   GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
   |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
 1280      1290      1300      1310        1320      1330      1340

          470          480        490       500       510       520
   GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
    | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
   AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
 1350      1360      1370      1380      1390      1400      1410      1420

  530       540       550       560       570       580       590       600
   CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
     ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
   AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
         1430      1440        1450      1460      1470      1480

          610       620          630       640       650       660
   AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
   || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
   AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
1490      1500      1510      1520        1530      1540      1550

 670      680        690         700       710       720       730
   AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
  |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
  AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
1560      1570      1580      1590      1600      1610      1620      1630

       740       750        760       770       780           790
  AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
  ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
  AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
        1640       1650      1660       1670        1680      1690

800       810         820       830        840       850       860
  GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
  || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
  GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
1700        1710      1720         1730      1740      1750      1760

 870       880       890       900       910       920        930
  AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
  |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
  AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
   1770      1780         1790       1800      1810      1820       1830

940       950       960           970        980       X
  GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
  | | | |   | | ||  |   || | |||    || |  | ||   || |  |
  GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGAAGTCGT
      1840       1850      1860      1870      1880    X 1890
```

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5. US-08-162-407-5’ (1-988)
   U02428        Cloning vector pDR2, complete sequence.

 LOCUS        U02428       10737 bp    DNA    circular   SYN        08-NOV-1993
 DEFINITION   Cloning vector pDR2, complete sequence.
 ACCESSION    U02428
 KEYWORDS     .
 SOURCE       Cloning vector pDR2.
   ORGANISM   Cloning vector pDR2
              Artificial sequences; Cloning vector.
 REFERENCE    1  (bases 1 to 10737)
   AUTHORS    Kitts,P.A.
   TITLE      CLONTECH Vectors On Disc version 1.1
   JOURNAL    Unpublished
   STANDARD   full automatic
 REFERENCE    2  (bases 1 to 10737)
   AUTHORS    Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
   TITLE      cDNA expression cloning in human cells using the plambdaDR2
              episomal vector system
   JOURNAL    Methods:A Companion to Methods in Enzymology 4, 111-131 (1992)
   STANDARD   full automatic
 REFERENCE    3  (bases 1 to 10737)
   AUTHORS    Kitts,P.A.
   TITLE      Direct Submission
   JOURNAL    Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
              4030 Fabian Way, Palo Alto, CA 94303, USA
   STANDARD   full automatic
 COMMENT      This vector can be obtained from CLONTECH Laboratories, Inc., 4030
              Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415)
              424-8222 or (800) 662-2566, extension 1. International customers,
              please contact your local distributor.  For technical information,
```

```
              call (415) 424- 8222 or (800) 662-2566, extension 3. This sequence
              was compiled by Andrew Murphy and revised at CLONTECH; this vector
              has not been completely sequenced. If you suspect there is an error
              in this sequence, please contact CLONTECH’s Technical Service
              Department at (415) 424-8222 or (800) 662-2566, extension 3 or
              E-mail CLONTECH@BIOTECHNET.COM.

              NCBI gi: 413794
 FEATURES               Location/Qualifiers
      source            1..10737
                        /organism="Cloning vector pDR2"
 BASE COUNT      2686 a    2596 c    3033 g    2422 t
 ORIGIN

Initial Score     =     170  Optimized Score  =       454  Significance  = 10.52
Residue Identity  =     50%  Matches          =       529  Mismatches    =   418
Gaps              =     105  Conservative Substitutions                  =     0
```

```
             X       10           20        30        40        50
             CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
             ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
   CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
  6400      6410      6420      6430      6440      6450      6460

   60        70          80        90           100       110       120
   CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
    |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
   GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
6470      6480      6490      6500      6510      6520      6530       6540

      130       140       150       160       170       180        190
   CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
   | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
   CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
             6550      6560       6570       6580      6590      6600

      200       210       220          230        240       250         260
   -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
     ||  |   |     |   |  |    |||  |    ||||||| || || |  |  ||||   ||  ||
   GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
   6610      6620        6630      6640      6650      6660      6670

          270         280           290       300       310       320
   CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
    |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
   6680      6690      6700      6710      6720            6730      6740

    330       340       350       360       370          380       390
   CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
     ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| |||||||
   GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
       6750      6760       6770        6780      6790      6800      6810

     400        410       420        430       440        450         460
   GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
   |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
        6820      6830      6840      6850        6860      6870      6880
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         470          480        490       500       510       520
  GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
   | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
  AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
       6890      6900      6910      6920      6930      6940      6950

 530       540       550       560       570       580       590       600
  CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
    ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
  AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
     6960      6970         6980      6990      7000      7010      7020

         610         620           630       640       650       660
  AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
  || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
  AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
       7030      7040      7050      7060        7070      7080      7090

   670       680        690         700       710       720       730
  AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
  |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
  AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
       7100      7110      7120      7130      7140      7150      7160

       740       750        760       770       780           790
  AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
  ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
  AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
     7170       7180      7190      7200         7210      7220      7230

800       810         820       830        840       850       860
  GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
  || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
  GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
         7240      7250         7260      7270      7280      7290

 870       880       890       900       910       920        930
  AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
  |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
  AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
7300      7310       7320         7330      7340      7350       7360

940       950       960           970        980       X
  GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
  | | | |   | | ||  |   || | |||    || |  | ||   || |  |
  GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGGAAGTCGT
     7370      7380       7390      7400      7410      7420


6. US-08-162-407-5' (1-988)
   U02455         Cloning vector rpDR2, complete sequence.

LOCUS       U02455      10850 bp    DNA   circular  SYN       08-NOV-1993
DEFINITION  Cloning vector rpDR2, complete sequence.
ACCESSION   U02455
KEYWORDS    .
SOURCE      Cloning vector rpDR2.
  ORGANISM  Cloning vector rpDR2
            Artificial sequences; Cloning vector.
REFERENCE   1  (bases 1 to 10850)
```

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  AUTHORS   Kitts,P.A.
  TITLE     CLONTECH Vectors On Disc version 1.1
  JOURNAL   Unpublished
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 10850)
  AUTHORS   Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
  TITLE     cDNA expression cloning in human cells using the plambdaDR2
            episomal vector system
  JOURNAL   Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
  STANDARD  full automatic
REFERENCE   3  (bases 1 to 10850)
  AUTHORS   Kitts,P.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
            4030 Fabian Way, Palo Alto, CA 94303, USA
  STANDARD  full automatic
COMMENT     Lambda DR2 can be obtained from CLONTECH Laboratories, Inc., 4030
            Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415)
            424-8222 or (800) 662-2566, extension 1. International customers,
            please contact your local distributor.  For technical information,
            call (415) 424- 8222 or (800) 662-2566, extension 3.
            This sequence was compiled by Andrew Murphy and revised at
            CLONTECH; this vector has not been completely sequenced. If you
            suspect there is an error in this sequence, please contact
            CLONTECH's Technical Service Department at (415) 424-8222 or (800)
            662-2566, extension 3 or E-mail CLONTECH@BIOTECHNET.COM.

            NCBI gi: 413821
FEATURES             Location/Qualifiers
     source          1..10850
                     /organism="Cloning vector rpDR2"
                     /note="plasmid released from lambda DR2"
BASE COUNT     2723 a   2615 c   3053 g   2459 t
ORIGIN

Initial Score     =    170  Optimized Score =    454  Significance = 10.52
Residue Identity  =    50%  Matches         =    529  Mismatches   =   418
Gaps              =    105  Conservative Substitutions             =     0

          X       10           20        30        40        50
          CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
          ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
      6520      6530      6540      6550      6560      6570      6580

60        70          80        90           100       110       120
CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
 |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
    6590      6600      6610      6620      6630      6640       6650

   130       140       150       160       170       180        190
CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
| |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
      6660       6670      6680        6690      6700      6710

   200       210       220          230        240       250         260
-TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
  ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
   GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
6720      6730        6740      6750      6760      6770      6780

          270         280           290       300       310       320
   CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
    |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
6790      6800      6810      6820      6830           6840       6850

    330       340       350       360       370          380       390
   CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGCAGCAGCAGTAG
     ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| ||||| ||
   GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
    6860      6870       6880        6890      6900      6910      6920

     400        410       420        430       440        450         460
   GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGGCCGG-GGA-CTCCATG-GGGT
   |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
     6930      6940      6950      6960        6970      6980      6990

          470          480        490       500       510       520
   GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
    | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
   AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
     7000      7010      7020      7030      7040      7050      7060

  530       540       550       560       570       580       590       600
   CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
     ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
   AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
   7070      7080         7090      7100      7110      7120      7130

          610         620           630       640       650       660
   AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
   || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
   AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
     7140      7150      7160      7170        7180      7190      7200

    670       680        690         700       710       720       730
   AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
   |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
   AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
     7210      7220      7230      7240      7250      7260      7270

        740       750        760       770       780           790
   AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
   ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
   AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
   7280       7290      7300      7310       7320        7330      7340

 800       810         820       830        840       850       860
   GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
   || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
   GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
       7350      7360       7370        7380      7390      7400      7410

  870       880       890       900       910       920        930
   AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
   |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
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  AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
       7420       7430         7440      7450      7460       7470

940       950       960           970        980       X
  GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
  | | | |   | | ||  |   || |  |||    || |  | ||   || |  |
  GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGGAAGTCGT
7480      7490       7500      7510      7520      7530      7540


7. US-08-162-407-5' (1-988)
   EBV          Epstein-Barr virus (EBV) genome. The complete sequ

 LOCUS       EBV        172281 bp    DNA   circular  VRL       04-JAN-1995
 DEFINITION  Epstein-Barr virus (EBV) genome. The complete sequence [1-10] was
             determined from DNA from B95-8 cells cloned by Arrand et al [11].
             B95-8 is a productive marmoset lymphoblastoid cell line
             immortalized with human EBV from a mononucleosis patient.
 ACCESSION   V01555 J02070 K01729 K01730 V01554 X00498 X00499 X00784
 KEYWORDS    DNA polymerase; EBNA; genome; ribonucleotide reductase;
             tandem repeat; terminal repeat.
 SOURCE      Human herpesvirus 4.
   ORGANISM  Human herpesvirus 4
             Viridae; ds-DNA enveloped viruses; Herpesviridae;
             Gammaherpesviridae.
 REFERENCE   1  (bases 1 to 172281)
   AUTHORS   Baer,R.J., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J.,
             Gibson,T.J., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C.,
             Tuffnell,P.S. and Barrell,B.G.
   TITLE     DNA sequence and expression of the B95-8 Epstein-Barr virus genome
   JOURNAL   Nature 310, 207-211 (1984)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 172281)
   AUTHORS   Deininger,P.L., Bankier,A., Farrell,P., Baer,R. and Barrell,B.
   TITLE     Sequence analysis and in vitro transcription of portions of the
             Epstein-Barr virus genome
   JOURNAL   J. Cell. Biochem. 19, 267-274 (1982)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 172281)
   AUTHORS   Farrell,P.J., Deininger,P.L., Bankier,A. and Barrell,B.
   TITLE     Homologous upstream sequences near Epstein-Barr virus promoters
   JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 80, 1565-1569 (1983)
   STANDARD  full automatic
 REFERENCE   4  (bases 1 to 172281)
   AUTHORS   Farrell,P.J., Bankier,A.T., Seguin,C., Deininger,P.L. and
             Barrell,B.G.
   TITLE     Latent and lytic cycle promoters of Epstein-Barr virus
   JOURNAL   EMBO J. 2, 1331-1338 (1983)
   STANDARD  full automatic
 REFERENCE   5  (bases 142687 to 159853)
   AUTHORS   Bankier,A.T., Deininger,P.L., Farrell,P.J. and Barrell,B.G.
   TITLE     Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
             Epstein-Barr virus
   JOURNAL   Mol. Biol. Med. 1, 21-45 (1983)
   STANDARD  full automatic
 REFERENCE   6  (bases 112620 to 125316)
   AUTHORS   Seguin,C., Farrell,P.J. and Barrell,B.G.
   TITLE     DNA sequence and transcription of the BamHI fragment B region of
             B95-8 Epstein-Barr virus
   JOURNAL   Mol. Biol. Med. 1, 369-392 (1983)
  STANDARD  full automatic
REFERENCE   7  (bases 159853 to 172281)
  AUTHORS   Bankier,A.T., Deininger,P.L., Satchwell,S.C., Baer,R., Farrell,P.J.
            and Barrell,B.G.
  TITLE     DNA sequence analysis of the EcoRI Dhet fragment of B95-8
            Epstein-Barr virus containing the terminal repeat sequences
  JOURNAL   Mol. Biol. Med. 1, 425-445 (1983)
  STANDARD  full automatic
REFERENCE   8  (bases 87650 to 92703)
  AUTHORS   Biggin,M., Farrell,P.J. and Barrell,B.G.
  TITLE     Transcription and DNA sequence of the BamHI L fragment of B95-8
            Epstein-Barr virus
  JOURNAL   EMBO J. 3, 1083-1090 (1984)
  STANDARD  full automatic
REFERENCE   9  (bases 76089 to 79808)
  AUTHORS   Gibson,T., Stockwell,P., Ginsburg,M. and Barrell,B.
  TITLE     Homology between two EBV early genes and HSV ribonucleotide
            reductase and 38K genes
  JOURNAL   Nucleic Acids Res. 12, 5087-5099 (1984)
  STANDARD  full automatic
REFERENCE   10 (bases 1 to 172281)
  AUTHORS   Hatfull,G.F., Barrell,B.G., Quinn,J. and McGeoch,D.
  JOURNAL   Unpublished
  STANDARD  full automatic
REFERENCE   11 (bases 1 to 172281)
  AUTHORS   Arrand,J.R., Rymo,L., Walsh,J.E., Bjorck,E., Lindahl,T. and
            Griffin,B.E.
  TITLE     Molecular cloning of the complete Epstein-Barr virus genome as a
            set of overlapping restriction endonuclease fragments
  JOURNAL   Nucleic Acids Res. 9, 2999-3014 (1981)
  STANDARD  full automatic
REFERENCE   12 (bases 1 to 172281)
  AUTHORS   Kozak,M.
  TITLE     Possible role of flanking nucleotides in recognition of the AUG
            initiator codon by eukaryotic ribosomes
  JOURNAL   Nucleic Acids Res. 9, 5233-5262 (1981)
  STANDARD  full automatic
REFERENCE   13 (bases 7315 to 9312)
  AUTHORS   Yates,J., Warren,N., Reisman,D. and Sugden,B.
  TITLE     A cis-acting element from the Epstein-Barr viral genome that
            permits stable replication of recombinant plasmids in latently
            infected cells
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 81, 3806-3810 (1984)
  STANDARD  full automatic
REFERENCE   14 (bases 45415 to 52824)
  AUTHORS   Jones,M.D., Foster,L., Sheedy,T. and Griffin,B.E.
  TITLE     The EB virus genome in Daudi Burkitt's lymphoma cells has a
            deletion similar to that observed in a non-transforming strain
            (P3HR-1) of the virus
  JOURNAL   EMBO J. 3, 813-821 (1984)
  STANDARD  full automatic
REFERENCE   15 (bases 45644 to 52450)
  AUTHORS   Jeang,K.T. and Hayward,S.D.
  TITLE     Organization of the Epstein-Barr virus DNA molecule. III. Location
            of the P3HR-1 deletion junction and characterization of the NotI
            repeat units that form part of the template for an abundant
            12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
  JOURNAL   J. Virol. 48, 135-148 (1983)
  STANDARD  full automatic
REFERENCE   16 (bases 1 to 172281)
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  AUTHORS   Farrell,P.J. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1984) to the EMBL/GenBank/DDBJ databases
  STANDARD  full automatic
REFERENCE   17 (bases 1 to 172281)
  AUTHORS   Bodescot,M. and Perricaudet,M.
  TITLE     Clustered alternative splice sites in Epstein-Barr virus RNAs
  JOURNAL   Nucleic Acids Res. 15, 5887 (1987)
  STANDARD  full automatic
REFERENCE   18 (bases 1 to 172281)
  AUTHORS   Laux,G., Perricaudet,M. and Farrell,P.J.
  TITLE     A spliced Epstein-Barr virus gene expressed in immortalized
            lymphocytes is created by circularization of the linear viral
            genome
  JOURNAL   EMBO J. 7, 769-774 (1988)
  STANDARD  full automatic
REFERENCE   19 (bases 1 to 172281)
  AUTHORS   Farrell,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-1988) to the EMBL/GenBank/DDBJ databases. Farrell
            P., Ludwig Institute for Cancer Research, St. Mary's Hospital
            Medical School, Norfolk Place London W2 1PG
  STANDARD  full automatic
COMMENT     CDS
            Listed under this feature are all known protein coding regions as
            well as all the major open reading frames in the sequence. In
            general the term major is taken as the longest frame in a
            particular region taking into account the adjacent longest frames
            and likely transcription signals. Note that on this basis some long
            overlapping frames have been excluded and on the other hand some
            small frames have been included which might represent exons or
            genes because they occur in a logical combination with other
            features or because of some other experimental data. The reading
            frames are named according to the Bam H1 fragment in which they
            start. eg BALF3 is the third leftward frame starting in Bam H1
            fragment A. BORF1 is the first rightward frame in Bam H1 fragment
            O. If there is an obvious TATA sequence followed by an in frame Met
            codon that satisfies the rules of Kozak [12] in that there is a
            purine at -3 and/or a G at +4 then the reading frame is numbered
            from the A of the ATG to the base preceding the termination codon.
            If there is no obvious initiation codon or there is a substantial
            reading frame in phase before the ATG then the reading frame is
            numbered from the first base of the first codon.
            SITEs of POLYA signals
            This feature lists all occurences of the sequence AATAAA which is
            found normally approximately 20 bases upstream of the mRNA
            processing/polyA addition site. The rarely used homolog ATTAAA is
            only listed when it is found in a position close to the end of a
            major reading frame.
            SITEs of DONOR and ACCEPT sequences
            This is not a comprehensive listing of all such sequences and only
            the positions of a few have been noted because they occur in
            potentially interesting positions. The number quoted in the table
            is the position of the terminal base in the intron in each case.
            Restriction enzyme SITEs.
            Only the positions of the sites Bam HI (BAM) are listed.
            RPT
            This feature is used to define repetitive sequences.
            SITE DEL
            This feature defines deletions in B95-8 with respect to other
            strains such as RAJI and also to deletions in other strains such as
            P3HR1 and DAUDI with respect to B95-8.
            SITE HPN
            Denotes sequences with twofold symmetry ie could form hairpin
            loops. This is not a comprehensive list - only a few occurences
            noted.
            ORGRPL
            Denotes the region that encompasses an origin of replication (ori
            P).[13].
            NUMBERING
            The DNA sequence of B95-8 EBV has been revised [19]. The original
            (Baer et al, 1984) base 359 has been deleted so the new sequence
            around that position reads TCAGTCTTT. To avoid renumbering the
            entire sequence, position 1 has benn moved 1 base to the left of
            the EcoRI site separating EcoRI Dhet from EcoRI I
            (ie the first A of AGAATTC).

            NCBI gi: 59074
FEATURES             Location/Qualifiers
     source          1..172281
                     /organism="Epstein-Barr virus"
                     /strain="B95-8"
     mRNA            58..272
                     /note="exon 2 terminal protein RNA"
     mRNA            360..458
                     /note="exon 3 terminal protein RNA"
     misc_feature    complement(535)
                     /note="polyA signal: AATAAA"
     mRNA            540..788
                     /note="exon 4 terminal protein RNA"
     mRNA            871..951
                     /note="exon 5 terminal protein RNA"
     mRNA            1026..1196
                     /note="exon 6 terminal protein RNA"
     promoter        complement(1192)
                     /note="TATA: TATAAAT"
     mRNA            1280..1495
                     /note="exon 7 terminal protein RNA"
     promoter        complement(1383)
                     /note="TATA: CATAAAA"
     mRNA            1574..1682
                     /note="exon 8 terminal protein RNA"
     promoter        1676
                     /note="TATA: TATAAAG"
     promoter        1691
                     /note="TATA: TATTAAA BN-R1 late promoter before BNRF1,
                     gives 4.1kb late RNA. Probably encodes non glycosylated
                     140kd protein in membrane antigen. Also two latent RNAs
                     spliced underneath this RNA, lengths 1.8 and 2.0kb (Hudson
                     et al, 1985). The longer one encodes terminal protein."
     CDS             1736..5692
                     /note="BNRF1 reading frame, 5 NXT/S;  NCBI gi: 59075"
                     /codon_start=1
                     /translation="MEERGRETQMPVARYGGPFIMVRLFGQDGEANIQEERLYELLSD
                     PRSALGLDPGPLIAENLLLVALRGTNNDPRPQRQERARELALVGILLGNGEQGEHLGT
                     ESALEASGNNYVYAYGPDWMARPSTWSAEIQQFLRLLGATYVLRVEMGRQFGFEVHRS
                     RPSFRQFQAINHLVLFDNALRKYDSGQVAAGFQRALLVAGPETADTRPDLRKLNEWVF
                     GGRAAGGRQLADELKIVSALRDTYSGHLVLQPTETLDTWKVLSRDTRTAHSLEHGFIH
                     AAGTIQANCPQLFMRRQHPGLFPFVNAIASSLGWYYQTATGPGADARAAARRQQAFQT
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                     FITVRQRGEKINGRTVLQALGRACDMAGCQHYVLGSTVPLGGLNFVNDLASPVSTAEM
                     MDDFSPFFTVEFPPIQEEGASSPVPLDVDESMDISPSYELPWLSLESCLTSILSHPTV
                     GSKEHLVRHTDRVSGGRVAQQPGVGPLDLPLADYAFVAHSQVWTRPGGAPPLPYRTWD
                     RMTEKLLVSAKPGGENVKVSGTVITLGEQGYKVSLDLREGTRLAMAEALLNAACAPIL
                     DPEDVLLTLHLHLDPRRADNSAVMEAMTAASDYARGLGVKLTFGSASCPETGSSASNF
                     MTVVASVSAPGEFSGPLITPVLQKTGSLLIAVRCGDGKIQGGSLFEQLFSDVATTPRA
                     PEALSLKNLFRAVQQLVKSGIVLSGHDISDGGLVTCLVEMALAGQRGVTITMPVASDY
                     LPEMFAEHPGLVFEVEERSVGEVLQTLRSMNMYPAVLGRVGEQGPDQMFEVQHGPETV
                     LRQSLRLLLGTWSSFASEQYECLRPDRINRSMHVSDYGYNEALAVSPLTGKNLSPRRL
                     VTEPDPRCQVAVLCAPGTRGHESLLAAFTNAGCLCRRVFFREVRDNTFLDKYVGLAIG
                     GVHGARDSALAGRATVALINRFPALRDAILKFLNRPDTFSVALGELGVQVLAGLGAVG
                     STDNPPAPGVEVNVQRSPLILAPNASGMFESRWLNISIPATTSSVMLRGLRGCVLPCW
                     VQGSCLGLQFTNLGMPYVLQNAHQIACHFHSNGTDAWRFAMNYPRNPTEQGNIAGLCS
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     misc_feature    complement(1795)
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     misc_feature    3955
                     /note="BAM: Bam H1 Nhet/h"
     misc_feature    3994
                     /note="BAM: Bam H1 h/C"
     mRNA            5408..5856
                     /note="exon 9 terminal protein RNA"
     misc_feature    5841
                     /note="polyA signal: AATAAA, end of 4.1kb late RNA and TP
                     latent RNA."
     misc_feature    5863
                     /note="alternative end to TP cDNAs"
     promoter        6097
                     /note="TATA: TATAAGA"
     misc_feature    6629..6795
                     /note="Pol III RNA EBER 1"
     promoter        complement(6823)
                     /note="TATA: CATAAAT"
     misc_feature    6956..7128
                     /note="Pol III RNA EBER 2"
     rep_origin      7315..9312
                     /note="origin of replication, ori P (Yates et al, 1984,
                     1985)"
     repeat_region   7421..8042
                     /note="21x30bp repeats, binding sites for EBNA-1 (site I,
                     Rawlins et al, 1985). Tandem repeat part of oriP (Reisman
                     et al, 1985). Also functions as a cell type specific
                     enhancer (Reisman et al, 1985; Lupton and Levine, 1985)"
     promoter        7738
                     /note="TATA: TATAAAT"
     promoter        7888
                     /note="TATA: TATAAAT"
     promoter        8573
                     /note="TATA: CATAAAT"
     misc_feature    complement(8680)
                     /note="polyA signal: AATAAA"
     misc_feature    complement(8755)
                     /note="polyA signal: AATAAA"
     misc_feature    8962
                     /note="polyA signal: AATAAA"
     misc_feature    9021..9133
                     /note="HPN: dyad symmetry, site II for EBNA-1 binding
                     (Rawlins et al, 1985). Dyad symmetry part of oriP (Reisman
                et al, 1985)"
promoter        complement(9398)
                /note="TATA: TATAAAT"
promoter        9631
                /note="TATA: TATAAAT BC-R1 late promoter before BCRF1"
CDS             9675..10187
                /note="BCRF1 reading frame;  NCBI gi: 59076"
                /codon_start=1
                /translation="MERRLVVTLQCLVLLYLAPECGGTDQCDNFPQMLRDLRDAFSRV
                KTFFQTKDEVDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPEAKDHV
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                IEAYMTIKAR"
promoter        10076
                /note="TATA: GATAAAA"
misc_feature    complement(10148)
                /note="polyA signal: AATAAA"
misc_feature    10173
                /note="polyA signal: ATTAAA"
misc_feature    10257
                /note="polyA signal: AATAAA, end of 0.8kb late RNA from
                BCR1 and end of 1.6 kb late RNA, start unknown"
misc_feature    complement(10277)
                /note="polyA signal: AATAAA"
promoter        complement(10975)
                /note="TATA: CATAAAT"
promoter        11305
                /note="TATA: TACAAAA; BCR2 promoter for highly spliced
                EBNA latent RNAs."
mRNA            11336..11480
                /note="exon C1 of Bodescot et al (1986) RNAs"
promoter        11524
                /note="TATA: TATAATT"
misc_feature    complement(11587)
                /note="polyA signal: AATAAA"
promoter        complement(11606)
                /note="TATA: CATAAAT"
mRNA            11626..11657
                /note="exon C2 of Bodescot et al (1986) RNAs"
promoter        11796
                /note="TATA: TATAAGT"
promoter        complement(11799)
                /note="TATA: TATAAAA"
repeat_region   12001..15072
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CDS             12541..13692
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                LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature    13215
                /note="BAM: BamH1 C/W"
promoter        14352
                /note="*TATA: TATAAAG BWR1 one of the promoters for highly
                spliced EBNA and LP RNAs (Sample et al, 1986; Speck et al,
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                1986)"
mRNA            14384..14410
                /note="*exon W0 of EBNA/LP RNAs"
mRNA            14554..14619
                /note="*exon W1 (also W66) part of leader protein (LP)
                gene. LP is also called EBNA-5 (Dillner et al, 1986) and
                EBNA-4 (Rowe et al, 1987)."
mRNA            14559..14619
                /note="*exon W1' (also W61) of EBNA/LP RNAs forms
                initiator met when fused to exon W0 or exon C2."
mRNA            14701..14832
                /note="*exon W2 (also W132) part of LP gene"
repeat_region   15073..18144
                /note="3072 repeat 2"
CDS             15613..16764
                /note="BWRF1 reading frame 2;  NCBI gi: 583874"
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                /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
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misc_feature    16287
                /note="BAM: BamH1 W/W"
promoter        17424
                /note="TATA: TATAAAG"
mRNA            17626..17691
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mRNA            17773..17904
                /note="Exon W2"
repeat_region   18145..21216
                /note="3072 repeat 3"
CDS             18685..19836
                /note="BWRF1 reading frame 3;  NCBI gi: 583875"
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misc_feature    19359
                /note="BAM: BamH1 W/W"
promoter        20496
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mRNA            20698..20763
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mRNA            20845..20976
                /note="Exon W2"
repeat_region   21217..24288
                /note="3072 repeat 4"
CDS             21757..22908
                /note="BWRF1 reading frame 4;  NCBI gi: 583876"
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                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
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     promoter        23568
                     /note="TATA: TATAAAG"
     mRNA            23771..23835
                     /note="Exon W1"
     mRNA            23917..24048
                     /note="Exon W2"
     repeat_region   24289..27360
                     /note="3072 repeat 5"
     CDS             24829..25980
                     /note="BWRF1 reading frame 5;  NCBI gi: 583877"
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                     PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
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     misc_feature    25503
                     /note="BAM: BamH1 W/W"
     promoter        26640
                     /note="TATA: TATAAAG"
     mRNA            26842..26907
                     /note="Exon W1"
     mRNA            26989..27120
                     /note="Exon W2"
     repeat_region   27361..30432
                     /note="3072 repeat 6"
     CDS             27901..29052
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     misc_feature    28575
                     /note="BAM: BamH1 W/W"
     promoter        29712
                     /note="TATA: TATAAAG"
     mRNA            29914..29979
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     mRNA            30061..30192
                     /note="Exon W2"
     repeat_region   30433..33504
                     /note="3072 repeat 7"
     CDS             30973..32124
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                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
     misc_feature    31647
                     /note="BAM: BamH1 W/W"
     promoter        32784
                     /note="TATA: TATAAAG"
     mRNA            32986..33051
                     /note="Exon W1"
     mRNA            33133..33264
                     /note="Exon W2"
     repeat_region   33505..36576
                     /note="3072 repeat 8"
     CDS             34045..35196
                     /note="BWRF1 reading frame 8;  NCBI gi: 583880"
                     /codon_start=1
                     /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
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                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
     misc_feature    34719
                     /note="BAM: BamH1 W/W"
     promoter        35856
                     /note="TATA: TATAAAG"
     mRNA            36058..36123
                     /note="Exon W1"
     mRNA            36205..36336
                     /note="Exon W2"
     repeat_region   36577..39648
                     /note="3072 repeat 9"
     CDS             37117..38268
                     /note="BWRF1 reading frame 9;  NCBI gi: 583881"
                     /codon_start=1
                     /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                     PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
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                     PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                     HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
     misc_feature    37791
                     /note="BAM: BamH1 W/W"
     promoter        38928
                     /note="TATA: TATAAAG"
     mRNA            39130..39195
                     /note="Exon W1"
     mRNA            39277..39408
                     /note="Exon W2"
     repeat_region   39649..42720
                     /note="3072 repeat 10"
     CDS             40189..41340
                     /note="BWRF1 reading frame 10;  NCBI gi: 583882"
                     /codon_start=1
                     /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                     PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
                     TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
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                 PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
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misc_feature     40863
                 /note="BAM: BamH1 W/W"
promoter         42000
                 /note="TATA: TATAAAG"
mRNA             42202..42267
                 /note="Exon W1"
mRNA             42349..42480
                 /note="Exon W2"
repeat_region    42721..45792
                 /note="3072 repeat 11"
CDS              43261..44412
                 /note="BWRF1 reading frame 11;  NCBI gi: 583883"
                 /codon_start=1
                 /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
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                 PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                 HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                 LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                 VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature     43935
                 /note="BAM: BamH1 W/W"
promoter         45072
                 /note="TATA: TATAAAG"
mRNA             45274..45339
                 /note="Exon W1"
misc_feature     45415..52824
                 /note="DEL: DAUDI deletion (Jones et al, 1984)"
mRNA             45421..45552
                 /note="Exon W2"
misc_feature     45644..52450
                 /note="DEL: P3HR1 deletion (Jeang and Hayward, 1983)"
repeat_region    45793..47643
                 /note="3072 repeat 12"
CDS              46333..47484
                 /note="BWRF1 reading frame 12;  NCBI gi: 583884"
                 /codon_start=1
                 /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
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misc_feature     47007
                 /note="BAM: BamH1 W/Y"
mRNA             47761..47793
                 /note="Exon Y1 Bodescot et al, 1984"
promoter         47831
                 /note="TATA: TATAAGT"
mRNA             47878..47999
                 /note="Exon Y2 Bodescot et al, 1984 and EBNA-1 (Speck and
                 Strominger,1985), last common exon"
misc_feature     complement(48023)
                 /note="polyA signal: AATAAA"
CDS              48386..50032
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                 /note="Coding exon for EBNA-2 (Sample et al,1986)"
                 /codon_start=1
mRNA             48386..48444
                 /note="exon Bodescot et al, 1984"
CDS              48429..49967
                 /note="BYRF1, encodes EBNA-2 (Dambaugh et al, 1984;
                 Dillner et al, 1984);  NCBI gi: 583885"
                 /codon_start=1
                 /translation="XCGWAGTCQQPSKHPRLCFALSAAIMPTFYLALHGGQTYHLIVD
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                 NDQQLHHLPSGPPWWPPICDPPQPSKTQGQSRGQSRGRGRGRGRGRGKGKSRDKQRKP
                 GGPWRPEPNTSSPSMPELSPVLGLHQGQGAGDSPTPGPSNAAPVCRNSHTATPNVSPI
                 HEPESHNSPEAPILFPDDWYPPSIDPADLDESWDYIFETTESPSSDEDYVEGPSKRPR
                 PSIQ"
repeat_region    48678..48800
                 /note="14 x CCCCCACCA repeats"
misc_feature     48848
                 /note="BAM: BamH1 Y/H"
promoter         49350
                 /note="TATA: TATAACA"
promoter         complement(49353)
                 /note="TATA: TATAAAA"
repeat_region    49525..49578
                 /note="9 x GGGGCA repeats"
mRNA             49852..50032
                 /note="exon (Bodescot et al 1984)"
misc_feature     50003
                 /note="polyA signal: AATAAA, end of Bodescot T1 RNA and
                 EBNA-2 RNA (3.0kb latent RNA in IB4 cells)"
promoter         complement(50156)
                 /note="TATA: TATAAGT"
misc_feature     complement(50317)
                 /note="polyA signal: AATAAA, end of 2.5kb early RNA from
                 52817"
repeat_region    50578..52115
                 /note="12 x 125bp repeats"
misc_feature     complement(50578..52557)
                 /note="BHLF1 early reading frame"
misc_feature     52654..53697
                 /note="region homologous to Eco R1 C of Raji"
promoter         complement(52817)
                 /note="TATA: GATAAAA promoter for 2.5kb early RNA
                 containing BHLF1 (Jeang and Hayward, 1983; Freese et
                 al,1983)"
promoter         53759
                 /note="TATA: TATTAAC likely promoter for class III and IV
                 early RNAs encoding BHRF1 (Pearson et al, 1987)"
misc_feature     53895
                 /note="DONOR: CGGGTAACT donor for splice to 54335 in class
                 IV early RNAs encoding BHRF1 (Pearson et al, 1987)"
misc_feature     54335
                 /note="ACCEPT: TTTTCTAG acceptor from 48444 in class I,
                 47999 in class II, and 53895 in class IV early RNAs
                 encoding BHRF1 (Pearson et al, 1987)"
misc_feature     54376..54948
                 /note="BHRF1 reading frame, limited homolgy to bcl-2 gene.
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                    Early gene in B95-8 cells and part of restricted EA
                    complex."
promoter            54591
                    /note="TATA: TATAACA"
promoter            complement(54594)
                    /note="TATA: TATAAAT"
misc_feature        54853
                    /note="BAM: BamH1 H/F"
misc_feature        complement(54929)
                    /note="polyA signal: AATAAA"
promoter            complement(54977)
                    /note="TATA: TATAAAG"
misc_feature        55518
                    /note="polyA signal: AATAAA, 3’ end of 2.5kb, 1.9kb, 1.7kb
                    and 0.6kb early RNAs"
misc_feature        complement(55982..56935)
                    /note="BFLF2 reading frame, 4 NXT/S, homologous to RF 27
                    in VZV and HFRF2 in CMV"
misc_feature        complement(55990)
                    /note="polyA signal: AATAAA, 3’ end of 2.3kb and 1.1kb
                    early RNAs from 58568 and 57081"
promoter            complement(56132)
                    /note="TATA: TATAAAG"
CDS                 complement(56948..58525)
                    /note="BFLF1 reading frame, 2 NXT/S homologous to RF 26 in
                    VZV and HFRF1 in CMV;  NCBI gi: 59090"
                    /codon_start=1
                    /translation="MAHKVTSANEPNPLTGKRLSSCPLTRSGVTEVAQIAGRTPKMED
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                    MPSRILAIDIQLHFYICRCFLPVSSSDMIRNANLGYYKLEFLKSILTGQSPANFCFKS
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                    SPEITTKADYCGLLLGTWQGTDLLGGPGHHAIGLNAEYSGDELAELALAITRPEAGDH
                    SQGPCLLAPMFGLRHKNASRTICPLCESLGAHPDAKDTLDRFKSLILDSFGNNIKILD
                    RIVFLIKTQNTLLDVPCPRLRAWLQMCTPQDFHKHLFCDPLCAINHSITNPSVLFGQI
                    YPPSFQAFKAALAAGQNLEQGVCDSLITLVYIFKSTQVARVGKTILVDVTKELDVVLR
                    IHGLDLVQSYQTSQVYV"
promoter            complement(57081)
                    /note="TATA: TATTTAA before BFLF2; BFL2 promoter gives
                    1.1kb early RNA"
promoter            complement(58088)
                    /note="TATA: GATAAAA"
promoter            complement(58568)
                    /note="TATA: TATTAAA before BFLF1, BFL1 promoter gives
                    2.3kb early RNA"
promoter            58832
                    /note="TATA: TATAAAA before BFRF1"
CDS                 58891..59901
                    /note="BFRF1 early reading frame, 1 NXT/S, homologous to
                    HFLF4 in CMV;  NCBI gi: 59091"
                    /codon_start=1
                    /translation="MASPEERLLDELNNVIVSFLCDSGSLEVERCSGAHVFSRGSSQP
                    LCTVKLRHGQIYHLEFVYKFLAFKLKNCNYPSSPVFVISNNGLATTLRCFLHEPSGLR
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                    RTTMQFLVFQAANAQKASRVMDMISDMSQQLSRSGQVEDTGARVTGGGGPRPGVTHSG
                    CLGDSHVRGRGGWDLDNFSEAETEDEASYAPWRDKDSWSESEAAPWKKELVRHPIRRH
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                    WT"
CDS                 59610..61583
                    /note="BFRF2 early reading frame, homologous to HFLF5 in
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                    CMV;  NCBI gi: 583886"
                    /codon_start=1
                    /translation="XRRRGELRSLEGQRLVVGIRGGAVEEGTREAPHPQAPDTRDSPY
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                    VERPGGLVRWARSQTSPSSLTLAPHLGPSLLSLSVVTGGGCGAVAFCNAFFLAYFLVV
                    RSVFPAFSDRIAAWICDRSPFCENTRAVARGYRGLVKRFLAFVFERSSYDPPLLRQNS
                    RPVERCFAIKNYVPGLDSQSCVTVPSFSRWAQSHASELDPREIRDRVTPATAPSFVAD
                    HASALLASLQKKASDTPCGNPIQWMWYRLLVNSCLRSAHCLLPIPAVSEGGRKTGGGV
                    GEELVGAGGPCLSRDVFVAIVSRNVLSCLLNVPAAGPRAYKCFRSHASRPVSGPDYPP
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                    SAAVGCQRLAEPPSARSGWRPRIRAVLPHNAAYELDRGSRLLDAIIPCLGPDRTCMRP
                    VVLRGVTVRQLLYLTLRTEARAVCSICQQRQAPEDARDEPHLFSSCLEVELPPGERCA
                    GCRLYQTRYGTPAAQAHPPGEAGGGFSRQSPAS"
promoter            complement(61062)
                    /note="TATA: GATAAAA"
promoter            61344
                    /note="TATA: TATTTAA before BFRF3"
CDS                 61456..62037
                    /note="BFRF3 early reading frame;  NCBI gi: 583887"
                    /codon_start=1
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                    QELNQNNLPNDVFREAQRSYLVFLTSQFCYEEYVQRTFGVPRRQRAIDKRQRASVAGA
                    GAHAHLGGSSATPVQQAQAAASAGTGALASSAPSTAVAQSATPSVSSSISSLRAATSG
                    ATAAASAAAAVDTGSGGGGQPHDTAPRGARKKQ"
misc_feature        complement(62068)
                    /note="polyA signal: AATAAA"
misc_feature        62069
                    /note="polyA signal: AATAAA, 3’ end of 10, 6.5, 3.7, 3.4,
                    3.1, 2.5 and 0.8kb early RNAs"
CDS                 complement(62078..71527)
                    /note="BPLF1 reading frame, 1 NXT/S, analogous to VZV
                    RF22;  NCBI gi: 59094"
                    /codon_start=1
                    /translation="MSNGDWGQSQRTRGTGPVRGIRTMDVNAPGGGSGGSALRILGTA
                    SCNQAHCKFGRFAGIQCVSNCVLYLVKSFLAGRPLTSRPELDEVLDEGARLDAIMRQS
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                    DGEAAGTPGADSSPPVMLPFERRIIPYNLRPLPSRSFTSDSFPAARYSPAKTNSPPSS
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                    IEYGAPPAASVPPFVHNVAVRSKNAALHVRRCTADIRDKVASAASDYLSYLEDPSLPT
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                    EAWARIRKALGARPEPAPTSPDDWNTLLASLLPDNTDSAAAAAAAVARNTDILDSLTQ
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                    ATAKEGGGGRGAEEAAGALFRARTAADAIRSALAQTRQALQSPDMKSAVVNTDLEAPY
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                    AIGPPQDDQERRRRTLASVASARLSAAAADSYWDTWPDVESNAGELLREYVSAPKALM
                    EDLADNPIVAMTLLAHASLIASRNHPPYPAPATDREVILLEQREMMALLVGTHPAYAA
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                    EDARRLTRHRIAGPPTGFIFFQDAWEEMDTRAALWPHPEFLGLVHNQSTARARACMLL
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     misc_feature   62249
                    /note="BAM: BamH1 F/Q"
     misc_feature   62430..62477
                    /note="Site III for EBNA-1 binding (Rawlins et al, 1985)"
     misc_feature   66121
                    /note="BAM: BamH1 Q/U"
     mRNA           67477..67649
                    /note="Exon in EBNA-1 RNA (Speck and Strominger,1985) and
                    cDNA clone T4 (Bodescot et al, 1986)"
     misc_feature   69410
                    /note="BAM: BamH1 U/P"
     repeat_region  69684..69930
                    /note="5 x 51bp repeats"
     repeat_region  70387..70521
                    /note="9 x 15bp repeat"
     promoter       70750
                    /note="TATA: CATAAAA"
     CDS            complement(71520..75239)
                    /note="BOLF1 reading frame, 1 NXT/S analogous to VZV RF
                    21;  NCBI gi: 59096"
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                    /translation="MASAMESDSSGGSGGADAQPPLAEVDGGLARVTRQLLLSGDDPA
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                    GEVLAVSGPTATFAFVEELVADTYLARWDAFPREGLSFYAFNAAKTTLGRWLVTVYAE
                    TNRYPWAAAGQGQPTAADIKAMAVELVEHSGGGAGGGEGEESGGGLFHRPESLSSVVA
                    SLPLARRRAVEILGVYAEASGGQTPPVAAVPVLAFDAARLRLLEPSGALFYDYVYEAL
                    LWDQTYGVPDSVIEAFLAGMAAEMEALAARVQEAAGSRASFSPAAIEQVATVLLSAGL
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                    ALELGYSLTGALRRSVAYRFRDYTFARLFQPPAIDAERAEAIVRRDARPPPVFIPAPR
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                    NGRNASKRRASRDLSPPPHGRWRAVLDSSPFSFSSSDFSDQDEGEGGEADLRGVPGGG
                    GEGAYEEDRERPSDIDTAARAQKVETSCPRRRSPRTTPSPSRRASGGGGPDRGEAEAH
                    TYPPYLSAAAAASRVRPRTRRGATRRPPRPTAEDE"
     promoter       complement(72192)
                    /note="TATA: TATTAAA before BPLF1"
     misc_feature   73468
                    /note="BAM: BamH1 P/O"
     promoter       75017
                    /note="TATA: TATTTAA BO-R1 late promoter before BORF1,
                    gives 3.9kb late RNA"
     CDS            75238..76332
                    /note="BORF1 late reading frame, 2 NXT/S homologous to VZV
                    RF20;  NCBI gi: 59095"
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                    FTFFQSSRGHCQIMNILRIYYSPSIMHRYAVVQPLHIEELTFGAVACLGTFSATDGWR
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     promoter       complement(75322)
                    /note="TATA: TATTTAG before BOLF1"
     promoter       75819
                    /note="TATA: TATAAAG"
     misc_feature   75838
                    /note="polyA signal: AATAAA"
     misc_feature   complement(76126)
                    /note="polyA signal: AATAAA"
     promoter       76169
                    /note="TATA: TACATAT BO-R2 early promoter before BORF2,
                    gives 2.8kb RNA"
     misc_feature   complement(76300)
                    /note="polyA signal: AATAAA"
     CDS            76407..78887
                    /note="BORF2 early reading frame, 2 NXT/S. Homology HSV
                    140K ribonucleotide reductase (Gibson et al, 1984) and RF
                    19 VZV;  NCBI gi: 59097"
                    /codon_start=1
                    /translation="MATTSHVEHELLSKLIDELKVKANSDPEADVLAGRLLHRLKAES
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                    TYLYVGRSGKQESVQHFYMRLAGFCASTTCLYAGLRAALQRARPEIESDMEVFDYYFE
                    HLTSQTVCCSTPFMRFAGVENSTLASCILTTPDLSSEWDVTQALYRHLGRYLFQRAGV
                    GVGVTGAGQDGKHISLLMRMINSHVEYHNYGCKRPVSVAAYMEPWHSQIFKFLETKLP
                    ENHERCPGIFTGLFVPELFFKLFRDTPWSDWYLFDPKDAGDLERLYGEEFEREYYRLV
                    TAGKFCGRVSIKSLMFSIVNCAVKAGSPFILLKEACNAHFWRDLQGEAMNAANLCAEV
                    LQPSRKSVATCNLANICLPRCLVNAPLAVRAQRADTQGDELLLALPRLSVTLPGEGAV
                    GDGFSLARLRDATQCATFVVACSILQGSPTYDSRDMASMGLGVQGLADVFADLGWQYT
                    DPPSRSLNKEIFEHMYFTALCTSSLIGLHTRKIFPGFKQSKYAGGWFHWHDWAGTDLS
                    IPREIWSRLSERIVRDGLFNSQFIALMPTSGCAQVTGCSDAFYPFYANASTKVTNKEE
                    ALRPNRSFWRHVRLDDREALNLVGGRVSCLPEALRQRYLRFQTAFDYNQEDLIQMSRD
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                     RAPFVDQSQSHSLFLREEDAARASTLANLLVRSYELGLKTIMYYCRIEKAADLGVMEC
                     KASAALSVPREEQNERSPAEQMPPRPMEPAQVAGPVDIMSKGPGEGPGGWCVPGGLEV
                     CYKYRQLFSEDDLLETDGFTERACESCQ"
     misc_feature    77835
                     /note="BAM: Bam H1 O/a"
     promoter        78804
                     /note="TATA: TATAAGT Ba-R1 early promoter before BaRF1,
                     gives 3.5kb RNA"
     misc_feature    78883
                     /note="polyA signal: AATAAA, end of 3.9kb late RNA from
                     75017 and 2.8kb early RNA from 76169"
     misc_feature    complement(78896)
                     /note="polyA signal: AATAAA"
     CDS             78900..79808
                     /note="BaRF1 early reading frame, homologous to HSV 38K
                     ribonucleotide reductase (Gibson et al, 1984) and RF 18
                     VZV;  NCBI gi: 59098"
                     /codon_start=1
                     /translation="MSKLLYVRDHEGFACLTVETHRNRWFAAHIVLTKDCGCLKLLNE
                     RDLEFYKFLFTFLAMAEKLVNFNIDELVTSFESHDIDHYYTEQKAMENVHGETYANIL
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                     SFYSIALLRVRGLMPGICLANNYISRDELLHTRAASLLYNSMTAKADRPRATWIQELF
                     RTAVEVETAFIEARGEGVTLVDVRAIKQFLEATADRILGDIGQAPLYGTPPPKDCPLT
                     YMTSIKQTNFFEQESSDYTMLVVDDL"
     promoter        complement(79495)
                     /note="TATA: TATAACA"
     misc_feature    79537
                     /note="BAM: Bam H1 a/M"
     promoter        79840
                     /note="TATA: CATAAAT BM-R1 early promoter before BMRF1,
                     gives 2.5kb RNA"
     CDS             79899..81113
                     /note="BMRF1 early reading frame. Early antigen protein
                     recognised by R3 monoclonal (Pearson et al 1983; Cho et
                     al, 1985a);  NCBI gi: 59099"
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                     PRLAAVANAGTAGLISFEVSPDAVAEWQNHQSPEEAPAAVSFRNLAYGRTCVLGKELF
                     GSAVEQASLQFYKRPQGGSRPEFVKLTMEYDDKVSKSHHTCALMPYMPPASDRLRNEQ
                     MIGQVLLMPKTASSLQKWARQQGSGGVKVTLNPDLYVTTYTSGEACLTLDYKPLSVGP
                     YEAFTGPVAKAQDVGAVEAHVVCSVAADSLAAALSLCRIPAVSVPILRFYRSGIIAVV
                     AGLLTSAGDLPLDLSVILFNHASEEAAASTASEPEDKSPRVQPLGTGLQQRPRHTVSP
                     SPSPPPPPRTPTWESPARPETPSPAIPSHSSNTALERPLAVQLARKRTSSEARQKQKH
                     PKKVKQAFNPLI"
     promoter        80779
                     /note="TATA: TATTTAA BM-R2 late promoter before BMRF2"
     misc_feature    complement(80782)
                     /note="polyA signal: AATAAA"
     promoter        80832
                     /note="TATA: GATAAAA, possible promoter for 1.4kb late RNA
                     encoding BMRF2"
     CDS             81118..82191
                     /note="BMRF2 early reading frame;  NCBI gi: 59100"
                     /codon_start=1
                     /translation="MFSCKQHLSLGACVFCLGLLASTPFIWCFVFANLLSLEIFSPWQ
                     THVYRLGFPTACLMAVLWTLVPAKHAVRAVTPAIMLNIASALIFFSLRVYSTSTWVSA
                     PCLFLANLPLLCLWPRLAIEIVYICPAIHQRFFELGLLLACTIFALSVVSRALEVSAV
                     FMSPFFIFLALGSGSLAGARRNQIYTSGLERRRSIFCARGDHSVASLKETLHKCPWDL
                     LAISALTVLVVCVMIVLHVHAEVFFGLSRYLPLFLCGAMASGGLYLGHSSIIACVMAT
                     LCTLTSVVVYFLHETLGPLGKTVLFISIFVYYFSGVAALSAAMRYKLKKFVNGPLVHL
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                     RVVYMCCFVFTFCEYLLVTFIKS"
     promoter        81751
                     /note="TATA: CATAAAT"
     misc_feature    82180
                     /note="polyA signal: ATTAAA, end of 3.5kb early RNA from
                     78804, 2.5kb early RNA from 79840 and 1.4kb late RNA"
     promoter        complement(82311)
                     /note="TATA: CATAAAT"
     repeat_region   82319..82461
                     /note="2x71bp repeats"
     CDS             complement(82743..84122)
                     /note="BMLF1 early reading frame. Diffuse early antigen
                     (Cho et al, 1985b). Also homologous to RF 4 VZV and IE63
                     of HSV.(BSLF2 + BMLF1) is also called EB2
                     (Chevallier-Greco et al, 1986). General transactivator of
                     transcription (Lieberman et al, 1986).  NCBI gi: 583888"
                     /codon_start=1
                     /translation="XSHILELEAVSDTNTDCDLDPMEGSEEHSTDGEISSSEEEDEDP
                     TPAHAIPARPSSVVITPTSASFVIPRKKWDLQDKTVTLHRSPLCRDEDEKEETGNSSY
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                     PRSESRGAGRSTRKQARQERSQRPLPNKPWFDMSLVKPVSKITFVTLPSPLASLTLEP
                     IQDPFLQSMLAVAAHPEIGAWQKVQPRHELRRSYKTLREFFTKSTNKDTWLDARMQAI
                     QNAGLCTLVAMLEETIFWLQEITYHGDLPLAPAEDILLACAMSLSKVILTKLKELAPC
                     FLPNTRDYNFVKQLFYITCATARQNKVVETLSSSYVKQPLCLLAAYAAVAPAYINANC
                     RRRHDEVEFLGHYIKNYNPGTLSSLLTEAVETHTRDCRSASCSRLVRAILSPGTGSLG
                     LFFVPGLNQ"
     misc_feature    complement(82747)
                     /note="polyA signal: AATAAA"
     repeat_region   83640..83729
                     /note="10x9bp repeats"
     misc_feature    complement(84122)
                     /note="ACCEPT: CTCCCCTCTGCAG acceptor in spliced form of
                     BMLF1 RNA"
     misc_feature    complement(84227)
                     /note="DONOR: CAGGTAAGA donor in spliced form of BMLF1
                     RNA"
     CDS             complement(84229..84288)
                     /note="BSLF2 early reading frame in 5' exon of spliced RNA
                     encoding BMLF1;  NCBI gi: 59102"
                     /codon_start=1
                     /translation="MVPSQRLSRTSSISSNEDPA"
     misc_feature    84233
                     /note="BAM: Bam H1 M/S"
     CDS             complement(84257..86881)
                     /note="BSLF1 reading frame, homologous to RF 6 VZV;  NCBI
                     gi: 59103"
                     /codon_start=1
                     /translation="MSAPVVIKALVASNTDIAEAILDAILSRPDEGFRLFCLCHNASP
                     LHHVAGSLVELQLHLPKKRLTSQSRCGLVLTLHLPAEEAFPFLRGLTPLTADRLSTYL
                     DRAGALRSLTPLVELLTLSAKKQPQGDARGRVAWLRPKIVGCLRRIYRVNISARWFIS
                     TFGSHEAQFVLVTAAYYFWGIPCTIETLAHLTELFTSESGQSLAAVTSLAELGEVFGS
                     SAWAEQTEAFAHFAHEKLRRDSREIRAVARTIDAYRGRLPLASADLVRYVYLAHAQCF
                     NEGTFKRYSQLTSMGEIGCLPSGGVVLPSLLDRGFAEHMRTYFTRETYLAEHVRVQQL
                     KIRMEPPAPYTWDPDPDDGLMRAWAGLSVDVARELVELARWHADEGPTYPPTLQGFLC
                     LAGQATCRGQWNPKEQFLPPTVLRRVQRLPVFLCHFADRHYFVMTAADPFSSHLAEVV
                     STPTNCRLPDTCLTRALSYTPVYYSQNSLSEQLFVSRHEYFNPRLPVCNLVLDLDLKI
                     KGAPWSLEEIYDLCRTVRREVLRLMRRLGPVSRAHPVYFFKSACPPADPDNMEDVLPF
                     CICTGKLGFRVITPLPRGHAIVGTSAVQGFVSVLQKLMGLTACLRRMRHKIKEIGAPL
                     FDSGVYHAGRCIRLPHTYKVDRGGGLSRQLRLFVCHPEEEDKHSYVKNALNIQNLLHH
                     SLHVGWPAPKTFCYHIADDGRDYLIQRTRETLPPTVENVCAMIEGHLGLDLVAWVSSC
                     IWPSLMSTLATAVPEDKFPQFLHVTFEQTGPNLVQVCHARGRNFACLRHTHRASSKNV
                     RVFLVLYYTSQAITVTFMSQCFAGRCGANQPTAHFSISVPASRIINRAEASQDSTTSQ
                     LARRRDRQDGSFSETLPN"
     promoter        complement(84356)
                     /note="TATA: CATAAAT before BSLF2 and BMLF1. Two RNAs
                     start here; one is spliced and the other is unspliced,
                     both traverse BMLF1."
     promoter        86882
                     /note="TATA: TATTTAA BS-R1 late promoter before BSRF1"
     CDS             86924..87580
                     /note="BSRF1 reading frame;  NCBI gi: 59104"
                     /codon_start=1
                     /translation="MAFYLPDWSCCGLWLFGRPRNRYSQLPEEPETFECPDRWRAEID
                     LGLPPGVQVGDLLRNEQTMGSLRQVYLLAVQANSITDHLKRFDAVRVPESCRGVVEAQ
                     VAKLEAVRSVIWNTMISLAVSGIEMDENGLKALLDKQAGDSLALMEMEKVATALKMDE
                     TGAWAQEISAVVSSVTAPSASAPFINSAFEPEVPTPVLAPPPVVRQPEHSGPTELALT
                     "
     misc_feature    complement(87134)
                     /note="polyA signal: AATAAA"
     misc_feature    87599
                     /note="polyA signal: AATAAA"
     misc_feature    complement(87613)
                     /note="polyA signal: AATAAA, end 1.0kb early RNA from
                     BLL3"
     CDS             complement(87638..88474)
                     /note="BLLF3 early reading frame (BLLF2 in Baer et al,
                     1984). Homologous to RF 8 VZV and dUTPase HSV.  NCBI gi:
                     59105"
                     /codon_start=1
                     /translation="MEACPHIRYAFQNDKLLLQQASVGRLTLVNKTTILLRPMKTTTV
                     DLGLYARPPEGHGLMLWGSTSRPVTSHVGIIDPGYTGELRLILQNQRRYNSTLRPSEL
                     KIHLAAFRYATPQMEEDKGPINHPQYPGDVGLDVSLPKDLALFPHQTVSVTLTVPPPS
                     IPHHRPTIFGRSGLAMQGILVKPCRWRRGGVDVSLTNFSDQTVFLNKYRRFCQLVYLH
                     KHHLTSFYSPHSDAGVLGPRSLFRWASCTFEEVPSLAMGDSGLSEALEGRQGRGFGSS
                     GQ"
     misc_feature    87650
                     /note="BAM: Bam H1 S/L"
     promoter        88507
                     /note="TATA: TATATAT BL-R1 late promoter before BLRF1,
                     gives 1.0kb late RNA"
     promoter        88511
                     /note="TATA: TATAAGA"
     promoter        complement(88514)
                     /note="TATA: TATATAT BL-L3 early promoter before BLLF3,
                     gives 1.0kb early RNA"
     CDS             88547..88855
                     /note="BLRF1 late reading frame;  NCBI gi: 59106"
                     /codon_start=1
                     /translation="MGKVLRKPFAKAVPLLFLAATWLLTGVLPAGASSPTNAAAASLT
                     EAQDQFYSYTCNADTFSPSLTSFASIWALLTLVLVIIASAIYLMYVCFNKFVNTLLTD
                     "
     promoter        88863
                     /note="TATA: TATTTAA BL-R2 late promoter before BLRF2,
                     gives 0.6kb late RNA"
     CDS             88925..89413
                     /note="BLRF2 late reading frame, 2 NXS/T;  NCBI gi: 59107"
                     /codon_start=1
                     /translation="MSAPRKVRLPSVKAVDMSMEDMAARLARLESENKALKQQVLRGG
                     ACASSTSVPSAPVPPPEPLTARQREVMITQATGRLASQAMKKIEDKVRKSVDGVTTRN
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                     SD"
     misc_feature    89412
                     /note="polyA signal: AATAAA, end of 1.0kb and 0.6kb late
                     RNAs"
     misc_feature    complement(89425)
                     /note="polyA signal: AATAAA, end of 0.7kb early, 2.2kb
                     late and 2.8kb late RNA"
     CDS             complement(89430..92153)
                     /note="BLLF1a, late reading frame, gp350 membrane antigen,
                     36 NXT/S (Hummel et al, 1984; Biggin et al, 1984; Beisel
                     et al, 1985);  NCBI gi: 59110"
                     /codon_start=1
                     /translation="MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA
                     DVNVTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLLELLGAGEL
                     ALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPYI
                     KWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEI
                     SQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLG
                     NNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVP
                     MVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDIT
                     VSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGFADPNTTTGLPS
                     STHVPTNLTAPASTGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTS
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                     NSTSHMPLLTSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTST
                     KPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKANSTTGGKHTTGHGARTSTE
                     PTTDYGGDSTTPRPRYNATTYLPPSTSSKLRPRWTFTSPPVTTAQATVPVPPTSQPRF
                     SNLSMLVLQWASLAVLTLLLLLVMADCAFRRNLSTSHTYTTPPYDDAETYV"
     CDS             complement(89430..92153)
                     /note="BLLF1b, late reading frame gp220 membrane antigen,
                     spliced form of BLLF1a (Hummel et al, 1984; Biggin et al,
                     1984; Beisel et al, 1985);  NCBI gi: 59109"
                     /codon_start=1
                     /translation="MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA
                     DVNVTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLLELLGAGEL
                     ALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPYI
                     KWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEI
                     SQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLG
                     NNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVP
                     MVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDIT
                     VSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGFADPNTTTGLPS
                     STHVPTNLTAPASTGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTS
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                     NSTSHMPLLTSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTST
                     KPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKANSTTGGKHTTGHGARTSTE
                     PTTDYGGDSTTPRPRYNATTYLPPSTSSKLRPRWTFTSPPVTTAQATVPVPPTSQPRF
                     SNLSMLVLQWASLAVLTLLLLLVMADCAFRRNLSTSHTYTTPPYDDAETYV"
     promoter        complement(89434)
                     /note="TATA: TATAAAG"
     CDS             complement(89567..90013)
                     /note="BLLF2 early reading frame (BLLF3 in Baer et al,
                     1984);  NCBI gi: 59108"
                     /codon_start=1
                     /translation="MCPPVRQHPAQAPPAKRQALETVPHPQNRGRLMSPKARPPKMQR
                     RPRPPVAKRRRFPRSPQQVERPILPPVESTPQDMEPGQVQSPPQITAVIQLRQDRDTM
                     RPPIYLPALLANCGPAGLLRAHRLPQPKPPCQSRQRPSPDSQTSPC"
     promoter        complement(90051)
                     /note="TATA: TATAACA BL-L2 early promoter before BLLF2,
                    gives 0.7kb early RNA"
intron              complement(90062..90652)
                    /note="intervening sequence in gp220 gene"
repeat_region       90177..90639
                    /note="21 copies of 21bp approximate repeat"
promoter            complement(92192)
                    /note="TATA: TATTAAA BL-L1 late promoter before BLLF1a,b.
                    Gives 2.8 and 2.2kb late RNAs"
mRNA                92238..92581
                    /note="Exon in Bodescot et al (1986) RNA (spliced from
                    20763 to 92670)"
CDS                 92243..92581
                    /note="BLRF3 reading frame;  NCBI gi: 59111"
                    /codon_start=1
                    /translation="MDKDRPGPPALDDNMEEEVPSTSVVQEQVSAGDWENVLIELSDS
                    SSEKEAEDAHLEPAQKGTKRKRVDHDAGGSAPARPMLPPQPDLPGREAILRRFPLDLR
                    TLLQAIGAAAT"
CDS                 92670..95165
                    /note="BERF1 frame, homology with BERF2b and BERF4. A
                    fusion of BLRF3 with BERF1 encodes EBNA-3A, latent cycle
                    gene. (Hennessy et al, 1986, Joab et al, 1987);  NCBI gi:
                    583889"
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                    /translation="XIDTRAIDQFFGSQISNTEMYIMYAMAIRQAIRDRRRNPASRRD
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                    VSFMEFLGFLQRTDLSYIKSFVSDALGTTSIQTPWIDDNPSTETAQAWNAGFLRGRAY
                    GIDLLRTEGEHVEGATGETREESEDTESDGDDEDLPCIVSRGGPKVKRPPIFIRRLHR
                    LLLMRAGKRTEQGKEVLEKARGSTYGTPRPPVPKPRPEVPQSDETATSHGSAQVPEPP
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                    AGPIVRPWEPSLTQAAGQAFAPVRPQHMPVEPVPVPTVALERPVYPKPVRPAPPKIAM
                    QGPGETSGIRRARERWRPAPWTPNPPRSPSQMSVRDRLARLRAEAQVKQASVEVQPPQ
                    LTQVSPQQPMEGPLVPEQQMFPGAPFSQVADVVRAPGVPAMQPQYFDLPLIQPISQGA
                    PVAPLRASMGPVPPVPATQPQYFDIPLTEPINQGASAAHFLPQQPMEGPLVPEQWMFP
                    GAALSQSVRPGVAQSQYFDLPLTQPINHGAPAAHFLHQPPMEGPWVPEQWMFQGAPPS
                    QGTDVVQHQLDALGYTLHGLNHPGVPVSPAVNQYHLSQAAFGLPIDEDESGEGSDTSE
                    PCEALDLSIHGRPCPQAPEWPVQEEGGQDATEVLDLSIHGRPRPRTPEWPVQGEGGQN
                    VTGPETRRVVVSAVVHMCQDDEFPDLQDPPDEA"
mRNA                92670..95248
                    /note="Exon in (Bodescot et al, 1986) RNA from 92581, to
                    3' end"
misc_feature        92703
                    /note="BAM: Bam H1 L/E"
promoter            complement(93161)
                    /note="TATA: CATAAAT"
promoter            93479
                    /note="TATA: TATAAGA"
promoter            complement(93482)
                    /note="TATA: TATAAAT"
repeat_region       94208..94277
                    /note="repeat type A"
repeat_region       94281..94306
                    /note="repeat type B"
repeat_region       94307..94381
                    /note="repeat type C"
repeat_region       94386..94411
                    /note="repeat type B"
repeat_region       94412..94489
                    /note="repeat type C"
repeat_region       94490..94560
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repeat_region       94571..94648
                    /note="repeat type C"
repeat_region       94649..94719
                    /note="repeat type A"
repeat_region       94896..94982
                    /note="repeat type D"
repeat_region       94983..95069
                    /note="repeat type D"
misc_feature        95221
                    /note="polyA signal: AATAAA"
misc_feature        complement(95272)
                    /note="polyA signal: AATAAA"
CDS                 95353..95724
                    /note="BERF2a reading frame;  NCBI gi: 59113"
                    /codon_start=1
                    /translation="MKKAWLSRAQQADAGGASGSEDPPDYGDQGNVTQVGSEPISPEI
                    GPFELSAASEDDPQSGPVEENLDAAAREEEEPHEQEHNGGDDPLDVHTRQPRFVDVNP
                    TQAPVIQLVHAVYDSMLVRGT"
CDS                 95725..98247
                    /note="BERF2b frame, homology with BERF1 and BERF4. BERF2a
                    and BERF2b are spliced together to make EBNA3B (EBNA4A)
                    latent protein.  NCBI gi: 583890"
                    /codon_start=1
                    /translation="XISRCFAWIFWPVLIDCHWFQQSDLRPLGSLFLEQNLNIEEFIW
                    MCMTVRHRCQAIRKKPLPIVKQRRWKLLSSCRSWRMGYRTHNLKVNSFESGGDNVHPV
                    LVTATLGCDEGTRHATTYSAGIVQIPRISDQNQKIETAFLMARRARSLSAERYTLFFD
                    LVSSGNTLYAIWIGLGTKNRVSFIEFVGWLCKKDHTHIREWFRQCTGRPKAAKPWLRA
                    HPVAIPYDDPLTNEEIDLAYARGQAMNIEAPRLPDDPIIVEDDDESEEIEAESDEEED
                    KSGMESLKNIPQTLPYNPTVYGRPAVFDRKSDAKSTKKCRAIVTDFSVIKAIEEEHRK
                    KKAARTEQPRATPESQAPTVVLQRPPTQQEPGPVGPLSVQARLEPWQPLPGPQVTAVL
                    LHEESMQGVQVHGSMLDLLEKDDEVMEQRVMATLLPPVPQQPRAGRRGPCVFTGDLGI
                    ESDEPASTEPVHDQLLPAPGPDPLEIQPLTSPTTSQLSSSAPSCAQTPWPVVQPSQTP
                    DDPTKQSRPPETAAPRQWPMPLRPIPMRPLRMQPIPFNHPVGPTPHQTPQVEITPYKP
                    TWAQIGHIPYQPTPTGPATMLLRQWAPATMQTPPRAPTPMSPPEVPPVPRQRPRGAPT
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                    KKGRPSLKLQAALERQAAAGWQPSPGSGTSDKIVQAPIFYPPVLQPIQVMGQGGSPTA
                    MAASAVTQAPTEYTRERRGVGPMPPTDIPPSKRAKIEAYTEPEMPHGGASHSPVVILE
                    NVGQGQQQTLECGGTAKQERDMLGLGDIAVSSPSSSETSNDE"
misc_feature        complement(95819)
                    /note="polyA signal: AATAAA"
promoter            complement(95853)
                    /note="TATA: TATAAAT"
misc_feature        complement(96276)
                    /note="polyA signal: AATAAA"
repeat_region       97522..97698
                    /note="3x60bp repeat"
CDS                 98323..98769
                    /note="BERF3 reading frame;  NCBI gi: 59115"
                    /codon_start=1
                    /translation="MTILDEVEILHIFRPTMESFEGQGDSRQSPDNERGDNVQTTGEH
                    DQDPGPGPPSSGASERLVPEESYSRDQQPWGQSRGDENRGWMQRIRRRRRRRAALSGH
                    LLDTEDNVPPWLPPHDITPYTARNIRDAACRAVKVSMPLTGFMGAI"
mRNA                98364..98730
                    /note="Exon in EBNA-1 RNA (Speck and Strominger, 1985)"
misc_feature        98731
                    /note="DONOR: AAGGTGAGT donor"
CDS                 98805..101423
                    /note="BERF4 frame, homology with BERF1 and BERF2b. BERF3
                    and BERF4 are spliced together to make the EBNA3C (EBNA
                4B) latent protein.  NCBI gi: 583891"
                /codon_start=1
                /translation="XSHLQALSNLILDSGLDTQHILCFVMAARQRLQDIRRGPLVAEG
                GVGWRHWLLTSPSQSWPMGYRTATLRTLTPVPNRVGADSIMLTATFGCQNAARTLNTF
                SATVWTPPHAGPREQERYAREAEVRFLRGKWQRRYRRIYDLIELCGSLHHIWQNLLQT
                EENLLDFVRFMGVMSSCNNPAVNYWFHKTIGNFKPYYPWNAPPNENPYHARRGIKEHV
                IQNAFRKAQIQGLSMLATGGEPRGDATSETSSDEDTGRQGSDVELESSDDELPYIDPN
                MEPVQQRPVMFVSRVPAKKPRKLPWPTPKTHPVKRTNVKTSDRSDKAEAQSTPERPGP
                SEQSSVTVEPAHPTPVEMPMVILHQPPPVPKPVPVKPTPPPSRRRRGACVVYDDDVIE
                VIDVETTEDSSSVSQPNKPHRKHQDGFQRSGRRQKRAAPPTVSPSDTGPPAVGPPAAG
                PPAAGPPAAGPPAAGPPAAGPPAAGPRILAPLSAGPPAAGPHIVTPPSARPRIMAPPV
                VRMFMRERQLPQSTGRKPQCFWEMRAGREITQMQQEPSSHLQSATQPTTPRPSWAPSV
                CALSVMDAGKAQPIESSHLSSMSPTQPISHEEQPRYEDPDAPLDLSLHPDVAAQPAPQ
                APYQGYQEPPAPQAPYQGYQEPPPPQAPYQGYQEPPAHGLQSSSYPGYAGPWTPRSQH
                PCYRHPWAPWSQDPVHGHTQGPWDPRAPHLPPQWDGSAGHGQDQVSQFPHLQSETGPP
                RLQLSLVPLVSSSAPSWSSPQPRAPIRPIPTRFPPPPMPLQDSMAVGCDSSGTACPSM
                PFASDYSQGAFTPLDINATTPKRPRVEESSHGPARCSQATAEAQEILSDNSEISVFPK
                DAKQTDYDASTESELD"
mRNA            98805..99050
                /note="Exon in T4 cDNA (Bodescot et al 1986). 99050 is not
                the end of the RNA."
misc_feature    99126..102118
                /note="DEL: Deletion in Raji"
promoter        99443
                /note="TATA: CATAAAA"
misc_feature    100104
                /note="DONOR: ACCGTGAGT possible donor before repeat."
repeat_region   100122..100304
                /note="10 x 15bp repeat"
misc_feature    100528
                /note="DONOR: CTGGTAAGG possible donor"
misc_feature    100613
                /note="BAM: Bam H1 E/e1"
repeat_region   100665..100781
                /note="3x39bp repeat"
promoter        complement(100860)
                /note="TATA: TATAACA"
misc_feature    100919
                /note="BAM: Bam H1 e1/e2"
misc_feature    101426
                /note="BAM: Bam H1 e2/e3"
CDS             complement(101445..102116)
                /note="BZLF2 reading frame 3x NXT/S. 2.5kb late RNA
                traverses BZLF2, ends unknown.  NCBI gi: 59117"
                /codon_start=1
                /translation="MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVRGGGRVAAAAITW
                VPKPNVEVWPVDPPPPVNFNKTAEQEYGDKEVKLPHWTPTLHTFQVPQNYTKANCTYC
                NTREYTFSYKGCCFYFTKKKHTWNGCFQACAELYPCTYFYGPTPDILPVVTRNLNAIE
                SLWVGVYRVGEGNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPVSHHECSFLKPCLCVS
                QRSNS"
promoter        101690
                /note="TATA: CATAAAA"
misc_feature    101765
                /note="polyA signal: AATAAA"
promoter        complement(101786)
                /note="TATA: TATAAAG"
misc_feature    101947
                /note="BAM: Bam H1 e3/Z"
misc_feature    complement(102098)
                /note="DONOR: CAGGTGAGG possible donor"
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mRNA            complement(102126..102341)
                /note="3' terminal exon of 0.9kb and 2.8kb early RNAs"
promoter        102153
                /note="TATA: TATTAAT"
misc_feature    complement(102156)
                /note="polyA signal: AATAAA 3' end of 0.9kb and 2.8kb RNAs
                encoding BZLF1 and BRLF1"
promoter        complement(102160)
                /note="TATA: TATTAAT"
CDS             complement(102213..103155)
                /note="BZLF1 reading frame, modified from Baer et al,
                1984. Has two splices within frame. 2xNXT/S. Immediate
                early gene which disrupts latency (Countryman and Miller,
                1985), called EB1 by Chevallier-Greco et al, 1986 and
                ZEBRA by Miller."
                /codon_start=1
promoter        complement(102380)
                /note="TATA: CATAAAT"
promoter        102415
                /note="TATA:TATATAC"
promoter        complement(102420)
                /note="TATA: TATATAC"
mRNA            complement(102426..102530)
                /note="Exon of 0.9kb and 2.8kb early RNAs"
misc_feature    complement(102504)
                /note="polyA signal: AATAAA, apparently not functional"
repeat_region   102581..102652
                /note="semi-repetitive sequence, homologous to human c-fos
                3' sequence"
mRNA            complement(102655..103194)
                /note="First exon of 0.9kb early RNA encoding BZLF1"
misc_feature    complement(102918)
                /note="splice acceptor used in RZ fusion gene (Sargeant)"
promoter        complement(103231)
                /note="TATA: TTTAAA of BZL1 immediate early promoter gives
                0.9kb RNA"
misc_feature    complement(103256..103311)
                /note="Upstream of BZL1, homology to 106243 to 106188"
CDS             complement(103366..105183)
                /note="BRLF1 reading frame, (immediate?) early gene, acts
                as transcription activator.  NCBI gi: 59119"
                /codon_start=1
                /translation="MRPKKDGLEDFLRLTPEIKKQLGSLVSDYCNVLNKEFTAGSVEI
                TLRSYKICKAFINEAKAHGREWGGLMATLNICNFWAILRNNRVRRRAENAGNDACSIA
                CPIVMRYVLDHLIVVTDRFFIQAPSNRVMIPATIGTAMYKLLKHSRVRAYTYSKVLGV
                DRAAIMASGKQVVEHLNRMEKEGLLSSKFKAFCKWVFTYPVLEEMFQTMVSSKTGHLT
                DDVKDVRALIKTLPRASYSSHAGQRSYVSGVLPACLLSTKSKAVETPILVSGADRMDE
                ELMGNDGGASHTEARYSESGQFHAFTDELESLPSPTMPLKPGAQSADCGDSSSSSSDS
                GNSDTEQSEREEARAEAPRLRAPKSRRTSRPNRGQTPCPSNAAEPEQPWIAAVHQESD
                ERPIFPHPSKPTFLPPVKRKKGLRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRP
                FHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDP
                DEETSQAVKALREMADTVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNL
                DSPLTPELNEILDTFLNDECLLHAMHISTGLSIFDTSLF"
misc_feature    complement(103453..103462)
                /note="TAATGAAATC sequence"
misc_feature    103741
                /note="BAM: Bam H1 Z/g"
misc_feature    103816
                /note="BAM: Bam H1 g/R"
mRNA            complement(104926..105185)
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                     /note="exon in RZ fusion gene (Sargeant)"
     mRNA            complement(104927..104989)
                     /note="BRLF2 poss. small 5' exon"
     promoter        105016
                     /note="TATA: TATAAAT before BRRF1, possible promoter for
                     1.1 kb early RNA encoding BRRF1"
     promoter        complement(105019)
                     /note="TATA: TATAAAT before BRLF2"
     CDS             105182..106114
                     /note="BRRF1 early reading frame;  NCBI gi: 59118"
                     /codon_start=1
                     /translation="MASSNRGNARPLKSFLHELYLKHYPEVGDVVHLLNTIGVDCDLP
                     PSHPLLTAQRGLFLARVLQAVQQHKLLEDTIVPKILKKLAYFLELLSYYSPKDEQRDI
                     AEVLDHLKTNRDLGLDDRLWALIRKLRQDRHHASVNVLMPGSDYTAVSLQYYDGISIG
                     MRKVIADVCRSGYASMPSMTATHNLSHQLLMASGPSEEPCAWRGFFNQVLLWTVALCK
                     FRRCIYYNYIQGSIATISQLLHLEIKALCSWIISQDGMRLFQHSRPLLTLWESVAANQ
                     EVTDAITLPDCAEYIDLLKHTKHVLENCSAMQYK"
     misc_feature    complement(105185)
                     /note="ACCEPT: splice acceptor in 2.8kb early RNA encoding
                     BRLF1 and RZ fusion gene (Sargeant)"
     promoter        105213
                     /note="TATA: CATTAAA"
     misc_feature    106110
                     /note="polyA signal: AATAAA, 3' end of early 1.1kb RNA
                     encoding BRRF1"
     misc_feature    complement(106125)
                     /note="DONOR: CAGGTAAGA possible donor"
     misc_feature    complement(106188..106243)
                     /note="Homology to upstream region of BZL1"
     promoter        complement(106213)
                     /note="TATA: CATAAAA"
     promoter        106243
                     /note="TATA: TATAAAA before BRRF2, possible promoter for
                     1.8 kb RNA encoding BRRF2"
     CDS             106302..107915
                     /note="BRRF2 reading frame;  NCBI gi: 59120"
                     /codon_start=1
                     /translation="MSGQQRGSVILVPEHLAGALTKLMSDFITGQDVTLSGGNIAVKI
                     RDAINQTPGGGDVAILSSLFALWNALPTSGRQSSRDDLIPAAVQALTTAHNLCLGVIP
                     GETSHKDTPESLLRAIVTGLQKLWVDSCGCPECLQCLKGLKAIKPGLYEIPRIIPHTK
                     QCSPVNLLNMLVHKLVALRGHVQLAYDARVLTPDFHEIPDLDDSDAVFARTLLAALFH
                     LNMFFILKDYITQDSMSLKQALSGHWMSATGNPLPAAPETLRDYLEAFRNSDNHFYLP
                     TTGPLNTFQFPEELLGRVVVIDSSLCAASHVQDVITHGVGAGVPRPRFSALPPAPSRE
                     PQQTCSQLTSRGNESSRRNLGQPGGTSPAVPPVCPIVSLTASGAKQNRGGMGSLHLAK
                     PEETSPAVSPVCPIASPAASRSKQHCGVTGSSQAAPSFSSVAPVASLSGDLEEEEEGS
                     RESPSLPSSKKGDEEFEAWLEAQDANLEDVQREFSGLRVIGDEDEDGSEDGEFSDLDL
                     SDSDHEGDEGGGAVGGGRSLHSLYSLSVV"
     promoter        complement(106385)
                     /note="TATA: GATAAAA"
     misc_feature    complement(106973)
                     /note="polyA signal: AATAAA"
     promoter        complement(107124)
                     /note="TATA: GATAAAA"
     misc_feature    107457
                     /note="BAM: Bam H1 R/f"
     misc_feature    107565
                     /note="BAM: Bam H1 f/K"
     misc_feature    107914
                     /note="polyA signal: AATAAA, 3' end of 1.8kb RNA encoding
                     BBRF2"
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     misc_feature    107942
                     /note="ACCEPT: splice acceptor for EBNA-1 RNA (from
                     98730)"
     CDS             107950..109875
                     /note="BKRF1 encodes EBNA-1 protein, latent cycle gene.
                     NCBI gi: 59121"
                     /codon_start=1
                     /translation="MSDEGPGTGPGNGLGEKGDTSGPEGSGGSGPQRRGGDNHGRGRG
                     RGRGRGGGRPGAPGGSGSGPRHRDGVRRPQKRPSCIGCKGTHGGTGAGAGAGGAGAGG
                     AGAGGAGAGGAGGAGGAGAGGAGAGGAGGAGAGGAGAGGAGGAGAGGAGAGGAGGAGAG
                     GGAGGAGGAGAGGAGAGGAGGAGAGGAGGAGAGGAGAGGAGGAGGAGAGGA
                     GAGGGAGGAGGAGAGGAGAGGAGAGGAGAGGAGGAGAGGAGGAGAGGAGGAGAGGGAG
                     GAGAGGGAGGAGAGGAGGAGAGGAGGAGAGGAGGAGAGGGAGAGGAGAGGGGRGRGGS
                     GGRGRGGSGGRGRGGSGGRRGRGRERARGGSRERARGRGRGRGEKRPRSPSSQSSSSG
                     SPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGP
                     RGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVF
                     VYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFL
                     QTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLPPWFPPMVEGAAAEGDDG
                     DDGDEGGDGDEGEEGQE"
     repeat_region   108217..108924
                     /note="EBNA triplet repeat GGA,GCA,GGG."
     misc_feature    109856
                     /note="DONOR: AGGGTGAGG possible donor at end BKRF1"
     promoter        109905
                     /note="TATA: TATTAAA before BKRF2, possible start for
                     2.3kb late RNA"
     misc_feature    109906
                     /note="polyA signal: ATTAAA"
     misc_feature    109937
                     /note="polyA signal: AATAAA 3' end of EBNA-1 RNA"
     CDS             109958..110371
                     /note="BKRF2 reading frame;  NCBI gi: 59122"
                     /codon_start=1
                     /translation="MRAVGVFLAICLVTIFVLPTWGNWAYPCCHVTQLRAQHLLALEN
                     ISDIYLVSNQTCDGFSLASLNSPKNGSNQLVISRCANGLNVVSFFISILKRSSSALTG
                     HLRELLTTLETLYGSFSVEDLFGANLNRYAWHRGG"
     misc_feature    110271
                     /note="DONOR: TCCGTGAGT possible donor at end of BKRF2"
     CDS             110275..111120
                     /note="BKRF3 reading frame, homologous to RF 59 VZV;  NCBI
                     gi: 583892"
                     /codon_start=1
                     /translation="XVNHPGDSLRFILSGRPVWCQLKQIRMASRGLDLWLDEHVWKRK
                     QEIGVKGENLLLPDLWLDFLQLSPIFQRKLAAVIACVRRLRTQATVYPEEDMCMAWAR
                     FCDPSDIKVVILGQDPYHGGQANGLAFSVAYGFPVPPSLRNIYAELHRSLPEFSPPDH
                     GCLDAWASQGVLLLNTILTVQKGKPGSHADIGWAWFTDHVISLLSERLKACVFMLWGA
                     KAGDKASLINSKKHLVLTSQHPSPLAQNSTRKSAQQKFLGNNHFVLANNFLREKGLGE
                     IDWRL"
     misc_feature    111098
                     /note="DONOR: TCGGTGAGA possible donor at end BKRF3"
     CDS             111107..111787
                     /note="BKRF4 reading frame, contains complex repetitive
                     sequence;  NCBI gi: 583893"
                     /codon_start=1
                     /translation="XGGCRGVITMAMFLKSRGVRSCRDRRLLSDEEEETSQSSSYTLG
                     SQASQSIQEEDVSDTDESDYSDEDEEIDLEEEYPSDEDPSEGSDSDPSWHPSDSDESD
                     YSESDEDEATPGSQASRSSRVSPSTQQSSGLTPTPSFSRPRTRAPPRPPAPAPVRGRA
                     SAPPRPPAPVQQSTKDKGPHRPTRPVLRGPAPRRPPPPSSPNTYNKHMMETTPPIKGN
                     NNYNWPWL"
     misc_feature    111272
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                     /note="DONOR: GACGTGAGT poss.donor before rpt.seq. in
                     BKRF4"
     misc_feature    111719
                     /note="polyA signal: AATAAA"
     misc_feature    111787
                     /note="polyA signal: AATAAA : currently unknown which is
                     3' end of the 2.3kb late and 1.1kb early RNAs"
     CDS             complement(111830..114259)
                     /note="BBLF4 early reading frame, very good homology to
                     RF55 VZV;  NCBI gi: 59126"
                     /codon_start=1
                     /translation="MAEEPRAPEALSSTFMLNMTSDASVRRIVRRIGTLARRRVQQLP
                     DMETFSPEFDPELSEPPFLPFSAYVITGTAGAGKSTSVSCLHHTMDCLVTGATTVAAQ
                     NLSQTLRAYCPTVYSAFGFKSRHINMTQRVSSHGRSTDAALEELQRRDLAKYWPVLSD
                     IAAEFRRTKPRGLYSGVSGPAFEVLRDMHQGQLWTTNVIVVDEAGTLSVHILTAVVFC
                     YWFFNAWLRTPLYRRGRIPCIVCVGSPTQTDAFQSSFSHETQVNKIRECDNILTFLVG
                     NPRAATYVDVARNWALFINNKRCTDVQFGHLMKTLEYGLELSPDILAYVDRFVVPRAA
                     IMDPAQYVGWTRLFLSHAEVKTFLTTLHATLKTAGQGRAARGTGGDGGGVTMFTCPVE
                     CEVFLDPLAQYKTLVGLPGLTAHTWLQKNYARLGNYSQFADQDMVPVGTEQDEERVKV
                     TYNVTYVKHSSVSVNCKTKKSICGYTGTFGDFMDTLEADSFVEAHGHEQPEYVYSFLA
                     RLIYGGIYAFSHGGHSLCENGEYVAELGAVPLPGRTWDPEVTAGMELGELPLEVAWDG
                     ERSPAAVFYARVLAPPAANSAPLCSLLNIYNDLRAYFRQCLDVAVRYGGREFRDLPFC
                     TFTNNMLIRDNIEFTSDEPLLHGLLDYASTTENYTLLGYTHLNVFFGIRGKQQPQDAG
                     SSRMPRLMVKDEAGFVCCLEHNTNKLYETIEDKSLNLCSIRDYGISSKLAMTIAKAQG
                     LSLNKVAICFGSHRNIKPGHVYVALSRARHSNCVVMDRNPLSEMITGEGNPASGYIVD
                     ALKNSRALLVY"
     misc_feature    complement(111830)
                     /note="polyA signal: AATAAA"
     promoter        112471
                     /note="TATA: TATATAT"
     promoter        complement(112476)
                     /note="TATA: TATATAA"
     misc_feature    112620
                     /note="BAM: Bam H1 K/B"
     promoter        113876
                     /note="TATA: TATTTAT before BBRF1"
     promoter        complement(113885)
                     /note="TATA: CATAAAT"
     CDS             114204..116045
                     /note="BBRF1 late reading frame, homologous to RF 54 VZV;
                     NCBI gi: 59125"
                     /codon_start=1
                     /translation="MFNMNVDESASGALGSSAIPVHPTPASVRLFEILQGKYAYVQGQ
                     TIYANLRNPGVFSRQVFTHLFKRAISHCTYDDVLHDWNKFEACIQKRWPSDDSCASRF
                     RESTFESWSTTMKLTVRDLLTTNIYRVLHSRSVLSYERYVDWICATGMVPAVKKPITQ
                     ELHSKIKSLRDRCVCRELGHERTIRSIGTELYEATKEIIESLNSTFIPQFTEVTIEYL
                     PRSDEYVAYYCGRRIRLHVLFPPAIFAGTVTFDSPVQRLYQNIFMCYRTLEHAKICQL
                     LNTAPLKAIVGHGGRDMYKDILAHLEQNSQRKDPKKELLNLLVKLSENKTISGVTDVV
                     EEFITDASNNLVDRNRLFGQPGETAAQGLKKKVSNTVVKCLTDQINEQFDQINGLEKE
                     RELYLKKIRSMESQLQASLGPGGNNPAASAPAAVAAEAASVDILTGSTASAIEKLFNS
                     PSASLGARVSGHNESILNSFVSQYIPPSREMTKDLTELWESELFNTFKLTPVVDNQGQ
                     RLYVRYSSDTISILLGPFTYLVAELSPVELVTDVYATLGIVEIIDELYRSSRLAIYIE
                     DLGRKYCPASATGGDHGIRQAPSARGDTEPDHAKSKPARDPPPGAGS"
     CDS             115843..116784
                     /note="BBRF2 late reading frame, homologous to RF 53 VZV;
                     NCBI gi: 583894"
                     /codon_start=1
                     /translation="XSWRSSTSSTGAVAWPSTSRTSVENTAPRARPGEIMASGKHHQP
                     GGTRSLTMQKVSLRVTPRLVLEVNRHNAICVATNVPEFYNARGDLNIRDLRAHVKARM
                     ISSQFCGYVLVSLLDSEDQVDHLNIFPHVFSERMILYKPNNVNLMEMCALLSMIENAK
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                     SPSIGLCREVLGRLTLLHSKCNNLDSLFLYNGARTLLSTLVKYHDLEEGAATPGPWNE
                     GLSLFKLHKELKRAPSEARDLMQSLFLTSGKMGCLARSPKDYCADLNKEEDANSGFTF
                     NLFYQDSLLTKHFQCQTVLQTLRRKCLGSDTVSKIIP"
     promoter        complement(116683)
                     /note="TATA: GATAAAA"
     misc_feature    complement(116696)
                     /note="polyA signal: AATAAA"
     CDS             complement(116781..117386)
                     /note="BBLF3 early reading frame, spliced to BBLF2. BBLF3
                     contains a consensus nucleotide binding site;  NCBI gi:
                     583895"
                     /codon_start=1
                     /translation="XFLQGVKDSEDASRLDRDVMGGEATVARRHIRVKARRGPGCLLM
                     AIFQGDLYVGGCREHSGPFLVWHEAFSWTLDQLAARPEADKAPPSHDHLLTLVRDLTR
                     RLAPGRRRNRFWALPRAWLQRLRRAGLRLSGSHVCLLDKDGARPAPCQTATEHGLSPT
                     AYFREIMAFLLDVISALHPGYTIPMEITRETDLLMTVLSLF"
     misc_feature    116785
                     /note="polyA signal: AATAAA"
     intron          complement(117386..117515)
                     /note="intron spliced out in RNA linking BBLF2 and BBLF3"
     CDS             complement(117515..119080)
                     /note="BBLF2 early reading frame, spliced to BBLF3;  NCBI
                     gi: 583896"
                     /codon_start=1
                     /translation="XDVLKGPVLLRSQTMMETPAESVRARVSSVTFYNVTQTAGRWWA
                     IWVVGIVPIKREDVETLIVVQACQPPLGGSLEPPVVNAPSTTELNFLRWERELRRSGG
                     LIAMLADAAEKDLFDLSFRTRDRRLLSAARVEDEQGLIFQPLFPAQVVCQSCSGDDGR
                     DQQPPPVDGFGSEMEGEQTCPHAQRHSESPGQLDVYIRTPRGDVFTYSTETPDDPSPV
                     PFRDILRPVTYEVDLVSSDGATGRGGDARRHRVSLKILEPAGGFESWLVNSWSMAGGG
                     LYAFLRSIYASCYANHRGTKPIFYLLDPELCPGGSDFQPYVPGFPFLPIHYVGRARPA
                     FWHRAPHSEGLLLLDLNLGVSGTPLADALLGLDARSGQRRGSLLLQQIWPPTRKEINP
                     RHVCTREGGEGGGEDETTVVGRAEATAILEADATWWLYELARCHLSARGAPVGTPDGG
                     GQARDAQTWLRALHRYGTSDTRRALGGLYTAVTRVLLHAAADLGLTWAYADEFILGFV
                     APTSAHPSEEPLAQ"
     promoter        118981
                     /note="TATA: TATAAAA BBR1 late promoter before BBRF3"
     promoter        119067
                     /note="TATA: TTTAAAA BBR2 late promoter ?"
     promoter        119098
                     /note="TATA: TATTTAA BBR3 late promoter before BBRF3"
     misc_feature    119108
                     /note="DONOR: AAGGTGAAT possible donor"
     CDS             119137..120354
                     /note="BBRF3 late reading frame;  NCBI gi: 59130"
                     /codon_start=1
                     /translation="MKSSKNDTFVYRTWVKTLVVYFVMFVMSAVVPITAMFPNLGYPC
                     YFNALVDYGALNLTNYNLAHHLTPTLYLEPPEMFVYITLVFIADCVAFIYYACGEVAL
                     IKARKKVSGLTDLSAWVSAVGSPTVLFLAILKLWSIQVFIQVLSYKHVFLSAFVYFLH
                     FLASVLHACACVTRFSPVWVVKAQDNSIPQDTFLWWVVFYLKPVVTNLYLGCLALETL
                     VFSLSVFLALGNSFYFMVGDMVLGAVNLFLILPIFWYILTEVWLASFLRHNFGFYCGM
                     FIASIILILPLVRYEAVFVSAKLHTTVAINVAIIPILCSVAMLIRICRIFKSMRQGTD
                     YVPVSETVELELESEPRPRPSRTPSPGRNRRRSSTSSSSSRSTRRQRPVSTQALVSSV
                     LPMTTDSEEEIFP"
     misc_feature    120260
                     /note="ACCEPT: ATCTTCCTCCAGGT possible acceptor"
     misc_feature    120358
                     /note="polyA signal: AATAAA"
     CDS             complement(120747..120974)
                     /note="BBLF1 late reading frame, possibly homologous to RF
                     49 VZV;  NCBI gi: 59131"
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                    /codon_start=1
                    /translation="MGALWSLCRRRVNSIGDVDGGIINLYNDYEEFNLETTKLIAAEE
                    GRACGETNEGLEYDEDSENDELLFLPNKKPN"
     misc_feature   complement(120764)
                    /note="polyA signal: AATAAA, 3' end of 0.6kb late, 1.6kb
                    early, 3.0kb early RNAs"
     CDS            complement(120929..122341)
                    /note="BGLF5 early reading frame, homologous to RF 48 VZV
                    and alkaline exonuclease of HSV;  NCBI gi: 59132"
                    /codon_start=1
                    /translation="MADVDELEDPMEEMTSYTFARFLRSPETEAFVRNLDRPPQMPAM
                    RFVYLYCLCKQIQEFSGETGFCDFVSSLVQENDSKDGPSLKSIYWGLQEATDEQRTVL
                    CSYVESMTRGQSENLMWDILRNGIISSSKLLSTIKNGPTKVFEPAPISTNHYFGGPVA
                    FGLRCEDTVKDIVCKLICGDASANRQFGFMISPTDGIFGVSLDLCVNVESQGDFILFT
                    DRSCIYEIKCRFKYLFSKSEFDPIYPSYTALYKRPCKRSFIRFINSIARPTVEYVPDG
                    RLPSEGDYLLTQDEAWNLKDVRKRKLGPGHDLVADSLAANRGVESMLYVMTDPSENAG
                    RIGIKDRVPVNIFINPRHNYFYQVLLQYKIVGDYVRHSGGGKPGRDCSPRVNIVTAFF
                    RKRSPLDPATCTLGSDLLLDASVEIPVAVLVTPVVLPDSVIRKTLSTAAGSWKAYADN
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     promoter       complement(121331)
                    /note="TATA: TATTAAA BBL1 late promoter before BBLF1"
     promoter       121669
                    /note="TATA: CATAAAT"
     promoter       121697
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     misc_feature   122313
                    /note="BAM: Bam H1 B/G"
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                    /note="BGLF4 early reading frame, homologous to RF 47 VZV;
                     NCBI gi: 583897"
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                    PITCEYLLGRGSYGAVYAHADNATVKLYDSVTELYHELMVCDMIQIGKATAEDGQDKA
                    LVDYLSACTSCHALFMPQFRCSLQDYGHWHDGSIEPLVRGFQGLKDAVYFLNRHCGLF
                    HSDISPSNILVDFTDTMWGMGRLVLTDYGTASLHDRNKMLDVRLKSSKGRQLYRLYCQ
                    REPFSIAKDTYKPLCLLSKCYILRGAGHIPDPSACGPVGAQTALRLDLQSLGYSLLYG
                    IMHLADSTHKIPYPNPDMGFDRSDPLYFLQFAAPKVVLLEVLSQMWNLNLDMGLTSCG
                    ESPCVDVTAEHMSQFLQWCRSLKKRFKESYFFNCRPRFEHPHLPGLVAELLADDFFGP
                    DGRRG"
     misc_feature   complement(123506)
                    /note="DONOR: AAGGTGACT possible donor"
     CDS            complement(123941..124939)
                    /note="BGLF3 reading frame;  NCBI gi: 59135"
                    /codon_start=1
                    /translation="MFNAVKADMPDDPMLARRYGQCLELALEACQDTPEQFKLVETPL
                    KSFLLVSNILPQDNRPWHEARSSGRVAEDDYDFSSLALELLPLNPRLPEEWQFGGQGW
                    SSRMEPSQPEMGMGLCFEVFDGDLMRIALAWNKDEVIGQALQILAHSQTWTSLVPEDP
                    LPWMWALFYGPRSHCEERHCVYAAARGKRGPILLPTAVYTPCANIEAFLAHLTRCVYA
                    LYLDVRDWKGEDIAPPFDVSRLNKMAKQLCLLPQEPFCITRVCLLCLLHKQNLNAQYK
                    RPVDTYDPCLILTGEAERYMVDAVGNYREASTGTTVLYPTYDLGSIVADMVTYEDE"
     promoter       complement(124117)
                    /note="TATA: TATAAAA"
     misc_feature   complement(124219)
                    /note="polyA signal: AATAAA"
     CDS            124938..125915
                    /note="BGRF1 reading frame, homologous to RF 45 VZV and
                    spliced HSV gene (Costa et al, 1985). Spliced to BDRF1.
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                    Northern blots in BGRF1 detect 2.7, 2.6, 2.1kb late and
                    1.9kb early RNAs. 2.6, 2.1kb RNAs very weak.  NCBI gi:
                    59134"
                    /codon_start=1
                    /translation="MLYASQRGRLTENLRNALQQDSTTQGCLGAETPSIMYTGAKSDR
                    WAHPLVGTIHASNLYCPMLRAYCRHYGPRPVFVASDESLPMFGASPALHTPVQVQMCL
                    LPELRDTLQRLLPPPNLEDSEALTEFKTSVSSARAILEDPNFLEMREFVTSLASFLSG
                    QYKHKPARLEAFQKQVVLHSFYFLISIKSLEITDTMFDIFQSAFGLEEMTLEKLHIFK
                    QKASVFLIPRRHGKTWIVVAIISLILSNLSNVQIGYVAHQKHVASAVFTEIIDTLTKS
                    FDSKRVEVNKETSTITFRHSGKISSTVMCATCFNKNVRPDVSVLGNCRA"
     promoter       complement(125113)
                    /note="TATA: TATAAAT before BGLF3"
     misc_feature   complement(125484)
                    /note="polyA signal: AATAAA, 3' end of 1.6kb late, 1.8kb
                    late, 3.0kb late and 3.7kb early RNAs"
     CDS            complement(125863..126873)
                    /note="BGLF2 late reading frame, poor homology to RF 44
                    VZV;  NCBI gi: 59136"
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                    /translation="MASAANSSREQLRKFLNKECLWVLSDASTPQMKVYTATTAVSAV
                    YVPQIAGPPKTYMNVTLIVLKPKKKPTYVTVYINGTLATVARPEVLFTKAVQGPHSLT
                    LMYFGVFSDAVGEAVPVEIRGNPVVTCTDLTTAHVFTTSTAVKTVEELQDITPSEIIP
                    LGRGGAWYAEGALYMFFVNMDMLMCCPNMPTFPSLTHFINLLTRCDNGECVTCYGAGA
                    HVNILRGWTEDDSPGTSGTCPCLLPCTALNNDYVPITGHRALLGLMFKPEDAPFVVGL
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                    SY"
     promoter       126277
                    /note="TATA: GATAAAA"
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                    /note="BGLF1 late reading frame;  NCBI gi: 59137"
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                    /translation="MDVHIDNQVLSGLGTPLLVHLFVPDTVMAELCPNRVPNCEGAWC
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                    IEHMPVAAAQVEHPKTYDLKQILLEITQEENRGEQRLGHAGSPALCLGLRLRAGAETK
                    AAAETSVSKHHPALENPSNIRGSAGGEGGGGRAGTGGTVGVGSGALSRVPVSFSKTRR
                    AIRESRALVRGIAHIFSPHALYVVTYPELSAQGRLHRMTAVTHASPATDLAEVSILGA
                    PEREFRFLISVALRISASFREKLAMQAWTAQQEIPVVIPTSYSRIYKNSDLIREAFFT
                    VQTRVSWESCWVKATISNAPKTPDACLWIDSHPLYEEGASAWGKVIDSRPPGGLVGAA
                    SQLVALGTDGHCVHLATTSDGQAFLVLPGGFVIKGQLALTPEERGYILARHGIRREQ"
     promoter       complement(126929)
                    /note="TATA: TATTAAA EEL8 late promoter before BGLF2,
                    gives 1.6kb late RNA"
     promoter       complement(127237)
                    /note="TATA: TATAAAA, potential promoter for 1.8kb late
                    RNA"
     misc_feature   128029
                    /note="polyA signal: AATAAA"
     CDS            complement(128344..129021)
                    /note="BDLF4 early reading frame;  NCBI gi: 59138"
                    /codon_start=1
                    /translation="MSDQGRLSLPRGEGGTDEPNPRHLCSYSKLEFHLPLPESMASVF
                    ACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPWTEIRQDTQDQRD
                    KWEPEQVQGLVKTVVNHLYHYFLNENVISGVSEALFDQEGALRPHIPALVSFVFPCCL
                    MLFRGASSEKVVDVVLSLYIHVIISIYSQKTVYGALLFKSTRNKRYDAVAKRMRELWM
                    STLTTKC"
     promoter       complement(128432)
                    /note="TATA: TATTTAA before BGLF1, potential promoter for
                    3.0kb late RNA"
     misc_feature   128848
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                     /note="BAM: Bam H1 G/D"
     promoter        complement(129054)
                     /note="TATA: TATTTGC before BDLF4, potential promoter for
                     3.7kb early RNA"
     CDS             129188..130351
                     /note="BDRF1 reading frame, homologous to RF 42 VZV and
                     spliced gene in HSV (Costa et al, 1985). Spliced from
                     BGRF1. Northern blots in BDRF1 detect 2.7, 2.6 kb late and
                     1.9kb early RNAs. Possibly also 1.8kb early RNA.  NCBI gi:
                     583898"
                     /codon_start=1
                     /translation="XLASYPVFQSIRGQTFHLLFVDEANFIKKEALPAILGFMLQKDA
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                     IPSYITMDSNIRATTNLFLDGAFSTELMGDTSSLSQGSLSRTVRDDAINQLELCRVDT
                     LNPRVAGRLASSLYVYVDPAYTNNTSASGTGIAAVTHDRADPNRVIVLGLEHFFLKDL
                     TGDAALQIATCVVALVSSIVTLHPHLEEVKVAVEGNSSQDSAVAIASIIGESCPLPCA
                     FVHTKDKTSSLQWPMYLLTNEKSKAFERLIYAVNTASLSASQVTVSNTIQLSFDPVLY
                     LISQIRAIKPIPLRDGTYTYTGKQRNLSDDVLVALVMAHFLATTQKHTFKKVH"
     promoter        129374
                     /note="TATA: TATAAGC"
     promoter        complement(129377)
                     /note="TATA: TATAAAG"
     misc_feature    129413
                     /note="DONOR: GTGGTAAGT possible donor"
     misc_feature    130347
                     /note="polyA signal: ATTAAA"
     misc_feature    complement(130359)
                     /note="polyA signal: AATAAA, 3' end of 0.9kb late RNA,
                     2.3kb late RNA and 3.2kb late RNA"
     CDS             complement(130362..131066)
                     /note="BDLF3 late reading frame 9xNXT/S;  NCBI gi: 59140"
                     /codon_start=1
                     /translation="MAHARDKAGAVMAMILICETSLIWTSSGSSTASAGNVTGTTAVT
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                     TTKVTAQNITATEAGTGTSTGVTSNVTTRSSSTTSATTRITNATTLAPTLSSKGTSNA
                     TKTTAELPTVPDERQPSLSYGLPLWTLVFVGLTFLMLILIFAAGLMMSAKNKPLDEAL
                     LTNAVTRDPSLYKGLV"
     promoter        complement(131104)
                     /note="TATA: TATAAAA EEL4 late promoter before BDLF3,
                     gives 0.9kb late RNA"
     CDS             complement(131127..132389)
                     /note="BDLF2 late reading frame;  NCBI gi: 59141"
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                     /translation="MVDEQVAVEHGTVSHTISREEDGVVHERRVLASGERVEVFYKAP
                     APRPREGRASTFHDFTVPAAAAVPGPEPEPEPHPPMPIHANGGGETKTNTQDQNQNQT
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                     GERMRFKEDVYDGEAETLAEPPRCFMLSFVFIYYCCYLAFLALLAFGFNPLFLPSFMP
                     VGAKVLRGKGRDFGVPLSYGCPTNPFCKVYTLIPAVVINNVTYYPNNTDSHGGHGGFE
                     AAALHVAALFESGCPNLQAVTNRNRTFNVTRASGRVERRLVQDMQRVLASAVVVMHHH
                     CHYETYYVFDGVGPEFGTIPTPCFKDVLAFRPSLVTNCTAPLKTSVKGPNWSGAAGGM
                     KRKQCRVDRLTDRSFPAYLEEVMYVMVQ"
     promoter        132266
                     /note="TATA: TATAAAA"
     CDS             complement(132400..133305)
                     /note="BDLF1 late reading frame, poor homology to RF 41
                     VZV;  NCBI gi: 59142"
                     /codon_start=1
                     /translation="MDLKVVVSLSSRLYTDEIAKMQQRIGCILPLASTHGTQNVQGLG
                     LGQVYSLETVPDYVSMYNYLSDCTLAVLDEVSVDSLILTKIVPGQTYAIKNKYQPFFQ
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                     MQAPGNADMLDVHMHLGSVSYLGHHYELALPEVPGPLGLALLDNLSLYFCIMVTLLPR
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                     LFNLGPRLATAAYSQETLTATCWLR"
     promoter        complement(132476)
                     /note="TATA: TATTTAA before BDLF2, likely promoter for
                     2.3kb late RNA"
     misc_feature    complement(133312)
                     /note="polyA signal: AATAAA, 3' end of 4.5kb late RNA"
     CDS             complement(133321..137466)
                     /note="BcLF1 late reading frame, homologous to RF 40 VZV
                     and major capsid protein of HSV;  NCBI gi: 59143"
                     /codon_start=1
                     /translation="MASNEGVENRPFPYLTVDADLLSNLRQSAAEGLFHSFDLLVGKD
                     AREAGIKFEVLLGVYTNAIQYVRFLETALAVSCVNTEFKDLSRMTDGKIQFRISVPTI
                     AHGDGRRPSKQRTFIVVKNCHKHHISTEMELSMLDLEILHSIPETPVEYAEYVGAVKT
                     VASALQFGVDALERGLINTVLSVKLRHAPPMFILQTLADPTFTERGFSKTVKSDLIAM
                     FKRHLLEHSFFLDRAENMGSGFSQYVRSRLSEMVAAVSGESVLKGVSTYTTAKGGEPV
                     GGVFIVTDNVLRQLLTFLGEEADNQIMGPSSYASFVVRGENLVTAVSYGRVMRTFEHF
                     MARIVDSPEKAGSTKSDLPAVAAGVEDQPRVPISAAVIKLGNHAVAVESLQKMYNDTQ
                     SPYPLNRRMQYSYYFPVGLFMPNPKYTTSAAIKMLDNPTQQLPVEAWIVNKNNLLLAF
                     NLQNALKVLCHPRLHTPAHTLNSLNAAPAPRDRRETYSLQHRRPNHMNVLVIVDEFYD
                     NKYAAPVTDIALKCGLPTEDFLHPSNYDLLRLELHPLYDIYIGRDAGERARHRAVHRL
                     MVGNLPTPLAPAAFQEARGQQFETATSLAHVVDQAVIETVQDTAYDTAYPAFFYVVEA
                     MIHGFEEKFVMNVPLVSLCINTYWERSGRLAFVNSFSMIKFICRHLGNNAISKEAYSM
                     YRKIYGELIALEQALMRLAGSDVVGDESVGQYVCALLDPNLLPPVAYTDIFTHLLTVS
                     DRAPQIIIGNEVYADTLAAPQFIERVGNMDEMAAQFVALYGYRVNGDHDHDFRLHLGP
                     YVDEGHADVLEKIFYYVFLPTCTNAHMCGLGVDFQHVAQTLAYNGPAFSHHFTRDEDI
                     LDNLENGTLRDLLEISDLRPTVGMIRDLSASFMTCPTFTRAVRVSVDNDVTQQLAPNP
                     ADKRTEQTVLVNGLVAFAFSERTRAVTQCLFHAIPFHMFYGDPRVAATMHQDVATFVM
                     RNPQQRAVEAFNRPEQLFAEYREWHRSPMGKYAAECLPSLVSISGMTAMHIKMSPMAY
                     IAQAKLKIHPGVAMTVVRTDEILSENILFSSRASTSMFIGTPNVSRREARVDAVTFEV
                     HHEMASIDTGLSYSSTMTPARVAAITTDMGIHTQDFFSVFPAEAFGNQQVNDYIKAKV
                     GAQRNGTLLRDPRTYLAGMTNVNGAPGLCHGQQATCEIIVTPVTADVAYFQKSNSPRG
                     RAACVVSCENYNQEVAEGLIYDHSRPDAAYEYRSTVNPWASQLGSLGDIMYNSSYRQT
                     AVPGLYSPCRAFFNKEELLRNNRGLYNMVNEYSQRLGGHPATSNTEVQFVVIAGTDVF
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     misc_feature    complement(133332)
                     /note="DONOR: AAGGTGGTT possible donor"
     promoter        complement(133352)
                     /note="TATA: TATTAAA before BDLF1"
     promoter        complement(133386)
                     /note="TATA: TATATAA"
     misc_feature    135178
                     /note="polyA signal: AATAAA"
     promoter        135394
                     /note="TATA: TATAAGT"
     misc_feature    136624
                     /note="polyA signal: AATAAA"
     misc_feature    136868
                     /note="BAM: Bam H1 D/c"
     promoter        complement(137710)
                     /note="TATA: TATTAAA EHL1 promoter before BcLF1, gives
                     4.5kb late RNA"
     promoter        137857
                     /note="TATA: CATAAAC"
     CDS             137862..139718
                     /note="BcRF1 reading frame;  NCBI gi: 583899"
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                     /translation="XRAQCFALSSATCLITNLSAASSSSAAWSRVGFLGTCKRNSAKM
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                    LAHLNQVTRIPPCPPFSGREARLKFHFFSWSTFMLSWPNNATLREIRTRAATNLTHHP
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                    GGRPASFQFPSSPTGSLLRCIVAASLLPEVSVGHQELSPLRSRSQGGQTDVRSGPDPA
                    RRLVALLRREDGAPKDPPLGPFGHPRGPGPAKSEDEESERRDAPPPPLDSSFQASRLV
                    PVGPGFRLLVFNTNRVINTKLVCSEPLVKMRVCNVPRLINNFVARKYVVKETAFTVSL
                    FFTDGVGANLAINVNISGTYLSFLLAMTSLRCFLPVEAIYPAAVSNWNSTLDLHGLEN
                    QSLVRENRSGVFWTTNFPSVVSCRDGLNVSWFKAATATISRVHGQTLEQHLIREITPI
                    VTHREAKISRIKNRLFTLLELRNRSQIQVLHKRFLEGLLDCASLLRLDPSCINRIASE
                    GLFDFSKRSIAHSKNRHECALLGHRHSANVTKLVVNERKTRLDILGRNANFLTRCKHQ
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     misc_feature   138019
                    /note="BAM: Bam H1 c/b"
     misc_feature   139352
                    /note="BAM: Bam H1 b/T"
     CDS            139642..140919
                    /note="BTRF1 reading frame. Northern blots detect 0.95
                    late and 3.8kb early RNA;  NCBI gi: 583900"
                    /codon_start=1
                    /translation="XERLPFSWPTCAKRQPPSTAVMLKCKQPGARFIHGAVHLPSGQI
                    VFHTIHSPTLASALGLPGENVPIPALFRASGLNVRESLPMTNMRAPIISLARLILAPN
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                    ASEHPAFSMVESVKRVRVDEGANTRRTIRDILEIPVTVLSSLQLSPTKSILKKAPEPP
                    PPEPQATFDATPYARIFYDIGRQVPKLGNAPAAQVSNVLIANRSHNSLRLVPNPDLLP
                    LQHLYLKHVVLKSLNLENIVQDFEAIFTSPSDTISEAETKAFEKLVEQAKNTVENIVF
                    CLNSICSTSTLPDVVPDVNNPNISLALEKYFLMFPPSGTIMRNVRFATPIVRLLCQGA
                    ELGTMAQFLGKYIKVKKETGMYTLVKLYYLLRI"
     misc_feature   complement(140902)
                    /note="polyA signal: AATAAA, 3' end of 2.5kb late RNA"
     CDS            complement(140916..143036)
                    /note="BXLF2 late reading frame, encodes gp85; homologous
                    to RF 37 VZV and glycoprotein H of HSV (gpIII of VZV);
                    NCBI gi: 59146"
                    /codon_start=1
                    /translation="MQLLCVFCLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTELM
                    AKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGTLGIALAEPVDIPAVSEGSMQV
                    DASKVHPGVISGLNSPACMLSAPLEKQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVAL
                    SINGDKFQYTGAMTSKFLMGTYKRVTEKGDEHVLSLVFGKTKDLPDLRGPFSYPSLTS
                    AQSGDYSLVIVTTFVHYANFHNYFVPNLKDMFSRAVTMTAASYARYVLQKLVLLEMKG
                    GCREPELDTETLTTMFEVSVAFFKVGHAVGETGNGCVDLRWLAKSFFELTVLKDIIGI
                    CYGATVKGMQSYGLERLAAMLMATVKMEELGHLTTEKQEYALRLATVGYPKAGVYSGL
                    IGGATSVLLSAYNRHPLFQPLHTVMRETLFIGSHVVLRELRLNVTTQGPNLALYQLLS
                    TALCSALEIGEVLRGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAAVSN
                    AVDGFLGRLSLEREDRDAWHLPAYKCVDRLDKVLMIIPLINVTFIISSDREVRGSALY
                    EASTTYLSSSLFLSPVIMNKCSQGAVAGEPRQIPKIQNFTRTQKSCIFCGFALLSYDE
                    KEGLETTTYITSQEVQNSILSSNYFDFDNLHVHYLLLTTNGTVMEIAGLYEERAHVVL
                    AIILYFIAFALGIFLVHKIVMFFL"
     misc_feature   140970
                    /note="polyA signal: AATAAA"
     misc_feature   complement(141286)
                    /note="polyA signal: AATAAA"
     promoter       142589
                    /note="TATA: GATAAAA"
     misc_feature   142740
                    /note="BAM: Bam H1 T/X"
     CDS            complement(143038..144861)
                    /note="BXLF1 early reading frame, thymidine kinase
                    (Littler et al, 1986). Weak homology to RF 36 VZV and HSV
                    thymidine kinase. 4.0kb early RNA presumably encodes the
                    TK. Also a 2.2kb late RNA here.  NCBI gi: 59148"
                    /codon_start=1
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                    /translation="MAGFPGKEAGPPGGWRKCQEDESPENERHENFYAEIDDFAPSVL
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                    SRSFMYQKGFEEGLAGLGLDDKSDCESEDESNFRRPSSHSALKQKNGGKGKPSGLFEH
                    LAAHGREFSKLSKHAAQLKRLSGSVMNVLNLDDAQDTRQAKAQRKESMRVPIVTHLTN
                    HVPVIKPACSLFLEGAPGVGKTTMLNHLKAVFGDLTIVVPEPMRYWTHVYENAIKAMH
                    KNVTRARHGREDTSAEVLACQMKFTTPFRVLASRKRSLLVTESGARSVAPLDCWILHD
                    RHLLSASVVFPLMLLRSQLLSYSDFIQVLATFTADPGDTIVWMKLNVEENMRRLKKRG
                    RKHESGLDAGYLKSVNDAYHAVYCAWLLTQYFAPEDIVKVCAGLTTITTVCHQSHTPI
                    IRSGVAEKLYKNSIFSVLKEVIQPFRADAVLLEVCLAFTRTLAYLQFVLVDLSEFQDD
                    LPGCWTEIYMQALKNPAIRSQFFDWAGLSKVISDFERGNRD"
     promoter       complement(143310)
                    /note="TATA: TATAAGA ECL2 late promoter before BXLF2,
                    gives 2.5kb late RNA"
     misc_feature   143608
                    /note="polyA signal: AATAAA"
     misc_feature   144791
                    /note="ACCEPT: TCTTTCGTTTTCAGG poss. acceptor before
                    BXRF1"
     CDS            144860..145606
                    /note="BXRF1 late reading frame, homologous to RF 35 VZV.
                    Basic (core?) protein.  NCBI gi: 59147"
                    /codon_start=1
                    /translation="MDPTRGLCALSTHDLAKFHSLPPARKAAGKRAHLRCYSKLLSLK
                    SWEQLASFLSLPPGPTFTDFRLFFEVTLGRRIADCVVVALQPYPRCYIVEFKTAMSNT
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                    EFPALGQKTLPTSTTGLLNLLSRWQDGALRARLDRPRPTAQGHRPRTHVGPKPSQLTA
                    RVPRSARAGRAGGRKGQVGAVGQVCPGAQK"
     misc_feature   144862
                    /note="BAM: Bam H1 X/V"
     misc_feature   144945
                    /note="DONOR: CAGGTAAGC possible donor at 3' BXRF1"
     promoter       complement(145135)
                    /note="TATA: TATAACA before BXLF1"
     promoter       145302
                    /note="TATA: TATTTAA before BVRF1, potential promoter for
                    1.9kb early RNA"
     CDS            145416..147128
                    /note="BVRF1 early reading frame, homologous to RF 34 VZV;
                     NCBI gi: 59149"
                    /codon_start=1
                    /translation="MALSGHVLIDPARLPRDTGPELMWAPSLRNSLRVSPEALELAER
                    EAERARSERWDRCAQVLKNRLLRVELDGIMRDHLARAEEIRQDLDAVVAFSDGLESMQ
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                    GNINQWVPSFGPWYRTMSANAMQRRVFPKQLRGNLNFTNSVSLKLMTEVVAVLEGTTQ
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                    KAKSPGGNFMILTSGNKEARQSIAPLNRQAAYPPGTFADNKIYNLFVGAGLLPTTAAL
                    NVPGAAGRDRDLVYRIANQIFGEDVPPFSSHQWNLRVGLAALEALMLVYTLCETANLA
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                    AMLAARTQLRLAFEDGVGVALGRPSPMLAAREILERQFSASDDYDRLYFLTLGYLASP
                    VAPS"
     misc_feature   complement(146926)
                    /note="polyA signal: AATAAA"
     misc_feature   147167
                    /note="DONOR: AAGGTAAAT possible donor"
     misc_feature   147170
                    /note="polyA signal: AATAAA, 3' end of 2.4kb late and
                    1.9kb early RNAs"
     promoter       147721
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                   /note="TATA: TATTTAT before BVRF2, potential promoter for
                   2.1kb early RNA"
     CDS           147927..149744
                   /note="BVRF2 early reading frame, N-terminus homologous to
                   RF 33 VZV;  NCBI gi: 59150"
                   /codon_start=1
                   /translation="MVQAPSVYVCGFVERPDAPPKDACLHLDPLTVKSQLPLKKPLPL
                   TVEHLPDAPVGSVFGLYQSRAGLFSAASITSGDFLSLLDSIYHDCDIAQSQRLPLPRE
                   PKVEALHAWLPSLSLASLHPDIPQTTADGGKLSFFDHVSICALGRRRGTTAVYGTDLA
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                   AVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPPPV
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     misc_feature  148007
                   /note="BAM: Bam H1 V/d"
     promoter      148620
                   /note="TATA: TATTTAA ECR1 late promoter before BdRF1,
                   gives 1.2kb late RNA"
     CDS           148707..149744
                   /note="BdRF1 reading frame; this is the C terminus of
                   BVRF2;  NCBI gi: 59151"
                   /codon_start=1
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     misc_feature  149115
                   /note="BAM: Bam H1 d/I"
     misc_feature  149727
                   /note="polyA signal: AATAAA, 3' end of 2.1kb early and
                   1.2kb late RNAs"
     misc_feature  complement(149758)
                   /note="polyA signal: AATAAA, 3' end of 1.0kb late, 1.5kb
                   late and 1.8kb late RNAs"
     CDS           complement(149779..150525)
                   /note="BILF2 late reading frame 11xNXT/S;  NCBI gi: 59152"
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                   /translation="MTHLVLLLCCCVGSVCAFFSDLVKFENVTAHAGARVNLTCSVPS
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                   IAPTTLVSHTTSTSHRPHRRPVSKRPTHKPVTLGPFPIDPWRPKTTWVHWALLLITCA
                   VVAPVLLIIIISCLGWLAGWGRRRKGWIPL"
     promoter      complement(150571)
                   /note="TATA: TATTTAG before BILF2. Potential promoter for
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     repeat_region 151236..151618
                   /note="repetitive sequence 3X"
     misc_feature  151767
                   /note="polyA signal: AATAAA"
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     misc_feature  152012..152013
                   /note="DEL: B95-8 deletion with respect to Raji"
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     promoter      152230
                   /note="TATA: CATAAAA"
     misc_feature  153259
                   /note="polyA signal: AATAAA"
     misc_feature  153637
                   /note="HPN: 22bp 2-fold symmetric"
     misc_feature  complement(153690)
                   /note="DONOR: AAAGTGAGG possible donor"
     CDS           complement(153699..156746)
                   /note="BALF5 DNA polymerase (early), homologous to many
                   DNA polymerases, CMV HFLF2 and RF 28 VZV. 4.5kb early RNA
                   apparently encodes BALF5, RNA ends unknown.  NCBI gi:
                   59154"
                   /codon_start=1
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     misc_feature  complement(156707)
                   /note="polyA signal: AATAAA; 3' end of 2.5kb late (gB) RNA
                   and 1.8kb late RNA"
     CDS           complement(156749..159322)
                   /note="BALF4 late reading frame 9xNXT/S homologous to HSV1
                   glycoprotein B (Pellet et al, 1985), CMV HFLF1 and RF 31
                   VZV (gpII);  NCBI gi: 59155"
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     promoter        158204
                     /note="TATA: TATAAAA"
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                     HLHALTHSLYTFITGPLAEESGLFPPPSNVALARCCDAAGTLPHQKAFLTSLIWPGIE
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     promoter        complement(159370)
                     /note="TATA: TATTTAA ECL1 late promoter before BALF4,
                     gives 2.5kb late RNA"
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                     /note="polyA signal: AATAAA"
     misc_feature    160990
                     /note="polyA signal: ATTAAA"
     misc_feature    complement(161013)
                     /note="polyA signal: AATAAA, presumed end of 3.9kb early
                     RNA"
     CDS             complement(161384..164770)
                     /note="BALF2 early reading frame, homologous to RF 29 VZV
                     and major DNA binding protein HSV. 3.9kb early RNA;  NCBI
                     gi: 59157"
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                     TGTNGPGNYAVEHLVYAASFSPNLLARYAYYLQFCQGQKSSLTPVPETGSYVAGAAAS
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                     GEPTCDLPDLDAALQGRVYGRRLPVRMSKVLMLCPRNIKIKNRVVFTGENAALQNSFI
                     KSTTRRENYIINGPYMKFLNTYHKTLFPDTKLSSLYLWHNFSRRRSVPVPSGASAEEY
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                     RTQSVPARDYPHVLGTRAVESAAAYAEATSSLTATTVVCAATDCLSQVCKARPVVTLP
                     VTINKYTGVNGNNQIFQAGNLGYFMGRGVDRNLLQAPGAGLRKQAGGSSMRKKFVFAT
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                     RDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAARDFLEGVWGGPGAAQDNFISV
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                     /note="DEL: deletion in Raji"
     promoter        complement(164814)
                     /note="TATA: CATTTAA before BALF2, presumed promoter for
                     3.9kb early RNA"
     misc_feature    complement(164851)
                     /note="polyA signal: AATAAA"
     CDS             complement(164855..165517)
                     /note="BALF1 early reading frame, 0.7kb early RNA;  NCBI
                     gi: 59159"
                     /codon_start=1
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                     VRNYLDDHKSAAFVLGAIAHYLALYRRLWFARLGGMPRSLRRQFPVTWALASLTDFLK
                     SL"
     promoter        165442
                     /note="TATA: GATAAAA"
     promoter        165466
                     /note="TATA: TATAAGA EDR1 early promoter before BARF1,
                     gives 0.8kb early RNA"
     CDS             165504..166169
                     /note="BARF1 reading frame;  NCBI gi: 59158"
                     /codon_start=1
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                     LSQ"
     promoter        complement(165713)
                     /note="TATA: TATAAAG before BALF1"
     misc_feature    166165
                     /note="polyA signal: AATAAA 3' end of 0.8kb early RNA.
                     Also 1kb late RNA in this region."
     promoter        166469..166475
                     /note="TATA: TTATTTT"
     mRNA            166498..166916
                     /note="Exon 1 of terminal protein RNA"
     misc_feature    166561..166563
                     /note="Likely initiator met of terminal protein"
     misc_feature    166614
                     /note="BAM: Bam H1 A/Nhet"
     misc_feature    complement(166946)
                     /note="polyA signal: AATAAA These 2 polyA sites are 3' end
                     of 0.8kb early, 2.5kb late and 2.5kb latent RNAs"
     misc_feature    complement(166950)
                     /note="polyA signal: AATAAA"
     CDS             complement(166998..167303)
                     /note="BNLF2b reading frame;  NCBI gi: 583902"
                     /codon_start=1
                     /translation="XATMRPGRPLAGFYATLRRSFRRMSKRSKNKAKKERVPVEDRPP
                     TPMPTSQRLIRRNALGGGVRPDAEDCIQRFHPLEPALGVSTKNFDLLSLRCELGWCG"
     CDS             complement(167304..167486)
                     /note="BNLF2a reading frame;  NCBI gi: 59161"
                     /codon_start=1
                     /translation="MVHVLERALLEQQSSACGLPGSSTETRPSHPCPEDPDVSRLRLL
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     promoter        167320
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                      /note="TATA: CATAAAA"
      promoter        complement(167525)
                      /note="TATA: TATAAAA EDL2 early promoter before BNLF2a,b.
                      Gives 0.8kb RNA"
      mRNA            complement(168163..168965)
                      /note="BNLF1 coding part of exon c of latent membrane
                      protein"
      repeat_region   168399..168574
                      /note="5 x 33bp repeats"
      intron          complement(168966..169041)
                      /note="intervening sequence in BNLF1"
      misc_feature    complement(168966)
                      /note="ACCEPT: TTTTTTCAACGCAGT possible acceptor"
      misc_feature    complement(169041)
                      /note="DONOR: TTGGTAAGA donor"
      mRNA            complement(169042..169128)
                      /note="BNLF1 exon b of latent membrane protein mRNA"
      intron          complement(169129..169206)
                      /note="intervening sequence in BNLF1"
      misc_feature    complement(169129)
                      /note="ACCEPT: TCCTCTTTCCCCAGT acceptor"
      promoter        complement(169201)
                      /note="TATA: TATTACA EDL1A late promoter, gives 2.5kb late
                      RNA"
      misc_feature    complement(169206)
                      /note="DONOR: TGAGTAAGT donor"
      mRNA            complement(169207..169474)
                      /note="BNLF1 exon a of latent membrane protein mRNA"
      promoter        complement(169546)
                      /note="TATA: TACATAAGC EDL1 promoter before BNLF1 gives
                      2.5kb latent RNA (LMP)"
      repeat_region   170094..170631
                      /note="terminal repeat 1 538bp"
      repeat_region   170632..171154
                      /note="terminal repeat 2 523bp"
      repeat_region   171155..171692
                      /note="terminal repeat 3 538bp"
      repeat_region   171693..172231
                      /note="terminal repeat 4 538bp"
 BASE COUNT    34054 a  52511 c  50755 g  34961 t
 ORIGIN

Initial Score    =    170  Optimized Score  =    454  Significance = 10.52
Residue Identity =    50%  Matches          =    529  Mismatches   =   418
Gaps             =    105  Conservative Substitutions              =     0

              X       10           20        30        40        50
              CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
              ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
    CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
107030    107040    107050    107060    107070    107080    107090    107100

    60        70          80        90           100       110       120
    CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
     |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
    GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
        107110    107120    107130    107140    107150    107160     107170

       130       140       150       160       170       180        190
    CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
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   | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || ||  | | | | ||
   CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
          107180    107190    107200      107210    107220    107230

      200       210       220          230        240       250         260
   -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
     ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
   GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
107240    107250      107260    107270    107280    107290    107300

          270         280           290       300       310       320
   CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
    |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
107310    107320    107330    107340    107350          107360    107370

    330       340       350       360       370          380       390
   CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
     ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| ||||| ||
   GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
    107380    107390     107400      107410    107420    107430    107440

     400        410       420        430       440        450         460
   GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
   |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
   GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
     107450    107460    107470    107480      107490    107500    107510

          470          480        490       500       510       520
   GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
    | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
   AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
     107520    107530    107540    107550    107560    107570    107580

  530       540       550       560       570       580       590       600
   CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
     ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
   AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
   107590    107600       107610    107620    107630    107640    107650

          610         620           630       640       650       660
   AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
   || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
   AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
     107660    107670    107680    107690      107700    107710    107720

    670       680        690         700       710       720       730
   AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
   |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
   AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
     107730    107740    107750    107760    107770    107780    107790

        740       750        760       770       780           790
   AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
   ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
   AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
   107800     107810    107820    107830       107840    107850    107860

 800       810         820       830        840       850       860
   GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
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    || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
    GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
        107870    107880       107890    107900    107910    107920

   870       880       890       900       910       920        930
    AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
    |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
    AGCAGGAGGTGGAGGC-CGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
07930    107940     107950       107960    107970    107980     107990

  940       950       960           970        980       X
    GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
    | | | |   | | ||  |   || | |||    || |  | ||   || |  |
    GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGAAGTCGT
  108000    108010     108020    108030    108040    108050
```

```
8. US-08-162-407-5' (1-988)
   HS4B958RAJ   Epstein-Barr virus, artifactual joining of B95-8 c

 LOCUS       HS4B958RAJ 184113 bp ds-DNA              VRL        23-DEC-1994
 DEFINITION  Epstein-Barr virus, artifactual joining of B95-8 complete genome
             and the sequences from Raji of the large deletion found in B95-8.
 ACCESSION   M80517
 KEYWORDS    .
 SOURCE      Human herpesvirus 4 DNA.
   ORGANISM  Human herpesvirus 4
             Viridae; ds-DNA enveloped viruses; Herpesviridae;
             Gammaherpesvirinae.
 REFERENCE   1  (sites)
   AUTHORS   Baer,R.J., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J.,
             Gibson,T.J., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C.,
             Tuffnell,P.S. and Barrell,B.G.
   TITLE     DNA sequence and expression of the B95-8 Epstein-Barr virus genome
   JOURNAL   Nature 310, 207-211 (1984)
   STANDARD  full automatic
 REFERENCE   2  (sites)
   AUTHORS   Parker,B.D., Bankier,A., Satchwell,S., Barrell,B. and Farrell,P.J.
   TITLE     Sequence and transcription of Raji Epstein-Barr virus DNA spanning
             the B95-8 deletion region
   JOURNAL   Virology 179, 339-346 (1990)
   STANDARD  full automatic
 REFERENCE   3  (sites)
   AUTHORS   Sample,J., Brooks,L., Sample,C., Young,L., Rowe,M., Gregory,C.,
             Rickinson,A. and Kieff,E.
   TITLE     Restricted Epstein-Barr virus protein expression in Burkitt
             lymphoma is due to a different Epstein-Barr nuclear antigen 1
             transcriptional initiation site
   JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88, 6343-6347 (1991)
   STANDARD  full automatic
 REFERENCE   4  (bases 1 to 184113)
   AUTHORS   Jenson,H.B.
   TITLE     GenBank Curator Program
   JOURNAL   Unpublished (1992)
   STANDARD  full automatic
 COMMENT     The B95-8 genome (V01555) has a large deletion in the right side of
             the genome which has been sequenced in Raji (M35547).  These
             sequences have been joined to form an extended and more complete,
             although artifactual, EBV sequence.
             For features, refer to feature tables of V01555 and M35547.
```

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            NCBI gi: 330330
FEATURES             Location/Qualifiers
     source          1..184113
                     /organism="Human herpesvirus 4"
                     /sequenced_mol="DNA"
     misc_feature    1..152008
                     /note="B95-8 sequences (corresponds to 1-152,008 of
                     V01555)"
     misc_feature    152009..152012
                     /note="Overlap of B95-8 and Raji sequences at B95-8
                     deletion point (corresponds to 152,009-152,012 in V01555,
                     and 1-4 in M35547)"
     misc_feature    153013..163839
                     /note="Raji sequences (corresponds to 5-11,831 of M35547)"
     misc_feature    163840..163843
                     /note="Overlap of B95-8 and Raji sequences at B95-8
                     deletion point (corresponds to 152,009-152,012 of V01555,
                     and 11,832-11,835 of M35547)"
     misc_feature    163844..184113
                     /note="B95-8 sequences (corresponds to 152,013-172,282 of
                     V01555)"
BASE COUNT    36002 a  55824 c  54622 g  37665 t
ORIGIN
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Initial Score    =    170  Optimized Score  =    454  Significance = 10.52
Residue Identity =    50%  Matches          =    529  Mismatches   =   418
Gaps             =    105  Conservative Substitutions              =     0

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              CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
              ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
    CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
107030    107040    107050    107060    107070    107080    107090    107100

    60        70         80        90           100       110       120
    CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
     |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
    GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
        107110    107120    107130    107140    107150    107160     107170

       130       140       150       160       170       180        190
    CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
    | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
    CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
           107180    107190    107200      107210    107220    107230

       200       210       220          230        240       250         260
    -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
      ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
    GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
 107240    107250      107260    107270    107280    107290    107300

           270        280          290       300       310       320
    CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
     |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
    GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
 107310    107320    107330    107340    107350          107360    107370

     330       340       350       360       370          380       390
    CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
      ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| ||||| ||
    GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
     107380    107390     107400      107410    107420    107430    107440

      400        410       420        430       440        450         460
    GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
    |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
    GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      107450    107460    107470    107480      107490    107500    107510

           470          480        490       500       510       520
    GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
     | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
    AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
      107520    107530    107540    107550    107560    107570    107580

   530       540       550       560       570       580       590       600
    CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
      ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
    AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
    107590    107600       107610    107620    107630    107640    107650

           610         620           630       640       650       660
    AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
    || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
    AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
      107660    107670    107680    107690      107700    107710    107720

      670       680        690        700       710       720       730
    AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
    |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
    AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      107730    107740    107750    107760    107770    107780    107790

         740       750        760       770       780           790
    AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
    ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
    AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
    107800     107810    107820    107830       107840    107850    107860

  800       810         820       830        840       850       860
    GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
    || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
    GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
        107870    107880       107890    107900    107910    107920

   870       880       890       900       910       920       930
    AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
    |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
    AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
07930    107940     107950       107960    107970    107980     107990

  940       950       960           970        980         X
    GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
    | | | |   | | ||  |   || | |||    || |  | ||   || |  |
    GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGAAGTCGT
  108000    108010     108020    108030    108040    108050
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9. US-08-162-407-5' (1-988)
   HS4B958RAJ   Epstein-Barr virus, artifactual joining of B95-8 c

 LOCUS       HS4B958RAJ 184113 bp ds-DNA             VRL       03-OCT-1991
 DEFINITION  Epstein-Barr virus, artifactual joining of B95-8 complete genome
             and the sequences from Raji of the large deletion found in B95-8.
 ACCESSION   M80517
 KEYWORDS    .
 SOURCE      Epstein-Barr virus DNA.
   ORGANISM  Epstein-Barr virus
             Viridae; ds-DNA enveloped viruses; Herpesviridae;
             Gammaherpesvirinae.
 REFERENCE   1  (sites)
   AUTHORS   Baer,R.J., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J.,
             Gibson,T.J., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C.,
             Tuffnell,P.S. and Barrell,B.G.
   TITLE     DNA sequence and expression of the B95-8 Epstein-Barr virus genome
   JOURNAL   Nature 310, 207-211 (1984)
   STANDARD  full automatic
 REFERENCE   2  (sites)
   AUTHORS   Parker,B.D., Bankier,A.T., Satchwell,S.C., Barrell,B.G. and
             Farrell,P.J.
   TITLE     Sequence and transcription of Raji Epstein-Barr virus DNA spanning
             the B95-8 deletion region
   JOURNAL   Virology 179, 339-346 (1990)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 184113)
   AUTHORS   Jenson,H.B.
   TITLE     GenBank Curator Program
   JOURNAL   Unpublished (1992)
   STANDARD  full automatic
 COMMENT     The B95-8 genome (V01555) has a large deletion in the right side of
             the genome which has been sequenced in Raji (M35547).  These
             sequences have been joined to form an extended and more complete,
             although artifactual, EBV sequence.
             For features, refer to feature tables of V01555 and M35547.

             NCBI gi: 330330
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      source          1..184113
                      /organism="Epstein-Barr virus"
                      /sequenced_mol="DNA"
      misc_feature    1..152008
                      /note="B95-8 sequences (corresponds to 1-152,008 of
                      V01555)"
      misc_feature    152009..152012
                      /note="Overlap of B95-8 and Raji sequences at B95-8
                      deletion point (corresponds to 152,009-152,012 in V01555,
                      and 1-4 in M35547)"
      misc_feature    153013..163839
                      /note="Raji sequences (corresponds to 5-11,831 of M35547)"
      misc_feature    163840..163843
                      /note="Overlap of B95-8 and Raji sequences at B95-8
                      deletion point (corresponds to 152,009-152,012 of V01555,
                      and 11,832-11,835 of M35547)"
      misc_feature    163844..184113
                      /note="B95-8 sequences (corresponds to 152,013-172,282 of
                      V01555)"
 BASE COUNT    36002 a  55824 c  54622 g  37665 t
 ORIGIN
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Initial Score    =    170  Optimized Score  =    454  Significance = 10.52
Residue Identity =    50%  Matches          =    529  Mismatches   =   418
Gaps             =    105  Conservative Substitutions             =     0

                  X        10          20        30        40        50
                  CGGGGGCTTG---TTCAGAGTTGGGTAAATGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
                  ||| |||  ||    ||| ||  | |    ||    | ||   ||    || |  |    |
         CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
       107030    107040    107050    107060    107070    107080    107090    107100

         60        70          80        90            100       110       120
         CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
         |    | ||||| | | ||   ||| ||||  ||   |    ||| | |   | || ||      |  |||||
         GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
             107110    107120    107130    107140    107150    107160     107170

            130       140       150       160       170       180        190
         CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
         | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
         CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGACCCACGGTGGAACAGGAGCAGGA
                107180    107190    107200     107210    107220    107230

            200       210       220           230        240       250        260
         -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
           || |   |     |   |  |    |||  |    |||||| || || |  |   ||||   ||  ||
         GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
       107240    107250      107260    107270    107280    107290    107300

                270         280            290       300       310       320
         CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
         |   |||| |||  | |  ||| | ||    ||| | ||||||    |     ||| | || | | |     |
         GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
       107310    107320    107330    107340    107350          107360    107370

          330       340       350       360       370          380       390
         CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
           ||        ||  | ||||| |   |||  || |  ||||| ||||||  |   | |||||| ||||| ||
         GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
          107380    107390     107400      107410    107420    107430    107440

          400       410        420         430       440         450       460
         GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
         |||| ||| ||||||    | ||||| |  |  ||  | ||    |||| || || |||     || | ||||
         GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
          107450    107460    107470    107480     107490    107500    107510

                470          480         490       500       510       520
         GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
          | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
         AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
          107520    107530    107540    107550    107560    107570    107580

        530       540       550       560       570       580       590       600
         CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
           ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |     |
         AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
         107590    107600       107610    107620    107630    107640    107650

                610         620           630       640       650       660
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         AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
         || |||  ||||  || ||  ||  ||||     ||   || | ||   | | |      |     | | ||
         AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
           107660    107670    107680    107690      107700    107710    107720

          670       680        690          700       710       720       730
         AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
         |||| |    |||   || |   |||   ||  | |  |||  ||   | |   | |  | | |||||    |
         AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
           107730    107740    107750    107760    107770    107780    107790

             740       750        760       770       780           790
         AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
         ||  ||  ||||      ||| |||    |  |  | ||| | |||  | ||  |    | ||      |
         AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
         107800     107810    107820    107830       107840    107850    107860

       800       810         820       830         840       850       860
         GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGCTGTGTTGGAAGG
         || |  || ||    |||    |  || |||    | ||  |  | ||  ||||| |   || || |   || |||
         GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
             107870    107880          107890    107900    107910    107920

        870       880       890       900       910       920       930
         AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
         |||||     ||    | | | ||  ||||     ||||   |  || || |  ||  |||| | |||   || |
         AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
       07930    107940     107950        107960    107970    107980    107990

       940       950       960           970       980      X
         GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
         | | | |   | | ||  |   || | |||   || |  | ||   || |  |
         GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGAAGTCGT
       108000    108010     108020    108030    108040    108050

10. US-08-162-407-5'  (1-988)
    EBV            Epstein-Barr virus (EBV) genome. The complete sequ

 LOCUS       EBV         172281 bp    DNA   circular  VRL       12-SEP-1993
 DEFINITION  Epstein-Barr virus (EBV) genome. The complete sequence [1-10] was
             determined from DNA from B95-8 cells cloned by Arrand et al [11].
             B95-8 is a productive marmoset lymphoblastoid cell line
             immortalized with human EBV from a mononucleosis patient.
 ACCESSION   V01555 J02070 K01729 K01730 V01554 X00498 X00499 X00784
 KEYWORDS    DNA polymerase; EBNA; genome; ribonucleotide reductase;
             tandem repeat; terminal repeat.
 SOURCE      Human herpesvirus 4.
   ORGANISM  Human herpesvirus 4
             Viridae; ds-DNA enveloped viruses; Herpesviridae;
             Gammaherpesviridae.
 REFERENCE   1  (bases 1 to 172281)
   AUTHORS   Baer,R.J., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J.,
             Gibson,T.J., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C.,
             Tuffnell,P.S. and Barrell,B.G.
   TITLE     DNA sequence and expression of the B95-8 Epstein-Barr virus genome
   JOURNAL   Nature 310, 207-211 (1984)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 172281)
   AUTHORS   Deininger,P.L., Bankier,A., Farrell,P., Baer,R. and Barrell,B.
   TITLE      Sequence analysis and in vitro transcription of portions of the
              Epstein-Barr virus genome
   JOURNAL    J. Cell. Biochem. 19, 267-274 (1982)
   STANDARD   full automatic
 REFERENCE    3  (bases 1 to 172281)
   AUTHORS    Farrell,P.J., Deininger,P.L., Bankier,A. and Barrell,B.
   TITLE      Homologous upstream sequences near Epstein-Barr virus promoters
   JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 80, 1565-1569 (1983)
   STANDARD   full automatic
 REFERENCE    4  (bases 1 to 172281)
   AUTHORS    Farrell,P.J., Bankier,A.T., Seguin,C., Deininger,P.L. and
              Barrell,B.G.
   TITLE      Latent and lytic cycle promoters of Epstein-Barr virus
   JOURNAL    EMBO J. 2, 1331-1338 (1983)
   STANDARD   full automatic
 REFERENCE    5  (bases 142687 to 159853)
   AUTHORS    Bankier,A.T., Deininger,P.L., Farrell,P.J. and Barrell,B.G.
   TITLE      Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
              Epstein-Barr virus
   JOURNAL    Mol. Biol. Med. 1, 21-45 (1983)
   STANDARD   full automatic
 REFERENCE    6  (bases 112620 to 125316)
   AUTHORS    Seguin,C., Farrell,P.J. and Barrell,B.G.
   TITLE      DNA sequence and transcription of the BamHI fragment B region of
              B95-8 Epstein-Barr virus
   JOURNAL    Mol. Biol. Med. 1, 369-392 (1983)
   STANDARD   full automatic
 REFERENCE    7  (bases 159853 to 172281)
   AUTHORS    Bankier,A.T., Deininger,P.L., Satchwell,S.C., Baer,R., Farrell,P.J.
              and Barrell,B.G.
   TITLE      DNA sequence analysis of the EcoRI Dhet fragment of B95-8
              Epstein-Barr virus containing the terminal repeat sequences
   JOURNAL    Mol. Biol. Med. 1, 425-445 (1983)
   STANDARD   full automatic
 REFERENCE    8  (bases 87650 to 92703)
   AUTHORS    Biggin,M., Farrell,P.J. and Barrell,B.G.
   TITLE      Transcription and DNA sequence of the BamHI L fragment of B95-8
              Epstein-Barr virus
   JOURNAL    EMBO J. 3, 1083-1090 (1984)
   STANDARD   full automatic
 REFERENCE    9  (bases 76089 to 79808)
   AUTHORS    Gibson,T., Stockwell,P., Ginsburg,M. and Barrell,B.
   TITLE      Homology between two EBV early genes and HSV ribonucleotide
              reductase and 38K genes
   JOURNAL    Nucleic Acids Res. 12, 5087-5099 (1984)
   STANDARD   full automatic
 REFERENCE    10 (bases 1 to 172281)
   AUTHORS    Hatfull,G.F., Barrell,B.G., Quinn,J. and McGeoch,D.
   JOURNAL    Unpublished
   STANDARD   full automatic
 REFERENCE    11 (bases 1 to 172281)
   AUTHORS    Arrand,J.R., Rymo,L., Walsh,J.E., Bjorck,E., Lindahl,T. and
              Griffin,B.E.
   TITLE      Molecular cloning of the complete Epstein-Barr virus genome as a
              set of overlapping restriction endonuclease fragments
   JOURNAL    Nucleic Acids Res. 9, 2999-3014 (1981)
   STANDARD   full automatic
 REFERENCE    12 (bases 1 to 172281)
   AUTHORS    Kozak,M.
   TITLE      Possible role of flanking nucleotides in recognition of the AUG
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              initiator codon by eukaryotic ribosomes
   JOURNAL    Nucleic Acids Res. 9, 5233-5262 (1981)
   STANDARD   full automatic
 REFERENCE    13 (bases 7315 to 9312)
   AUTHORS    Yates,J., Warren,N., Reisman,D. and Sugden,B.
   TITLE      A cis-acting element from the Epstein-Barr viral genome that
              permits stable replication of recombinant plasmids in latently
              infected cells
   JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 81, 3806-3810 (1984)
   STANDARD   full automatic
 REFERENCE    14 (bases 45415 to 52824)
   AUTHORS    Jones,M.D., Foster,L., Sheedy,T. and Griffin,B.E.
   TITLE      The EB virus genome in Daudi Burkitt's lymphoma cells has a
              deletion similar to that observed in a non-transforming strain
              (P3HR-1) of the virus
   JOURNAL    EMBO J. 3, 813-821 (1984)
   STANDARD   full automatic
 REFERENCE    15 (bases 45644 to 52450)
   AUTHORS    Jeang,K.T. and Hayward,S.D.
   TITLE      Organization of the Epstein-Barr virus DNA molecule. III. Location
              of the P3HR-1 deletion junction and characterization of the NotI
              repeat units that form part of the template for an abundant
              12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
   JOURNAL    J. Virol. 48, 135-148 (1983)
   STANDARD   full automatic
 REFERENCE    16 (bases 1 to 172281)
   AUTHORS    Farrell,P.J. and Barrell,B.G.
   TITLE      Direct Submission
   JOURNAL    Submitted (05-JUN-1984) to the EMBL/GenBank/DDBJ databases
   STANDARD   full automatic
 REFERENCE    17 (bases 1 to 172281)
   AUTHORS    Bodescot,M. and Perricaudet,M.
   TITLE      Clustered alternative splice sites in Epstein-Barr virus RNAs
   JOURNAL    Nucleic Acids Res. 15, 5887 (1987)
   STANDARD   full automatic
 REFERENCE    18 (bases 1 to 172281)
   AUTHORS    Laux,G., Perricaudet,M. and Farrell,P.J.
   TITLE      A spliced Epstein-Barr virus gene expressed in immortalized
              lymphocytes is created by circularization of the linear viral
              genome
   JOURNAL    EMBO J. 7, 769-774 (1988)
   STANDARD   full automatic
 REFERENCE    19 (bases 1 to 172281)
   AUTHORS    Farrell,P.J.
   TITLE      Direct Submission
   JOURNAL    Submitted (18-MAR-1988) to the EMBL/GenBank/DDBJ databases. Farrell
              P., Ludwig Institute for Cancer Research, St. Mary's Hospital
              Medical School, Norfolk Place London W2 1PG
   STANDARD   full automatic
 COMMENT      CDS

              Listed under this feature are all known protein coding regions as
              well as all the major open reading frames in the sequence. In
              general the term major is taken as the longest frame in a
              particular region taking into account the adjacent longest frames
              and likely transcription signals. Note that on this basis some long
              overlapping frames have been excluded and on the other hand some
              small frames have been included which might represent exons or
              genes because they occur in a logical combination with other
              features or because of some other experimental data. The reading
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frames are named according to the Bam H1 fragment in which they start. eg BALF3 is the third leftward frame starting in Bam H1 fragment A. BORF1 is the first rightward frame in Bam H1 fragment O. If there is an obvious TATA sequence followed by an in frame Met codon that satisfies the rules of Kozak [12] in that there is a purine at -3 and/or a G at +4 then the reading frame is numbered from the A of the ATG to the base preceding the termination codon. If there is no obvious initiation codon or there is a substantial reading frame in phase before the ATG then the reading frame is numbered from the first base of the first codon.

SITEs of POLYA signals

This feature lists all occurences of the sequence AATAAA which is found normally approximately 20 bases upstream of the mRNA processing/polyA addition site. The rarely used homolog ATTAAA is only listed when it is found in a position close to the end of a major reading frame.

SITEs of DONOR and ACCEPT sequences

This is not a comprehensive listing of all such sequences and only the positions of a few have been noted because they occur in potentially interesting positions. The number quoted in the table is the position of the terminal base in the intron in each case.

Restriction enzyme SITEs.

Only the positions of the sites Bam HI (BAM) are listed.

RPT

This feature is used to define repetitive sequences.

SITE DEL

This feature defines deletions in B95-8 with respect to other strains such as RAJI and also to deletions in other strains such as P3HR1 and DAUDI with respect to B95-8.

SITE HPN

Denotes sequences with twofold symmetry ie could form hairpin loops. This is not a comprehensive list - only a few occurences noted.

ORGRPL

Denotes the region that encompasses an origin of replication (ori P).[13].

NUMBERING

The DNA sequence of B95-8 EBV has been revised [19]. The original (Baer et al, 1984) base 359 has been deleted so the new sequence around that position reads TCAGTCTTT. To avoid renumbering the entire sequence, position 1 has benn moved 1 base to the left of the EcoRI site separating EcoRI Dhet from EcoRI I (ie the first A of AGAATTC).

```
                NCBI gi: 59074
FEATURES                 Location/Qualifiers
     source              1..172281
                         /organism="Epstein-Barr virus"
                         /strain="B95-8"
     mRNA                58..272
                         /note="exon 2 terminal protein RNA"
     mRNA                360..458
                         /note="exon 3 terminal protein RNA"
     misc_feature        complement(535)
                         /note="polyA signal: AATAAA"
     mRNA                540..788
                         /note="exon 4 terminal protein RNA"
     mRNA                871..951
                         /note="exon 5 terminal protein RNA"
     mRNA                1026..1196
                         /note="exon 6 terminal protein RNA"
     promoter            complement(1192)
                         /note="TATA: TATAAAT"
     mRNA                1280..1495
                         /note="exon 7 terminal protein RNA"
     promoter            complement(1383)
                         /note="TATA: CATAAAA"
     mRNA                1574..1682
                         /note="exon 8 terminal protein RNA"
     promoter            1676
                         /note="TATA: TATAAAG"
     promoter            1691
                         /note="TATA: TATTAAA BN-R1 late promoter before BNRF1,
                         gives 4.1kb late RNA. Probably encodes non glycosylated
                         140kd protein in membrane antigen. Also two latent RNAs
                         spliced underneath this RNA, lengths 1.8 and 2.0kb (Hudson
                         et al, 1985). The longer one encodes terminal protein."
     CDS                 1736..5692
                         /note="BNRF1 reading frame, 5 NXT/S;  NCBI gi: 59075"
                         /codon_start=1
                         /translation="MEERGRETQMPVARYGGPFIMVRLFGQDGEANIQEERLYELLSD
                         PRSALGLDPGPLIAENLLLVALRGTNNDPRPQRQERARELALVGILLGNGEQGEHLGT
                         ESALEASGNNYVYAYGPDWMARPSTWSAEIQQFLRLLGATYVLRVEMGRQFGFEVHRS
                         RPSFRQFQAINHLVLFDNALRKYDSGQVAAGFQRALLVAGPETADTRPDLRKLNEWVF
                         GGRAAGGRQLADELKIVSALRDTYSGHLVLQPTETLDTWKVLSRDTRTAHSLEHGFIH
                         AAGTIQANCPQLFMRRQHPGLFPFVNAIASSLGWYYQTATGPGADARAAARRQQAFQT
                         RAAAECHAKSGVPVVAGFYRTINATLKGGEGLQPTMFNGELGAIKHQALDTVRYDYGH
                         YLIMLGPFQPWSGLTAPPCPYAESSWAQAAVQTALELFSALYPAPCISGYARPPGPSA
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                 VIEHLGSLVPKGGLLLFLSHLPDDVKDGLGEMGPARATGPGMQQFVSSYFLNPACSNV
                 FITVRQRGEKINGRTVLQALGRACDMAGCQHYVLGSTVPLGGLNFVNDLASPVSTAEM
                 MDDFSPFFTVEFPPIQEEGASSPVPLDVDESMDISPSYELPWLSLESCLTSILSHPTV
                 GSKEHLVRHTDRVSGGRVAQQPGVGPLDLPLADYAFVAHSQVWTRPGGAPPLPYRTWD
                 RMTEKLLVSAKPGGENVKVSGTVITLGEQGYKVSLDLREGTRLAMAEALLNAACAPIL
                 DPEDVLLTLHLHLDPRRADNSAVMEAMTAASDYARGLGVKLTFGSASCPETGSSASNF
                 MTVVASVSAPGEFSGPLITPVLQKTGSLLIAVRCGDGKIQGGSLFEQLFSDVATTPRA
                 PEALSLKNLFRAVQQLVKSGIVLSGHDISDGGLVTCLVEMALAGQRGVTITMPVASDY
                 LPEMFAEHPGLVFEVEERSVGEVLQTLRSMNMYPAVLGRVGEQGPDQMFEVQHGPETV
                 LRQSLRLLLGTWSSFASEQYECLRPDRINRSMHVSDYGYNEALAVSPLTGKNLSPRRL
                 VTEPDPRCQVAVLCAPGTRGHESLLAAFTNAGCLCRRVFFREVRDNTFLDKYVGLAIG
                 GVHGARDSALAGRATVALINRFPALRDAILKFLNRPDTFSVALGELGVQVLAGLGAVG
                 STDNPPAPGVEVNVQRSPLILAPNASGMFESRWLNISIPATTSSVMLRGLRGCVLPCW
                 VQGSCLGLQFTNLGMPYVLQNAHQIACHFHSNGTDAWRFAMNYPRNPTEQGNIAGLCS
                 RDGRHLALLCDPSLCTDFWQWEHIPPAFGHPTGCSPWTLMFQAAHLWSLRHGRPSE"
misc_feature     complement(1795)
                 /note="polyA signal: AATAAA"
misc_feature     3955
                 /note="BAM: Bam H1 Nhet/h"
misc_feature     3994
                 /note="BAM: Bam H1 h/C"
mRNA             5408..5856
                 /note="exon 9 terminal protein RNA"
misc_feature     5841
                 /note="polyA signal: AATAAA, end of 4.1kb late RNA and TP
                 latent RNA."
misc_feature     5863
                 /note="alternative end to TP cDNAs"
promoter         6097
                 /note="TATA: TATAAGA"
misc_feature     6629..6795
                 /note="Pol III RNA EBER 1"
promoter         complement(6823)
                 /note="TATA: CATAAAT"
misc_feature     6956..7128
                 /note="Pol III RNA EBER 2"
rep_origin       7315..9312
                 /note="origin of replication, ori P (Yates et al, 1984,
                 1985)"
repeat_region    7421..8042
                 /note="21x30bp repeats, binding sites for EBNA-1 (site I,
                 Rawlins et al, 1985). Tandem repeat part of oriP (Reisman
                 et al, 1985). Also functions as a cell type specific
                 enhancer (Reisman et al, 1985; Lupton and Levine, 1985)"
promoter         7738
                 /note="TATA: TATAAAT"
promoter         7888
                 /note="TATA: TATAAAT"
promoter         8573
                 /note="TATA: CATAAAT"
misc_feature     complement(8680)
                 /note="polyA signal: AATAAA"
misc_feature     complement(8755)
                 /note="polyA signal: AATAAA"
misc_feature     8962
                 /note="polyA signal: AATAAA"
misc_feature     9021..9133
                 /note="HPN: dyad symmetry, site II for EBNA-1 binding
                 (Rawlins et al, 1985). Dyad symmetry part of oriP (Reisman
                 et al, 1985)"
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promoter         complement(9398)
                 /note="TATA: TATAAAT"
promoter         9631
                 /note="TATA: TATAAAT BC-R1 late promoter before BCRF1"
CDS              9675..10187
                 /note="BCRF1 reading frame;  NCBI gi: 59076"
                 /codon_start=1
                 /translation="MERRLVVTLQCLVLLYLAPECGGTDQCDNFPQMLRDLRDAFSRV
                 KTFFQTKDEVDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPEAKDHV
                 NSLGENLKTLRLRLRRCHRFLPCENKSKAVEQIKNAFNKLQEKGIYKAMSEFDIFINY
                 IEAYMTIKAR"
promoter         10076
                 /note="TATA: GATAAAA"
misc_feature     complement(10148)
                 /note="polyA signal: AATAAA"
misc_feature     10173
                 /note="polyA signal: ATTAAA"
misc_feature     10257
                 /note="polyA signal: AATAAA, end of 0.8kb late RNA from
                 BCR1 and end of 1.6 kb late RNA, start unknown"
misc_feature     complement(10277)
                 /note="polyA signal: AATAAA"
promoter         complement(10975)
                 /note="TATA: CATAAAT"
promoter         11305
                 /note="TATA: TACAAAA; BCR2 promoter for highly spliced
                 EBNA latent RNAs."
mRNA             11336..11480
                 /note="exon C1 of Bodescot et al (1986) RNAs"
promoter         11524
                 /note="TATA: TATAATT"
misc_feature     complement(11587)
                 /note="polyA signal: AATAAA"
promoter         complement(11606)
                 /note="TATA: CATAAAT"
mRNA             11626..11657
                 /note="exon C2 of Bodescot et al (1986) RNAs"
promoter         11796
                 /note="TATA: TATAAGT"
promoter         complement(11799)
                 /note="TATA: TATAAAA"
repeat_region    12001..15072
                 /note="3072 repeat 1"
CDS              12541..13692
                 /note="BCRF2 3072 repeat, reading frame 1;  NCBI gi:
                 583873"
                 /codon_start=1
                 /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                 PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
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                 PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                 HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                 LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                 VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature     13215
                 /note="BAM: BamH1 C/W"
promoter         14352
                 /note="*TATA: TATAAAG BWR1 one of the promoters for highly
                 spliced EBNA and LP RNAs (Sample et al, 1986; Speck et al,
                 1986)"
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mRNA            14384..14410
                /note="*exon W0 of EBNA/LP RNAs"
mRNA            14554..14619
                /note="*exon W1 (also W66) part of leader protein (LP)
                gene. LP is also called EBNA-5 (Dillner et al, 1986) and
                EBNA-4 (Rowe et al, 1987)."
mRNA            14559..14619
                /note="*exon W1' (also W61) of EBNA/LP RNAs forms
                initiator met when fused to exon W0 or exon C2."
mRNA            14701..14832
                /note="*exon W2 (also W132) part of LP gene"
repeat_region   15073..18144
                /note="3072 repeat 2"
CDS             15613..16764
                /note="BWRF1 reading frame 2;  NCBI gi: 583874"
                /codon_start=1
                /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
                TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
                PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature    16287
                /note="BAM: BamH1 W/W"
promoter        17424
                /note="TATA: TATAAAG"
mRNA            17626..17691
                /note="Exon W1"
mRNA            17773..17904
                /note="Exon W2"
repeat_region   18145..21216
                /note="3072 repeat 3"
CDS             18685..19836
                /note="BWRF1 reading frame 3;  NCBI gi: 583875"
                /codon_start=1
                /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
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                PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature    19359
                /note="BAM: BamH1 W/W"
promoter        20496
                /note="TATA: TATAAAG"
mRNA            20698..20763
                /note="Exon W1"
mRNA            20845..20976
                /note="Exon W2"
repeat_region   21217..24288
                /note="3072 repeat 4"
CDS             21757..22908
                /note="BWRF1 reading frame 4;  NCBI gi: 583876"
                /codon_start=1
                /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
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                PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
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                VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature    22431
                /note="BAM: BamH1 W/W"
promoter        23568
                /note="TATA: TATAAAG"
mRNA            23771..23835
                /note="Exon W1"
mRNA            23917..24048
                /note="Exon W2"
repeat_region   24289..27360
                /note="3072 repeat 5"
CDS             24829..25980
                /note="BWRF1 reading frame 5;  NCBI gi: 583877"
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                /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
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                LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature    25503
                /note="BAM: BamH1 W/W"
promoter        26640
                /note="TATA: TATAAAG"
mRNA            26842..26907
                /note="Exon W1"
mRNA            26989..27120
                /note="Exon W2"
repeat_region   27361..30432
                /note="3072 repeat 6"
CDS             27901..29052
                /note="BWRF1 reading frame 6;  NCBI gi: 583878"
                /codon_start=1
                /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
                TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
                PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
misc_feature    28575
                /note="BAM: BamH1 W/W"
promoter        29712
                /note="TATA: TATAAAG"
mRNA            29914..29979
                /note="Exon W1"
mRNA            30061..30192
                /note="Exon W2"
repeat_region   30433..33504
                /note="3072 repeat 7"
CDS             30973..32124
                /note="BWRF1 reading frame 7;  NCBI gi: 583879"
                /codon_start=1
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                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
     misc_feature    31647
                     /note="BAM: BamH1 W/W"
     promoter        32784
                     /note="TATA: TATAAAG"
     mRNA            32986..33051
                     /note="Exon W1"
     mRNA            33133..33264
                     /note="Exon W2"
     repeat_region   33505..36576
                     /note="3072 repeat 8"
     CDS             34045..35196
                     /note="BWRF1 reading frame 8;  NCBI gi: 583880"
                     /codon_start=1
                     /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                     PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
                     TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
                     PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                     HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
     misc_feature    34719
                     /note="BAM: BamH1 W/W"
     promoter        35856
                     /note="TATA: TATAAAG"
     mRNA            36058..36123
                     /note="Exon W1"
     mRNA            36205..36336
                     /note="Exon W2"
     repeat_region   36577..39648
                     /note="3072 repeat 9"
     CDS             37117..38268
                     /note="BWRF1 reading frame 9;  NCBI gi: 583881"
                     /codon_start=1
                     /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
                     PRVSRQGPASSGAAGSPPQAPQTRVSASRADRPRAWRLLGASRRGWFCPSLCPSEEPG
                     TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
                     PEGPRQPGRPQRPVPRPFPGLQSPGCPPEGTLGVPSPPLQARASPSRRGASLGPQVQP
                     HRDPSGPDPPTGPSLCPPAPLQPSLHPRPQLLASPGPPGQPEGPRQPGRVAFPLPWPL
                     LPASHPSPLSLPPHRVHQAGRRDPGGPVSVPPAAAQSLPPGKGASFSPPSLRPSLLCT
                     VCKVQPPTPVHGSRAQPRPPLPTVDRPSVHPGHPRPPVSTPVPSRGDFM"
     misc_feature    37791
                     /note="BAM: BamH1 W/W"
     promoter        38928
                     /note="TATA: TATAAAG"
     mRNA            39130..39195
                     /note="Exon W1"
     mRNA            39277..39408
                     /note="Exon W2"
     repeat_region   39649..42720
                     /note="3072 repeat 10"
     CDS             40189..41340
                     /note="BWRF1 reading frame 10;  NCBI gi: 583882"
                     /codon_start=1
                     /translation="XWEAEGRPRPGEVEGDRPGLCWQSPGDPLRPSGPGRSPSAPQTD
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                     TSGTPEPLGPASRRPPGLRSPLSPVKPKECLRGATLGAQAPESRGQGHLRVPPRVPGQ
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     promoter        42000
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     mRNA            42202..42267
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                     /note="Exon W2"
     repeat_region   42721..45792
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     promoter        45072
                     /note="TATA: TATAAAG"
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                     /note="DEL: DAUDI deletion (Jones et al, 1984)"
     mRNA            45421..45552
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                     /note="DEL: P3HR1 deletion (Jeang and Hayward, 1983)"
     repeat_region   45793..47643
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     misc_feature    47007
                     /note="BAM: BamH1 W/Y"
     mRNA            47761..47793
                     /note="Exon Y1 Bodescot et al, 1984"
     promoter        47831
                     /note="TATA: TATAAGT"
     mRNA            47878..47999
                     /note="Exon Y2 Bodescot et al, 1984 and EBNA-1 (Speck and
                     Strominger,1985), last common exon"
     misc_feature    complement(48023)
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     CDS             48386..50032
                     /note="Coding exon for EBNA-2 (Sample et al,1986)"
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mRNA              48386..48444
                  /note="exon Bodescot et al, 1984"
CDS               48429..49967
                  /note="BYRF1, encodes EBNA-2 (Dambaugh et al, 1984;
                  Dillner et al, 1984);  NCBI gi: 583885"
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                  NDQQLHHLPSGPPWWPPICDPPQPSKTQGQSRGQSRGRGRGRGRGRGKGKSRDKQRKP
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                  PSIQ"
repeat_region     48678..48800
                  /note="14 x CCCCCACCA repeats"
misc_feature      48848
                  /note="BAM: BamH1 Y/H"
promoter          49350
                  /note="TATA: TATAACA"
promoter          complement(49353)
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repeat_region     49525..49578
                  /note="9 x GGGGCA repeats"
mRNA              49852..50032
                  /note="exon (Bodescot et al 1984)"
misc_feature      50003
                  /note="polyA signal: AATAAA, end of Bodescot T1 RNA and
                  EBNA-2 RNA (3.0kb latent RNA in IB4 cells)"
promoter          complement(50156)
                  /note="TATA: TATAAGT"
misc_feature      complement(50317)
                  /note="polyA signal: AATAAA, end of 2.5kb early RNA from
                  52817"
repeat_region     50578..52115
                  /note="12 x 125bp repeats"
misc_feature      complement(50578..52557)
                  /note="BHLF1 early reading frame"
misc_feature      52654..53697
                  /note="region homologous to Eco R1 C of Raji"
promoter          complement(52817)
                  /note="TATA: GATAAAA promoter for 2.5kb early RNA
                  containing BHLF1 (Jeang and Hayward, 1983; Freese et
                  al,1983)"
promoter          53759
                  /note="TATA: TATTAAC likely promoter for class III and IV
                  early RNAs encoding BHRF1 (Pearson et al, 1987)"
misc_feature      53895
                  /note="DONOR: CGGGTAACT donor for splice to 54335 in class
                  IV early RNAs encoding BHRF1 (Pearson et al, 1987)"
misc_feature      54335
                  /note="ACCEPT: TTTTCTAG acceptor from 48444 in class I,
                  47999 in class II, and 53895 in class IV early RNAs
                  encoding BHRF1 (Pearson et al, 1987)"
misc_feature      54376..54948
                  /note="BHRF1 reading frame, limited homolgy to bcl-2 gene.
                  Early gene in B95-8 cells and part of restricted EA
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                  complex."
promoter          54591
                  /note="TATA: TATAACA"
promoter          complement(54594)
                  /note="TATA: TATAAAT"
misc_feature      54853
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promoter          complement(54977)
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misc_feature      55518
                  /note="polyA signal: AATAAA, 3' end of 2.5kb, 1.9kb, 1.7kb
                  and 0.6kb early RNAs"
misc_feature      complement(55982..56935)
                  /note="BFLF2 reading frame, 4 NXT/S, homologous to RF 27
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misc_feature      complement(55990)
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                  early RNAs from 58568 and 57081"
promoter          complement(56132)
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CDS               complement(56948..58525)
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                  VZV and HFRF1 in CMV;  NCBI gi: 59090"
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                  SQGPCLLAPMFGLRHKNASRTICPLCESLGAHPDAKDTLDRFKSLILDSFGNNIKILD
                  RIVFLIKTQNTLLDVPCPRLRAWLQMCTPQDFHKHLFCDPLCAINHSITNPSVLFGQI
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                  IHGLDLVQSYQTSQVYV"
promoter          complement(57081)
                  /note="TATA: TATTTAA before BFLF2; BFL2 promoter gives
                  1.1kb early RNA"
promoter          complement(58088)
                  /note="TATA: GATAAAA"
promoter          complement(58568)
                  /note="TATA: TATTAAA before BFLF1, BFL1 promoter gives
                  2.3kb early RNA"
promoter          58832
                  /note="TATA: TATAAAA before BFRF1"
CDS               58891..59901
                  /note="BFRF1 early reading frame, 1 NXT/S, homologous to
                  HFLF4 in CMV;  NCBI gi: 59091"
                  /codon_start=1
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                  RTTMQFLVFQAANAQKASRVMDMISDMSQQLSRSGQVEDTGARVTGGGGPRPGVTHSG
                  CLGDSHVRGRGGWDLDNFSEAETEDEASYAPWRDKDSWSESEAAPWKKELVRHPIRRH
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CDS               59610..61583
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                  CMV;  NCBI gi: 583886"
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                     VERPGGLVRWARSQTSPSSLTLAPHLGPSLLSLSVVTGGGCGAVAFCNAFFLAYFLVV
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     promoter        complement(61062)
                     /note="TATA: GATAAAA"
     promoter        61344
                     /note="TATA: TATTTAA before BFRF3"
     CDS             61456..62037
                     /note="BFRF3 early reading frame;  NCBI gi: 583887"
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                     ATAAASAAAAVDTGSGGGGQPHDTAPRGARKKQ"
     misc_feature    complement(62068)
                     /note="polyA signal: AATAAA"
     misc_feature    62069
                     /note="polyA signal: AATAAA, 3' end of 10, 6.5, 3.7, 3.4,
                     3.1, 2.5 and 0.8kb early RNAs"
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     misc_feature    62430..62477
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     misc_feature    66121
                     /note="BAM: BamH1 Q/U"
     mRNA            67477..67649
                     /note="Exon in EBNA-1 RNA (Speck and Strominger,1985) and
                     cDNA clone T4 (Bodescot et al, 1986)"
     misc_feature    69410
                     /note="BAM: BamH1 U/P"
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                     /note="9 x 15bp repeat"
     promoter        70750
                     /note="TATA: CATAAAA"
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                     21;  NCBI gi: 59096"
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                     TNRYPWAAAGQGQPTAADIKAMAVELVEHSGGGAGGGEGEESGGGLFHRPESLSSVVA
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promoter        complement(72192)
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misc_feature    73468
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promoter        75017
                /note="TATA: TATTTAA BO-R1 late promoter before BORF1,
                gives 3.9kb late RNA"
CDS             75238..76332
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promoter        complement(75322)
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misc_feature    75838
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promoter        76169
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                gives 2.8kb RNA"
misc_feature    complement(76300)
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CDS             76407..78887
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                19 VZV;  NCBI gi: 59097"
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                LQPSRKSVATCNLANICLPRCLVNAPLAVRAQRADTQGDELLLALPRLSVTLPGEGAV
                GDGFSLARLRDATQCATFVVACSILQGSPTYDSRDMASMGLGVQGLADVFADLGWQYT
                DPPSRSLNKEIFEHMYFTALCTSSLIGLHTRKIFPGFKQSKYAGGWFHWHDWAGTDLS
                IPREIWSRLSERIVRDGLFNSQFIALMPTSGCAQVTGCSDAFYPFYANASTKVTNKEE
                ALRPNRSFWRHVRLDDREALNLVGGRVSCLPEALRQRYLRFQTAFDYNQEDLIQMSRD
                RAPFVDQSQSHSLFLREEDAARASTLANLLVRSYELGLKTIMYYCRIEKAADLGVMEC
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                KASAALSVPREEQNERSPAEQMPPRPMEPAQVAGPVDIMSKGPGEGPGGWCVPGGLEV
                CYKYRQLFSEDDLLETDGFTERACESCQ"
misc_feature    77835
                /note="BAM: Bam H1 O/a"
promoter        78804
                /note="TATA: TATAAGT Ba-R1 early promoter before BaRF1,
                gives 3.5kb RNA"
misc_feature    78883
                /note="polyA signal: AATAAA, end of 3.9kb late RNA from
                75017 and 2.8kb early RNA from 76169"
misc_feature    complement(78896)
                /note="polyA signal: AATAAA"
CDS             78900..79808
                /note="BaRF1 early reading frame, homologous to HSV 38K
                ribonucleotide reductase (Gibson et al, 1984) and RF 18
                VZV;  NCBI gi: 59098"
                /codon_start=1
                /translation="MSKLLYVRDHEGFACLTVETHRNRWFAAHIVLTKDCGCLKLLNE
                RDLEFYKFLFTFLAMAEKLVNFNIDELVTSFESHDIDHYYTEQKAMENVHGETYANIL
                NMLFDGDRAAMNAYAEAIMADEALQAKISWLRDKVAAAVTLPEKILVFLLIEGIFFIS
                SFYSIALLRVRGLMPGICLANNYISRDELLHTRAASLLYNSMTAKADRPRATWIQELF
                RTAVEVETAFIEARGEGVTLVDVRAIKQFLEATADRILGDIGQAPLYGTPPPKDCPLT
                YMTSIKQTNFFEQESSDYTMLVVDDL"
promoter        complement(79495)
                /note="TATA: TATAACA"
misc_feature    79537
                /note="BAM: Bam H1 a/M"
promoter        79840
                /note="TATA: CATAAAT BM-R1 early promoter before BMRF1,
                gives 2.5kb RNA"
CDS             79899..81113
                /note="BMRF1 early reading frame. Early antigen protein
                recognised by R3 monoclonal (Pearson et al 1983; Cho et
                al, 1985a);  NCBI gi: 59099"
                /codon_start=1
                /translation="METTQTLRFKTKALAVLSKCYDHAQTHLKGGVLQVNLLSVNYGG
                PRLAAVANAGTAGLISFEVSPDAVAEWQNHQSPEEAPAAVSFRNLAYGRTCVLGKELF
                GSAVEQASLQFYKRPQGGSRPEFVKLTMEYDDKVSKSHHTCALMPYMPPASDRLRNEQ
                MIGQVLLMPKTASSLQKWARQQGSGGVKVTLNPDLYVTTYTSGEACLTLDYKPLSVGP
                YEAFTGPVAKAQDVGAVEAHVVCSVAADSLAAALSLCRIPAVSVPILRFYRSGIIAVV
                AGLLTSAGDLPLDLSVILFNHASEEAAASTASEPEDKSPRVQPLGTGLQQRPRHTVSP
                SPSPPPPPRTPTWESPARPETPSPAIPSHSSNTALERPLAVQLARKRTSSEARQKQKH
                PKKVKQAFNPLI"
promoter        80779
                /note="TATA: TATTTAA BM-R2 late promoter before BMRF2"
misc_feature    complement(80782)
                /note="polyA signal: AATAAA"
promoter        80832
                /note="TATA: GATAAAA, possible promoter for 1.4kb late RNA
                encoding BMRF2"
CDS             81118..82191
                /note="BMRF2 early reading frame;  NCBI gi: 59100"
                /codon_start=1
                /translation="MFSCKQHLSLGACVFCLGLLASTPFIWCFVFANLLSLEIFSPWQ
                THVYRLGFPTACLMAVLWTLVPAKHAVRAVTPAIMLNIASALIFFSLRVYSTSTWVSA
                PCLFLANLPLLCLWPRLAIEIVYICPAIHQRFFELGLLLACTIFALSVVSRALEVSAV
                FMSPFFIFLALGSGSLAGARRNQIYTSGLERRRSIFCARGDHSVASLKETLHKCPWDL
                LAISALTVLVVCVMIVLHVHAEVFFGLSRYLPLFLCGAMASGGLYLGHSSIIACVMAT
                LCTLTSVVVYFLHETLGPLGKTVLFISIFVYYFSGVAALSAAMRYKLKKFVNGPLVHL
                RVVYMCCFVFTFCEYLLVTFIKS"
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promoter        81751
                /note="TATA: CATAAAT"
misc_feature    82180
                /note="polyA signal: ATTAAA, end of 3.5kb early RNA from
                78804, 2.5kb early RNA from 79840 and 1.4kb late RNA"
promoter        complement(82311)
                /note="TATA: CATAAAT"
repeat_region   82319..82461
                /note="2x71bp repeats"
CDS             complement(82743..84122)
                /note="BMLF1 early reading frame. Diffuse early antigen
                (Cho et al, 1985b). Also homologous to RF 4 VZV and IE63
                of HSV.(BSLF2 + BMLF1) is also called EB2
                (Chevallier-Greco et al, 1986). General transactivator of
                transcription (Lieberman et al, 1986).  NCBI gi: 583888"
                /codon_start=1
                /translation="XSHILELEAVSDTNTDCDLDPMEGSEEHSTDGEISSSEEEDEDP
                TPAHAIPARPSSVVITPTSASFVIPRKKWDLQDKTVTLHRSPLCRDEDEKEETGNSSY
                TRGHKRRRGEVHGCTDESYGKRRHLPPGARAPRAPRAPRVPRAPRSPRAPRSNRATRG
                PRSESRGAGRSTRKQARQERSQRPLPNKPWFDMSLVKPVSKITFVTLPSPLASLTLEP
                IQDPFLQSMLAVAAHPEIGAWQKVQPRHELRRSYKTLREFFTKSTNKDTWLDARMQAI
                QNAGLCTLVAMLEETIFWLQEITYHGDLPLAPAEDILLACAMSLSKVILTKLKELAPC
                FLPNTRDYNFVKQLFYITCATARQNKVVETLSSSYVKQPLCLLAAYAAVAPAYINANC
                RRRHDEVEFLGHYIKNYNPGTLSSLLTEAVETHTRDCRSASCSRLVRAILSPGTGSLG
                LFFVPGLNQ"
misc_feature    complement(82747)
                /note="polyA signal: AATAAA"
repeat_region   83640..83729
                /note="10x9bp repeats"
misc_feature    complement(84122)
                /note="ACCEPT: CTCCCCTCTGCAG acceptor in spliced form of
                BMLF1 RNA"
misc_feature    complement(84227)
                /note="DONOR: CAGGTAAGA donor in spliced form of BMLF1
                RNA"
CDS             complement(84229..84288)
                /note="BSLF2 early reading frame in 5′ exon of spliced RNA
                encoding BMLF1;  NCBI gi: 59102"
                /codon_start=1
                /translation="MVPSQRLSRTSSISSNEDPA"
misc_feature    84233
                /note="BAM: Bam H1 M/S"
CDS             complement(84257..86881)
                /note="BSLF1 reading frame, homologous to RF 6 VZV;  NCBI
                gi: 59103"
                /codon_start=1
                /translation="MSAPVVIKALVASNTDIAEAILDAILSRPDEGFRLFCLCHNASP
                LHHVAGSLVELQLHLPKKRLTSQSRCGLVLTLHLPAEEAFPFLRGLTPLTADRLSTYL
                DRAGALRSLTPLVELLTLSAKKQPQGDARGRVAWLRPKIVGCLRRIYRVNISARWFIS
                TFGSHEAQFVLVTAAYYFWGIPCTIETLAHLTELFTSESGQSLAAVTSLAELGEVFGS
                SAWAEQTEAFAHFAHEKLRRDSREIRAVARTIDAYRGRLPLASADLVRYVYLAHAQCF
                NEGTFKRYSQLTSMGEIGCLPSGGVVLPSLLDRGFAEHMRTYFTRETYLAEHVRVQQL
                KIRMEPPAPYTWDPDPDDGLMRAWAGLSVDVARELVELARWHADEGPTYPPTLQGFLC
                LAGQATCRGQWNPKEQFLPPTVLRRVQRLPVFLCHFADRHYFVMTAADPFSSHLAEVV
                STPTNCRLPDTCLTRALSYTPVYYSQNSLSEQLFVSRHEYFNPRLPVCNLVLDLDLKI
                KGAPWSLEEIYDLCRTVRREVLRLMRRLGPVSRAHPVYFFKSACPPADPDNMEDVLPF
                CICTGKLGFRVITPLPRGHAIVGTSAVQGFVSVLQKLMGLTACLRRMRHKIKEIGAPL
                FDSGVYHAGRCIRLPHTYKVDRGGGLSRQLRLFVCHPEEEDKHSYVKNALNIQNLLHH
                SLHVGWPAPKTFCYHIADDGRDYLIQRTRETLPPTVENVCAMIEGHLGLDLVAWVSSC
                IWPSLMSTLATAVPEDKFPQFLHVTFEQTGPNLVQVCHARGRNFACLRHTHRASSKNV
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                RVFLVLYYTSQAITVTFMSQCFAGRCGANQPTAHFSISVPASRIINRAEASQDSTTSQ
                LARRRDRQDGSFSETLPN"
promoter        complement(84356)
                /note="TATA: CATAAAT before BSLF2 and BMLF1. Two RNAs
                start here; one is spliced and the other is unspliced,
                both traverse BMLF1."
promoter        86882
                /note="TATA: TATTTAA BS-R1 late promoter before BSRF1"
CDS             86924..87580
                /note="BSRF1 reading frame;  NCBI gi: 59104"
                /codon_start=1
                /translation="MAFYLPDWSCCGLWLFGRPRNRYSQLPEEPETFECPDRWRAEID
                LGLPPGVQVGDLLRNEQTMGSLRQVYLLAVQANSITDHLKRFDAVRVPESCRGVVEAQ
                VAKLEAVRSVIWNTMISLAVSGIEMDENGLKALLDKQAGDSLALMEMEKVATALKMDE
                TGAWAQEISAVVSSVTAPSASAPFINSAFEPEVPTPVLAPPPVVRQPEHSGPTELALT
                "
misc_feature    complement(87134)
                /note="polyA signal: AATAAA"
misc_feature    87599
                /note="polyA signal: AATAAA"
misc_feature    complement(87613)
                /note="polyA signal: AATAAA, end 1.0kb early RNA from
                BLL3"
CDS             complement(87638..88474)
                /note="BLLF3 early reading frame (BLLF2 in Baer et al,
                1984). Homologous to RF 8 VZV and dUTPase HSV.  NCBI gi:
                59105"
                /codon_start=1
                /translation="MEACPHIRYAFQNDKLLLQQASVGRLTLVNKTTILLRPMKTTTV
                DLGLYARPPEGHGLMLWGSTSRPVTSHVGIIDPGYTGELRLILQNQRRYNSTLRPSEL
                KIHLAAFRYATPQMEEDKGPINHPQYPGDVGLDVSLPKDLALFPHQTVSVTLTVPPPS
                IPHHRPTIFGRSGLAMQGILVKPCRWRRGGVDVSLTNFSDQTVFLNKYRRFCQLVYLH
                KHHLTSFYSPHSDAGVLGPRSLFRWASCTFEEVPSLAMGDSGLSEALEGRQGRGFGSS
                GQ"
misc_feature    87650
                /note="BAM: Bam H1 S/L"
promoter        88507
                /note="TATA: TATATAT BL-R1 late promoter before BLRF1,
                gives 1.0kb late RNA"
promoter        88511
                /note="TATA: TATAAGA"
promoter        complement(88514)
                /note="TATA: TATATAT BL-L3 early promoter before BLLF3,
                gives 1.0kb early RNA"
CDS             88547..88855
                /note="BLRF1 late reading frame;  NCBI gi: 59106"
                /codon_start=1
                /translation="MGKVLRKPFAKAVPLLFLAATWLLTGVLPAGASSPTNAAAASLT
                EAQDQFYSYTCNADTFSPSLTSFASIWALLTLVLVIIASAIYLMYVCFNKFVNTLLTD
                "
promoter        88863
                /note="TATA: TATTTAA BL-R2 late promoter before BLRF2,
                gives 0.6kb late RNA"
CDS             88925..89413
                /note="BLRF2 late reading frame, 2 NXS/T;  NCBI gi: 59107"
                /codon_start=1
                /translation="MSAPRKVRLPSVKAVDMSMEDMAARLARLESENKALKQQVLRGG
                ACASSTSVPSAPVPPPEPLTARQREVMITQATGRLASQAMKKIEDKVRKSVDGVTTRN
                EMENILQNLTLRIQVSMLGAKGQPSPGEGTRPRESNDPNATRRARSRSRGREAKKVQI
                SD"
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misc_feature    89412
                /note="polyA signal: AATAAA, end of 1.0kb and 0.6kb late
                RNAs"
misc_feature    complement(89425)
                /note="polyA signal: AATAAA, end of 0.7kb early, 2.2kb
                late and 2.8kb late RNA"
CDS             complement(89430..92153)
                /note="BLLF1a, late reading frame, gp350 membrane antigen,
                36 NXT/S (Hummel et al, 1984; Biggin et al, 1984; Beisel
                et al, 1985);  NCBI gi: 59110"
                /codon_start=1
                /translation="MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA
                DVNVTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLLELLGAGEL
                ALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPYI
                KWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEI
                SQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLG
                NNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVP
                MVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDIT
                VSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGFADPNTTTGLPS
                STHVPTNLTAPASTGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTS
                STSPVTTPTPNATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPT
                PNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPTSAVTTPTPNATGPTVGETSPQAN
                ATNHTLGGTSPTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSD
                NSTSHMPLLTSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTST
                KPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKANSTTGGKHTTGHGARTSTE
                PTTDYGGDSTTPRPRYNATTYLPPSTSSKLRPRWTFTSPPVTTAQATVPVPPTSQPRF
                SNLSMLVLQWASLAVLTLLLLLVMADCAFRRNLSTSHTYTTPPYDDAETYV"
CDS             complement(89430..92153)
                /note="BLLF1b, late reading frame gp220 membrane antigen,
                spliced form of BLLF1a (Hummel et al, 1984; Biggin et al,
                1984; Beisel et al, 1985);  NCBI gi: 59109"
                /codon_start=1
                /translation="MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA
                DVNVTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENATNLFLLELLGAGEL
                ALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPYI
                KWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEI
                SQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLG
                NNSILYVFYSGNGPKASGGDYCIQSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVP
                MVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDIT
                VSGLGTAPKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGFADPNTTTGLPS
                STHVPTNLTAPASTGPTVSTADVTSPTPAGTTSGASPVTPSPSPWDNGTESKAPDMTS
                STSPVTTPTPNATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPT
                PNATSPTLGKTSPTSAVTTPTPNATSPTLGKTSPTSAVTTPTPNATGPTVGETSPQAN
                ATNHTLGGTSPTPVVTSQPKNATSAVTTGQHNITSSSTSSMSLRPSSNPETLSPSTSD
                NSTSHMPLLTSAHPTGGENITQVTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTST
                KPGEVNVTKGTPPQNATSPQAPSGQKTAVPTVTSTGGKANSTTGGKHTTGHGARTSTE
                PTTDYGGDSTTPRPRYNATTYLPPSTSSKLRPRWTFTSPPVTTAQATVPVPPTSQPRF
                SNLSMLVLQWASLAVLTLLLLLVMADCAFRRNLSTSHTYTTPPYDDAETYV"
promoter        complement(89434)
                /note="TATA: TATAAAG"
CDS             complement(89567..90013)
                /note="BLLF2 early reading frame (BLLF3 in Baer et al,
                1984);  NCBI gi: 59108"
                /codon_start=1
                /translation="MCPPVRQHPAQAPPAKRQALETVPHPQNRGRLMSPKARPPKMQR
                RPRPPVAKRRRFPRSPQQVERPILPPVESTPQDMEPGQVQSPPQITAVIQLRQDRDTM
                RPPIYLPALLANCGPAGLLRAHRLPQPKPPCQSRQRPSPDSQTSPC"
promoter        complement(90051)
                /note="TATA: TATAACA BL-L2 early promoter before BLLF2,
                gives 0.7kb early RNA"
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intron          complement(90062..90652)
                /note="intervening sequence in gp220 gene"
repeat_region   90177..90639
                /note="21 copies of 21bp approximate repeat"
promoter        complement(92192)
                /note="TATA: TATTAAA BL-L1 late promoter before BLLF1a,b.
                Gives 2.8 and 2.2kb late RNAs"
mRNA            92238..92581
                /note="Exon in Bodescot et al (1986) RNA (spliced from
                20763 to 92670)"
CDS             92243..92581
                /note="BLRF3 reading frame;  NCBI gi: 59111"
                /codon_start=1
                /translation="MDKDRPGPPALDDNMEEEVPSTSVVQEQVSAGDWENVLIELSDS
                SSEKEAEDAHLEPAQKGTKRKRVDHDAGGSAPARPMLPPQPDLPGREAILRRFPLDLR
                TLLQAIGAAAT"
CDS             92670..95165
                /note="BERF1 frame, homology with BERF2b and BERF4. A
                fusion of BLRF3 with BERF1 encodes EBNA-3A, latent cycle
                gene. (Hennessy et al, 1986, Joab et al, 1987);  NCBI gi:
                583889"
                /codon_start=1
                /translation="XIDTRAIDQFFGSQISNTEMYIMYAMAIRQAIRDRRRNPASRRD
                QAKWRLQTLAAGWPMGYQAYSSWMYSYTDHQTTPTFVHLQATLGCTGGRRCHVTFSAG
                TFKLPRCTPGDRQWLYVQSSVGNIVQSCNPRYSIFFDYMAIHRSLTKIWEEVLTPDQR
                VSFMEFLGFLQRTDLSYIKSFVSDALGTTSIQTPWIDDNPSTETAQAWNAGFLRGRAY
                GIDLLRTEGEHVEGATGETREESEDTESDGDDEDLPCIVSRGGPKVKRPPIFIRRLHR
                LLLMRAGKRTEQGKEVLEKARGSTYGTPRPPVPKPRPEVPQSDETATSHGSAQVPEPP
                TIHLAAQGMAYPLHEQHGMAPCPVAQAPPTPLPPVSPGDQLPGVFSDGRVACAPVPAP
                AGPIVRPWEPSLTQAAGQAFAPVRPQHMPVEPVPVPTVALERPVYPKPVRPAPPKIAM
                QGPGETSGIRRARERWRPAPWTPNPPRSPSQMSVRDRLARLRAEAQVKQASVEVQPPQ
                LTQVSPQQPMEGPLVPEQQMFPGAPFSQVADVVRAPGVPAMQPQYFDLPLIQPISQGA
                PVAPLRASMGPVPPVPATQPQYFDIPLTEPINQGASAAHFLPQQPMEGPLVPEQWMFP
                GAALSQSVRPGVAQSQYFDLPLTQPINHGAPAAHFLHQPPMEGPWVPEQWMFQGAPPS
                QGTDVVQHQLDALGYTLHGLNHPGVPVSPAVNQYHLSQAAFGLPIDEDESGEGSDTSE
                PCEALDLSIHGRPCPQAPEWPVQEEGGQDATEVLDLSIHGRPRPRTPEWPVQGEGGQN
                VTGPETRRVVVSAVVHMCQDDEFPDLQDPPDEA"
mRNA            92670..95248
                /note="Exon in (Bodescot et al, 1986) RNA from 92581, to
                3' end"
misc_feature    92703
                /note="BAM: Bam H1 L/E"
promoter        complement(93161)
                /note="TATA: CATAAAT"
promoter        93479
                /note="TATA: TATAAGA"
promoter        complement(93482)
                /note="TATA: TATAAAT"
repeat_region   94208..94277
                /note="repeat type A"
repeat_region   94281..94306
                /note="repeat type B"
repeat_region   94307..94381
                /note="repeat type C"
repeat_region   94386..94411
                /note="repeat type B"
repeat_region   94412..94489
                /note="repeat type C"
repeat_region   94490..94560
                /note="repeat type A"
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repeat_region   94571..94648
                /note="repeat type C"
repeat_region   94649..94719
                /note="repeat type A"
repeat_region   94896..94982
                /note="repeat type D"
repeat_region   94983..95069
                /note="repeat type D"
misc_feature    95221
                /note="polyA signal: AATAAA"
misc_feature    complement(95272)
                /note="polyA signal: AATAAA"
CDS             95353..95724
                /note="BERF2a reading frame;  NCBI gi: 59113"
                /codon_start=1
                /translation="MKKAWLSRAQQADAGGASGSEDPPDYGDQGNVTQVGSEPISPEI
                GPFELSAASEDDPQSGPVEENLDAAAREEEEPHEQEHNGGDDPLDVHTRQPRFVDVNP
                TQAPVIQLVHAVYDSMLVRGT"
CDS             95725..98247
                /note="BERF2b frame, homology with BERF1 and BERF4. BERF2a
                and BERF2b are spliced together to make EBNA3B (EBNA4A)
                latent protein.  NCBI gi: 583890"
                /codon_start=1
                /translation="XISRCFAWIFWPVLIDCHWFQQSDLRPLGSLFLEQNLNIEEFIW
                MCMTVRHRCQAIRKKPLPIVKQRRWKLLSSCRSWRMGYRTHNLKVNSFESGGDNVHPV
                LVTATLGCDEGTRHATTYSAGIVQIPRISDQNQKIETAFLMARRARSLSAERYTLFFD
                LVSSGNTLYAIWIGLGTKNRVSFIEFVGWLCKKDHTHIREWFRQCTGRPKAAKPWLRA
                HPVAIPYDDPLTNEEIDLAYARGQAMNIEAPRLPDDPIIVEDDDESEEIEAESDEEED
                KSGMESLKNIPQTLPYNPTVYGRPAVFDRKSDAKSTKKCRAIVTDFSVIKAIEEEHRK
                KKAARTEQPRATPESQAPTVVLQRPPTQQEPGPVGPLSVQARLEPWQPLPGPQVTAVL
                LHEESMQGVQVHGSMLDLLEKDDEVMEQRVMATLLPPVPQQPRAGRRGPCVFTGDLGI
                ESDEPASTEPVHDQLLPAPGPDPLEIQPLTSPTTSQLSSSAPSCAQTPWPVVQPSQTP
                DDPTKQSRPPETAAPRQWPMPLRPIPMRPLRMQPIPFNHPVGPTPHQTPQVEITPYKP
                TWAQIGHIPYQPTPTGPATMLLRQWAPATMQTPPRAPTPMSPPEVPPVPRQRPRGAPT
                PTPPPQVPPVPRQRPRGAPTPTPPPQVLPTPMQLALRAPAGQQGPTKQILRQLLTGGV
                KKGRPSLKLQAALERQAAAGWQPSPGSGTSDKIVQAPIFYPPVLQPIQVMGQGGSPTA
                MAASAVTQAPTEYTRERRGVGPMPPTDIPPSKRAKIEAYTEPEMPHGGASHSPVVILE
                NVGQGQQQTLECGGTAKQERDMLGLGDIAVSSPSSSETSNDE"
misc_feature    complement(95819)
                /note="polyA signal: AATAAA"
promoter        complement(95853)
                /note="TATA: TATAAAT"
misc_feature    complement(96276)
                /note="polyA signal: AATAAA"
repeat_region   97522..97698
                /note="3x60bp repeat"
CDS             98323..98769
                /note="BERF3 reading frame;  NCBI gi: 59115"
                /codon_start=1
                /translation="MTILDEVEILHIFRPTMESFEGQGDSRQSPDNERGDNVQTTGEH
                DQDPGPGPPSSGASERLVPEESYSRDQQPWGQSRGDENRGWMQRIRRRRRRRAALSGH
                LLDTEDNVPPWLPPHDITPYTARNIRDAACRAVKVSMPLTGFMGAI"
mRNA            98364..98730
                /note="Exon in EBNA-1 RNA (Speck and Strominger, 1985)"
misc_feature    98731
                /note="DONOR: AAGGTGAGT donor"
CDS             98805..101423
                /note="BERF4 frame, homology with BERF1 and BERF2b. BERF3
                and BERF4 are spliced together to make the EBNA3C (EBNA
                4B) latent protein.  NCBI gi: 583891"
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                /codon_start=1
                /translation="XSHLQALSNLILDSGLDTQHILCFVMAARQRLQDIRRGPLVAEG
                GVGWRHWLLTSPSQSWPMGYRTATLRTLTPVPNRVGADSIMLTATFGCQNAARTLNTF
                SATVWTPPHAGPREQERYAREAEVRFLRGKWQRRYRRIYDLIELCGSLHHIWQNLLQT
                EENLLDFVRFMGVMSSCNNPAVNYWFHKTIGNFKPYYPWNAPPNENPYHARRGIKEHV
                IQNAFRKAQIQGLSMLATGGEPRGDATSETSSDEDTGRQGSDVELESSDDELPYIDPN
                MEPVQQRPVMFVSRVPAKKPRKLPWPTPKTHPVKRTNVKTSDRSDKAEAQSTPERPGP
                SEQSSVTVEPAHPTPVEMPMVILHQPPPVPKPVPVKPTPPPSRRRRGACVVYDDDVIE
                VIDVETTEDSSSVSQPNKPHRKHQDGFQRSGRRQKRAAPPTVSPSDTGPPAVGPPAAG
                PPAAGPPAAGPPAAGPPAAGPPAAGPRILAPLSAGPPAAGPHIVTPPSARPRIMAPPV
                VRMFMRERQLPQSTGRKPQCFWEMRAGREITQMQQEPSSHLQSATQPTTPRPSWAPSV
                CALSVMDAGKAQPIESSHLSSMSPTQPISHEEQPRYEDPDAPLDLSLHPDVAAQPAPQ
                APYQGYQEPPAPQAPYQGYQEPPPPQAPYQGYQEPPAHGLQSSSYPGYAGPWTPRSQH
                PCYRHPWAPWSQDPVHGHTQGPWDPRAPHLPPQWDGSAGHGQDQVSQFPHLQSETGPP
                RLQLSLVPLVSSSAPSWSSPQPRAPIRPIPTRFPPPPMPLQDSMAVGCDSSGTACPSM
                PFASDYSQGAFTPLDINATTPKRPRVEESSHGPARCSQATAEAQEILSDNSEISVFPK
                DAKQTDYDASTESELD"
mRNA            98805..99050
                /note="Exon in T4 cDNA (Bodescot et al 1986). 99050 is not
                the end of the RNA."
misc_feature    99126..102118
                /note="DEL: Deletion in Raji"
promoter        99443
                /note="TATA: CATAAAA"
misc_feature    100104
                /note="DONOR: ACCGTGAGT possible donor before repeat."
repeat_region   100122..100304
                /note="10 x 15bp repeat"
misc_feature    100528
                /note="DONOR: CTGGTAAGG possible donor"
misc_feature    100613
                /note="BAM: Bam H1 E/e1"
repeat_region   100665..100781
                /note="3x39bp repeat"
promoter        complement(100860)
                /note="TATA: TATAACA"
misc_feature    100919
                /note="BAM: Bam H1 e1/e2"
misc_feature    101426
                /note="BAM: Bam H1 e2/e3"
CDS             complement(101445..102116)
                /note="BZLF2 reading frame 3x NXT/S. 2.5kb late RNA
                traverses BZLF2, ends unknown.  NCBI gi: 59117"
                /codon_start=1
                /translation="MVSFKQVRVPLFTAIALVIVLLLAYFLPPRVRGGGRVAAAAITW
                VPKPNVEVWPVDPPPPVNFNKTAEQEYGDKEVKLPHWTPTLHTFQVPQNYTKANCTYC
                NTREYTFSYKGCCFYFTKKKHTWNGCFQACAELYPCTYFYGPTPDILPVVTRNLNAIE
                SLWVGVYRVGEGNWTSLDGGTFKVYQIFGSHCTYVSKFSTVPVSHHECSFLKPCLCVS
                QRSNS"
promoter        101690
                /note="TATA: CATAAAA"
misc_feature    101765
                /note="polyA signal: AATAAA"
promoter        complement(101786)
                /note="TATA: TATAAAG"
misc_feature    101947
                /note="BAM: Bam H1 e3/Z"
misc_feature    complement(102098)
                /note="DONOR: CAGGTGAGG possible donor"
mRNA            complement(102126..102341)
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                     /note="3' terminal exon of 0.9kb and 2.8kb early RNAs"
promoter             102153
                     /note="TATA: TATTAAT"
misc_feature         complement(102156)
                     /note="polyA signal: AATAAA 3' end of 0.9kb and 2.8kb RNAs
                     encoding BZLF1 and BRLF1"
promoter             complement(102160)
                     /note="TATA: TATTAAT"
CDS                  complement(102213..103155)
                     /note="BZLF1 reading frame, modified from Baer et al,
                     1984. Has two splices within frame. 2xNXT/S. Immediate
                     early gene which disrupts latency (Countryman and Miller,
                     1985), called EB1 by Chevallier-Greco et al, 1986 and
                     ZEBRA by Miller."
                     /codon_start=1
promoter             complement(102380)
                     /note="TATA: CATAAAT"
promoter             102415
                     /note="TATA:TATATAC"
promoter             complement(102420)
                     /note="TATA: TATATAC"
mRNA                 complement(102426..102530)
                     /note="Exon of 0.9kb and 2.8kb early RNAs"
misc_feature         complement(102504)
                     /note="polyA signal: AATAAA, apparently not functional"
repeat_region        102581..102652
                     /note="semi-repetitive sequence, homologous to human c-fos
                     3' sequence"
mRNA                 complement(102655..103194)
                     /note="First exon of 0.9kb early RNA encoding BZLF1"
misc_feature         complement(102918)
                     /note="splice acceptor used in RZ fusion gene (Sargeant)"
promoter             complement(103231)
                     /note="TATA: TTTAAA of BZL1 immediate early promoter gives
                     0.9kb RNA"
misc_feature         complement(103256..103311)
                     /note="Upstream of BZL1, homology to 106243 to 106188"
CDS                  complement(103366..105183)
                     /note="BRLF1 reading frame, (immediate?) early gene, acts
                     as transcription activator.  NCBI gi: 59119"
                     /codon_start=1
                     /translation="MRPKKDGLEDFLRLTPEIKKQLGSLVSDYCNVLNKEFTAGSVEI
                     TLRSYKICKAFINEAKAHGREWGGLMATLNICNFWAILRNNRVRRRAENAGNDACSIA
                     CPIVMRYVLDHLIVVTDRFFIQAPSNRVMIPATIGTAMYKLLKHSRVRAYTYSKVLGV
                     DRAAIMASGKQVVEHLNRMEKEGLLSSKFKAFCKWVFTYPVLEEMFQTMVSSKTGHLT
                     DDVKDVRALIKTLPRASYSSHAGQRSYVSGVLPACLLSTKSKAVETPILVSGADRMDE
                     ELMGNDGGASHTEARYSESGQFHAFTDELESLPSPTMPLKPGAQSADCGDSSSSSSDS
                     GNSDTEQSEREEARAEAPRLRAPKSRRTSRPNRGQTPCPSNAAEPEQPWIAAVHQESD
                     ERPIFPHPSKPTFLPPVKRKKGLRDSREGMFLPKPEAGSAISDVFEGREVCQPKRIRP
                     FHPPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLDPAPAVTPEASHLLEDP
                     DEETSQAVKALREMADTVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNL
                     DSPLTPELNEILDTFLNDECLLHAMHISTGLSIFDTSLF"
misc_feature         complement(103453..103462)
                     /note="TAATGAAATC sequence"
misc_feature         103741
                     /note="BAM: Bam H1 Z/g"
misc_feature         103816
                     /note="BAM: Bam H1 g/R"
mRNA                 complement(104926..105185)
                     /note="exon in RZ fusion gene (Sargeant)"
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mRNA                 complement(104927..104989)
                     /note="BRLF2 poss. small 5' exon"
promoter             105016
                     /note="TATA: TATAAAT before BRRF1, possible promoter for
                     1.1 kb early RNA encoding BRRF1"
promoter             complement(105019)
                     /note="TATA: TATAAAT before BRLF2"
CDS                  105182..106114
                     /note="BRRF1 early reading frame;  NCBI gi: 59118"
                     /codon_start=1
                     /translation="MASSNRGNARPLKSFLHELYLKHYPEVGDVVHLLNTIGVDCDLP
                     PSHPLLTAQRGLFLARVLQAVQQHKLLEDTIVPKILKKLAYFLELLSYYSPKDEQRDI
                     AEVLDHLKTNRDLGLDDRLWALIRKLRQDRHHASVNVLMPGSDYTAVSLQYYDGISIG
                     MRKVIADVCRSGYASMPSMTATHNLSHQLLMASGPSEEPCAWRGFFNQVLLWTVALCK
                     FRRCIYYNYIQGSIATISQLLHLEIKALCSWIISQDGMRLFQHSRPLLTLWESVAANQ
                     EVTDAITLPDCAEYIDLLKHTKHVLENCSAMQYK"
misc_feature         complement(105185)
                     /note="ACCEPT: splice acceptor in 2.8kb early RNA encoding
                     BRLF1 and RZ fusion gene (Sargeant)"
promoter             105213
                     /note="TATA: CATTAAA"
misc_feature         106110
                     /note="polyA signal: AATAAA, 3' end of early 1.1kb RNA
                     encoding BRRF1"
misc_feature         complement(106125)
                     /note="DONOR: CAGGTAAGA possible donor"
misc_feature         complement(106188..106243)
                     /note="Homology to upstream region of BZL1"
promoter             complement(106213)
                     /note="TATA: CATAAAA"
promoter             106243
                     /note="TATA: TATAAAA before BRRF2, possible promoter for
                     1.8 kb RNA encoding BRRF2"
CDS                  106302..107915
                     /note="BRRF2 reading frame;  NCBI gi: 59120"
                     /codon_start=1
                     /translation="MSGQQRGSVILVPEHLAGALTKLMSDFITGQDVTLSGGNIAVKI
                     RDAINQTPGGGDVAILSSLFALWNALPTSGRQSSRDDLIPAAVQALTTAHNLCLGVIP
                     GETSHKDTPESLLRAIVTGLQKLWVDSCGCPECLQCLKGLKAIKPGLYEIPRIIPHTK
                     QCSPVNLLNMLVHKLVALRGHVQLAYDARVLTPDFHEIPDLDDSDAVFARTLLAALFH
                     LNMFFILKDYITQDSMSLKQALSGHWMSATGNPLPAAPETLRDYLEAFRNSDNHFYLP
                     TTGPLNTFQFPEELLGRVVVIDSSLCAASHVQDVITHGVGAGVPRPRFSALPPAPSRE
                     PQQTCSQLTSRGNESSRRNLGQPGGTSPAVPPVCPIVSLTASGAKQNRGGMGSLHLAK
                     PEETSPAVSPVCPIASPAASRSKQHCGVTGSSQAAPSFSSVAPVASLSGDLEEEEEGS
                     RESPSLPSSKKGDEEFEAWLEAQDANLEDVQREFSGLRVIGDEDEDGSEDGEFSDLDL
                     SDSDHEGDEGGGAVGGGRSLHSLYSLSVV"
promoter             complement(106385)
                     /note="TATA: GATAAAA"
misc_feature         complement(106973)
                     /note="polyA signal: AATAAA"
promoter             complement(107124)
                     /note="TATA: GATAAAA"
misc_feature         107457
                     /note="BAM: Bam H1 R/f"
misc_feature         107565
                     /note="BAM: Bam H1 f/K"
misc_feature         107914
                     /note="polyA signal: AATAAA, 3' end of 1.8kb RNA encoding
                     BBRF2"
misc_feature         107942
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                     /note="ACCEPT: splice acceptor for EBNA-1 RNA (from
                     98730)"
     CDS             107950..109875
                     /note="BKRF1 encodes EBNA-1 protein, latent cycle gene.
                     NCBI gi: 59121"
                     /codon_start=1
                     /translation="MSDEGPGTGPGNGLGEKGDTSGPEGSGGSGPQRRGGDNHGRGRG
                     RGRGRGGGRPGAPGGSGSGPRHRDGVRRPQKRPSCIGCKGTHGGTGAGAGAGGAGAGG
                     AGAGGGAGAGGGAGGAGGAGGAGAGGGAGAGGGAGGAGGAGAGGGAGAGGGAGGAGAG
                     GGAGGAGGAGAGGGAGAGGGAGGAGAGGGAGGAGGAGAGGGAGAGGAGGAGGAGAGGA
                     GAGGGAGGAGGAGAGGAGAGGAGAGGAGAGGAGGAGAGGAGGAGAGGAGGAGAGGGAG
                     GAGAGGGAGGAGAGGAGGAGAGGAGGAGAGGAGGAGAGGGAGAGGAGAGGGGRGRGGS
                     GGRGRGGSGGRGRGGSGGRRGRGRERARGGSRERARGRGRGRGEKRPRSPSSQSSSSG
                     SPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGP
                     RGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVF
                     VYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFL
                     QTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLPPWFPPMVEGAAAEGDDG
                     DDGDEGGDGDEGEEGQE"
     repeat_region   108217..108924
                     /note="EBNA triplet repeat GGA,GCA,GGG."
     misc_feature    109856
                     /note="DONOR: AGGGTGAGG possible donor at end BKRF1"
     promoter        109905
                     /note="TATA: TATTAAA before BKRF2, possible start for
                     2.3kb late RNA"
     misc_feature    109906
                     /note="polyA signal: ATTAAA"
     misc_feature    109937
                     /note="polyA signal: AATAAA 3' end of EBNA-1 RNA"
     CDS             109958..110371
                     /note="BKRF2 reading frame;  NCBI gi: 59122"
                     /codon_start=1
                     /translation="MRAVGVFLAICLVTIFVLPTWGNWAYPCCHVTQLRAQHLLALEN
                     ISDIYLVSNQTCDGFSLASLNSPKNGSNQLVISRCANGLNVVSFFISILKRSSSALTG
                     HLRELLTTLETLYGSFSVEDLFGANLNRYAWHRGG"
     misc_feature    110271
                     /note="DONOR: TCCGTGAGT possible donor at end of BKRF2"
     CDS             110275..111120
                     /note="BKRF3 reading frame, homologous to RF 59 VZV;  NCBI
                     gi: 583892"
                     /codon_start=1
                     /translation="XVNHPGDSLRFILSGRPVWCQLKQIRMASRGLDLWLDEHVWKRK
                     QEIGVKGENLLLPDLWLDFLQLSPIFQRKLAAVIACVRRLRTQATVYPEEDMCMAWAR
                     FCDPSDIKVVILGQDPYHGGQANGLAFSVAYGFPVPPSLRNIYAELHRSLPEFSPPDH
                     GCLDAWASQGVLLLNTILTVQKGKPGSHADIGWAWFTDHVISLLSERLKACVFMLWGA
                     KAGDKASLINSKKHLVLTSQHPSPLAQNSTRKSAQQKFLGNNHFVLANNFLREKGLGE
                     IDWRL"
     misc_feature    111098
                     /note="DONOR: TCGGTGAGA possible donor at end BKRF3"
     CDS             111107..111787
                     /note="BKRF4 reading frame, contains complex repetitive
                     sequence;  NCBI gi: 583893"
                     /codon_start=1
                     /translation="XGGCRGVITMAMFLKSRGVRSCRDRRLLSDEEEETSQSSSYTLG
                     SQASQSIQEEDVSDTDESDYSDEDEEIDLEEEYPSDEDPSEGSDSDPSWHPSDSDESD
                     YSESDEDEATPGSQASRSSRVSPSTQQSSGLTPTPSFSRPRTRAPPRPPAPAPVRGRA
                     SAPPRPPAPVQQSTKDKGPHRPTRPVLRGPAPRRPPPPSSPNTYNKHMMETTPPIKGN
                     NNYNWPWL"
     misc_feature    111272
                     /note="DONOR: GACGTGAGT poss.donor before rpt.seq. in
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                     BKRF4"
     misc_feature    111719
                     /note="polyA signal: AATAAA"
     misc_feature    111787
                     /note="polyA signal: AATAAA : currently unknown which is
                     3' end of the 2.3kb late and 1.1kb early RNAs"
     CDS             complement(111830..114259)
                     /note="BBLF4 early reading frame, very good homology to
                     RF55 VZV;  NCBI gi: 59126"
                     /codon_start=1
                     /translation="MAEEPRAPEALSSTFMLNMTSDASVRRIVRRIGTLARRRVQQLP
                     DMETFSPEFDPELSEPPFLPFSAYVITGTAGAGKSTSVSCLHHTMDCLVTGATTVAAQ
                     NLSQTLRAYCPTVYSAFGFKSRHINMTQRVSSHGRSTDAALEELQRRDLAKYWPVLSD
                     IAAEFRRTKPRGLYSGVSGPAFEVLRDMHQGQLWTTNVIVVDEAGTLSVHILTAVVFC
                     YWFFNAWLRTPLYRRGRIPCIVCVGSPTQTDAFQSSFSHETQVNKIRECDNILTFLVG
                     NPRAATYVDVARNWALFINNKRCTDVQFGHLMKTLEYGLELSPDILAYVDRFVVPRAA
                     IMDPAQYVGWTRLFLSHAEVKTFLTTLHATLKTAGQGRAARGTGGDGGGVTMFTCPVE
                     CEVFLDPLAQYKTLVGLPGLTAHTWLQKNYARLGNYSQFADQDMVPVGTEQDEERVKV
                     TYNVTYVKHSSVSVNCKTKKSICGYTGTFGDFMDTLEADSFVEAHGHEQPEYVYSFLA
                     RLIYGGIYAFSHGGHSLCENGEYVAELGAVPLPGRTWDPEVTAGMELGELPLEVAWDG
                     ERSPAAVFYARVLAPPAANSAPLCSLLNIYNDLRAYFRQCLDVAVRYGGREFRDLPFC
                     TFTNNMLIRDNIEFTSDEPLLHGLLDYASTTENYTLLGYTHLNVFFGIRGKQQPQDAG
                     SSRMPRLMVKDEAGFVCCLEHNTNKLYETIEDKSLNLCSIRDYGISSKLAMTIAKAQG
                     LSLNKVAICFGSHRNIKPGHVYVALSRARHSNCVVMDRNPLSEMITGEGNPASGYIVD
                     ALKNSRALLVY"
     misc_feature    complement(111830)
                     /note="polyA signal: AATAAA"
     promoter        112471
                     /note="TATA: TATATAT"
     promoter        complement(112476)
                     /note="TATA: TATATAA"
     misc_feature    112620
                     /note="BAM: Bam H1 K/B"
     promoter        113876
                     /note="TATA: TATTTAT before BBRF1"
     promoter        complement(113885)
                     /note="TATA: CATAAAT"
     CDS             114204..116045
                     /note="BBRF1 late reading frame, homologous to RF 54 VZV;
                     NCBI gi: 59125"
                     /codon_start=1
                     /translation="MFNMNVDESASGALGSSAIPVHPTPASVRLFEILQGKYAYVQGQ
                     TIYANLRNPGVFSRQVFTHLFKRAISHCTYDDVLHDWNKFEACIQKRWPSDDSCASRF
                     RESTFESWSTTMKLTVRDLLTTNIYRVLHSRSVLSYERYVDWICATGMVPAVKKPITQ
                     ELHSKIKSLRDRCVCRELGHERTIRSIGTELYEATKEIIESLNSTFIPQFTEVTIEYL
                     PRSDEYVAYYCGRRIRLHVLFPPAIFAGTVTFDSPVQRLYQNIFMCYRTLEHAKICQL
                     LNTAPLKAIVGHGGRDMYKDILAHLEQNSQRKDPKKELLNLLVKLSENKTISGVTDVV
                     EEFITDASNNLVDRNRLFGQPGETAAQGLKKKVSNTVVKCLTDQINEQFDQINGLEKE
                     RELYLKKIRSMESQLQASLGPGGNNPAASAPAAVAAEAASVDILTGSTASAIEKLFNS
                     PSASLGARVSGHNESILNSFVSQYIPPSREMTKDLTELWESELFNTFKLTPVVDNQGQ
                     RLYVRYSSDTISILLGPFTYLVAELSPVELVTDVYATLGIVEIIDELYRSSRLAIYIE
                     DLGRKYCPASATGGDHGIRQAPSARGDTEPDHAKSKPARDPPPGAGS"
     CDS             115843..116784
                     /note="BBRF2 late reading frame, homologous to RF 53 VZV;
                     NCBI gi: 583894"
                     /codon_start=1
                     /translation="XSWRSSTSSTGAVAWPSTSRTSVENTAPRARPGEIMASGKHHQP
                     GGTRSLTMQKVSLRVTPRLVLEVNRHNAICVATNVPEFYNARGDLNIRDLRAHVKARM
                     ISSQFCGYVLVSLLDSEDQVDHLNIFPHVFSERMILYKPNNVNLMEMCALLSMIENAK
                     SPSIGLCREVLGRLTLLHSKCNNLDSLFLYNGARTLLSTLVKYHDLEEGAATPGPWNE
                     GLSLFKLHKELKRAPSEARDLMQSLFLTSGKMGCLARSPKDYCADLNKEEDANSGFTF
                     NLFYQDSLLTKHFQCQTVLQTLRRKCLGSDTVSKIIP"
     promoter        complement(116683)
                     /note="TATA: GATAAAA"
     misc_feature    complement(116696)
                     /note="polyA signal: AATAAA"
     CDS             complement(116781..117386)
                     /note="BBLF3 early reading frame, spliced to BBLF2. BBLF3
                     contains a consensus nucleotide binding site;  NCBI gi:
                     583895"
                     /codon_start=1
                     /translation="XFLQGVKDSEDASRLDRDVMGGEATVARRHIRVKARRGPGCLLM
                     AIFQGDLYVGGCREHSGPFLVWHEAFSWTLDQLAARPEADKAPPSHDHLLTLVRDLTR
                     RLAPGRRRNRFWALPRAWLQRLRRAGLRLSGSHVCLLDKDGARPAPCQTATEHGLSPT
                     AYFREIMAFLLDVISALHPGYTIPMEITRETDLLMTVLSLF"
     misc_feature    116785
                     /note="polyA signal: AATAAA"
     intron          complement(117386..117515)
                     /note="intron spliced out in RNA linking BBLF2 and BBLF3"
     CDS             complement(117515..119080)
                     /note="BBLF2 early reading frame, spliced to BBLF3;  NCBI
                     gi: 583896"
                     /codon_start=1
                     /translation="XDVLKGPVLLRSQTMMETPAESVRARVSSVTFYNVTQTAGRWWA
                     IWVVGIVPIKREDVETLIVVQACQPPLGGSLEPPVVNAPSTTELNFLRWERELRRSGG
                     LIAMLADAAEKDLFDLSFRTRDRRLLSAARVEDEQGLIFQPLFPAQVVCQSCSGDDGR
                     DQQPPPVDGFGSEMEGEQTCPHAQRHSESPGQLDVYIRTPRGDVFTYSTETPDDPSPV
                     PFRDILRPVTYEVDLVSSDGATGRGGDARRHRVSLKILEPAGGFESWLVNSWSMAGGG
                     LYAFLRSIYASCYANHRGTKPIFYLLDPELCPGGSDFQPYVPGFPFLPIHYVGRARPA
                     FWHRAPHSEGLLLLDLNLGVSGTPLADALLGLDARSGQRRGSLLLQQIWPPTRKEINP
                     RHVCTREGGEGGGEDETTVVGRAEATAILEADATWWLYELARCHLSARGAPVGTPDGG
                     GQARDAQTWLRALHRYGTSDTRRALGGLYTAVTRVLLHAAADLGLTWAYADEFILGFV
                     APTSAHPSEEPLAQ"
     promoter        118981
                     /note="TATA: TATAAAA BBR1 late promoter before BBRF3"
     promoter        119067
                     /note="TATA: TTTAAAA BBR2 late promoter ?"
     promoter        119098
                     /note="TATA: TATTTAA BBR3 late promoter before BBRF3"
     misc_feature    119108
                     /note="DONOR: AAGGTGAAT possible donor"
     CDS             119137..120354
                     /note="BBRF3 late reading frame;  NCBI gi: 59130"
                     /codon_start=1
                     /translation="MKSSKNDTFVYRTWVKTLVVYFVMFVMSAVVPITAMFPNLGYPC
                     YFNALVDYGALNLTNYNLAHHLTPTLYLEPPEMFVYITLVFIADCVAFIYYACGEVAL
                     IKARKKVSGLTDLSAWVSAVGSPTVLFLAILKLWSIQVFIQVLSYKHVFLSAFVYFLH
                     FLASVLHACACVTRFSPVWVVKAQDNSIPQDTFLWWVVFYLKPVVTNLYLGCLALETL
                     VFSLSVFLALGNSFYFMVGDMVLGAVNLFLILPIFWYILTEVWLASFLRHNFGFYCGM
                     FIASIILILPLVRYEAVFVSAKLHTTVAINVAIIPILCSVAMLIRICRIFKSMRQGTD
                     YVPVSETVELELESEPRPRPSRTPSPGRNRRRSSTSSSSSRSTRRQRPVSTQALVSSV
                     LPMTTDSEEEIFP"
     misc_feature    120260
                     /note="ACCEPT: ATCTTCCTCCAGGT possible acceptor"
     misc_feature    120358
                     /note="polyA signal: AATAAA"
     CDS             complement(120747..120974)
                     /note="BBLF1 late reading frame, possibly homologous to RF
                     49 VZV;  NCBI gi: 59131"
                     /codon_start=1
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                     /translation="MGALWSLCRRRVNSIGDVDGGIINLYNDYEEFNLETTKLIAAEE
                     GRACGETNEGLEYDEDSENDELLFLPNKKPN"
     misc_feature    complement(120764)
                     /note="polyA signal: AATAAA, 3' end of 0.6kb late, 1.6kb
                     early, 3.0kb early RNAs"
     CDS             complement(120929..122341)
                     /note="BGLF5 early reading frame, homologous to RF 48 VZV
                     and alkaline exonuclease of HSV;  NCBI gi: 59132"
                     /codon_start=1
                     /translation="MADVDELEDPMEEMTSYTFARFLRSPETEAFVRNLDRPPQMPAM
                     RFVYLYCLCKQIQEFSGETGFCDFVSSLVQENDSKDGPSLKSIYWGLQEATDEQRTVL
                     CSYVESMTRGQSENLMWDILRNGIISSSKLLSTIKNGPTKVFEPAPISTNHYFGGPVA
                     FGLRCEDTVKDIVCKLICGDASANRQFGFMISPTDGIFGVSLDLCVNVESQGDFILFT
                     DRSCIYEIKCRFKYLFSKSEFDPIYPSYTALYKRPCKRSFIRFINSIARPTVEYVPDG
                     RLPSEGDYLLTQDEAWNLKDVRKRKLGPGHDLVADSLAANRGVESMLYVMTDPSENAG
                     RIGIKDRVPVNIFINPRHNYFYQVLLQYKIVGDYVRHSGGGKPGRDCSPRVNIVTAFF
                     RKRSPLDPATCTLGSDLLLDASVEIPVAVLVTPVVLPDSVIRKTLSTAAGSWKAYADN
                     TFDTAPWVPSGLFADDESTP"
     promoter        complement(121331)
                     /note="TATA: TATTAAA BBL1 late promoter before BBLF1"
     promoter        121669
                     /note="TATA: CATAAAT"
     promoter        121697
                     /note="TATA: TATAAAG"
     promoter        121772
                     /note="TATA: CATAAAG"
     misc_feature    122313
                     /note="BAM: Bam H1 B/G"
     CDS             complement(122325..123692)
                     /note="BGLF4 early reading frame, homologous to RF 47 VZV;
                      NCBI gi: 583897"
                     /codon_start=1
                     /translation="XGWRSSVSRSLRPETSCDRPSSHLRNMDVNMAAELSPTNSSSSG
                     ELSVSPEPPRETQAFLGKVTVIDYFTFQHKHLKVTNIDDMTETLYVKLPENMTRCDHL
                     PITCEYLLGRGSYGAVYAHADNATVKLYDSVTELYHELMVCDMIQIGKATAEDGQDKA
                     LVDYLSACTSCHALFMPQFRCSLQDYGHWHDGSIEPLVRGFQGLKDAVYFLNRHCGLF
                     HSDISPSNILVDFTDTMWGMGRLVLTDYGTASLHDRNKMLDVRLKSSKGRQLYRLYCQ
                     REPFSIAKDTYKPLCLLSKCYILRGAGHIPDPSACGPVGAQTALRLDLQSLGYSLLYG
                     IMHLADSTHKIPYPNPDMGFDRSDPLYFLQFAAPKVVLLEVLSQMWNLNLDMGLTSCG
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                     DGRRG"
     misc_feature    complement(123506)
                     /note="DONOR: AAGGTGACT possible donor"
     CDS             complement(123941..124939)
                     /note="BGLF3 reading frame;  NCBI gi: 59135"
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                     /translation="MFNAVKADMPDDPMLARRYGQCLELALEACQDTPEQFKLVETPL
                     KSFLLVSNILPQDNRPWHEARSSGRVAEDDYDFSSLALELLPLNPRLPEEWQFGGQGW
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                     LPWMWALFYGPRSHCEERHCVYAAARGKRGPILLPTAVYTPCANIEAFLAHLTRCVYA
                     LYLDVRDWKGEDIAPPFDVSRLNKMAKQLCLLPQEPFCITRVCLLCLLHKQNLNAQYK
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     promoter        complement(124117)
                     /note="TATA: TATAAAA"
     misc_feature    complement(124219)
                     /note="polyA signal: AATAAA"
     CDS             124938..125915
                     /note="BGRF1 reading frame, homologous to RF 45 VZV and
                     spliced HSV gene (Costa et al, 1985). Spliced to BDRF1.
                     Northern blots in BGRF1 detect 2.7, 2.6, 2.1kb late and
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                    1.9kb early RNAs. 2.6, 2.1kb RNAs very weak.  NCBI gi:
                    59134"
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                    QYKHKPARLEAFQKQVVLHSFYFLISIKSLEITDTMFDIFQSAFGLEEMTLEKLHIFK
                    QKASVFLIPRRHGKTWIVVAIISLILSNLSNVQIGYVAHQKHVASAVFTEIIDTLTKS
                    FDSKRVEVNKETSTITFRHSGKISSTVMCATCFNKNVRPDVSVLGNCRA"
promoter            complement(125113)
                    /note="TATA: TATAAAT before BGLF3"
misc_feature        complement(125484)
                    /note="polyA signal: AATAAA, 3' end of 1.6kb late, 1.8kb
                    late, 3.0kb late and 3.7kb early RNAs"
CDS                 complement(125863..126873)
                    /note="BGLF2 late reading frame, poor homology to RF 44
                    VZV;  NCBI gi: 59136"
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                    YVPQIAGPPKTYMNVTLIVLKPKKKPTYVTVYINGTLATVARPEVLFTKAVQGPHSLT
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                    LGRGGAWYAEGALYMFFVNMDMLMCCPNMPTFPSLTHFINLLTRCDNGECVTCYGAGA
                    HVNILRGWTEDDSPGTSGTCPCLLPCTALNNDYVPITGHRALLGLMFKPEDAPFVVGL
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promoter            126277
                    /note="TATA: GATAAAA"
CDS                 complement(126851..128374)
                    /note="BGLF1 late reading frame;  NCBI gi: 59137"
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                    IEHMPVAAAQVEHPKTYDLKQILLEITQEENRGEQRLGHAGSPALCLGLRLRAGAETK
                    AAAETSVSKHHPALENPSNIRGSAGGEGGGGRAGTGGTVGVGSGALSRVPVSFSKTRR
                    AIRESRALVRGIAHIFSPHALYVVTYPELSAQGRLHRMTAVTHASPATDLAEVSILGA
                    PEREFRFLISVALRISASFREKLAMQAWTAQQEIPVVIPTSYSRIYKNSDLIREAFFT
                    VQTRVSWESCWVKATISNAPKTPDACLWIDSHPLYEEGASAWGKVIDSRPPGGLVGAA
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promoter            complement(126929)
                    /note="TATA: TATTAAA EEL8 late promoter before BGLF2,
                    gives 1.6kb late RNA"
promoter            complement(127237)
                    /note="TATA: TATAAAA, potential promoter for 1.8kb late
                    RNA"
misc_feature        128029
                    /note="polyA signal: AATAAA"
CDS                 complement(128344..129021)
                    /note="BDLF4 early reading frame;  NCBI gi: 59138"
                    /codon_start=1
                    /translation="MSDQGRLSLPRGEGGTDEPNPRHLCSYSKLEFHLPLPESMASVF
                    ACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPWTEIRQDTQDQRD
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                    MLFRGASSEKVVDVVLSLYIHVIISIYSQKTVYGALLFKSTRNKRYDAVAKRMRELWM
                    STLTTKC"
promoter            complement(128432)
                    /note="TATA: TATTTAA before BGLF1, potential promoter for
                    3.0kb late RNA"
misc_feature        128848
                    /note="BAM: Bam H1 G/D"
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promoter            complement(129054)
                    /note="TATA: TATTTGC before BDLF4, potential promoter for
                    3.7kb early RNA"
CDS                 129188..130351
                    /note="BDRF1 reading frame, homologous to RF 42 VZV and
                    spliced gene in HSV (Costa et al, 1985). Spliced from
                    BGRF1. Northern blots in BDRF1 detect 2.7, 2.6 kb late and
                    1.9kb early RNAs. Possibly also 1.8kb early RNA.  NCBI gi:
                    583898"
                    /codon_start=1
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                    IPSYITMDSNIRATTNLFLDGAFSTELMGDTSSLSQGSLSRTVRDDAINQLELCRVDT
                    LNPRVAGRLASSLYVYVDPAYTNNTSASGTGIAAVTHDRADPNRVIVLGLEHFFLKDL
                    TGDAALQIATCVVALVSSIVTLHPHLEEVKVAVEGNSSQDSAVAIASIIGESCPLPCA
                    FVHTKDKTSSLQWPMYLLTNEKSKAFERLIYAVNTASLSASQVTVSNTIQLSFDPVLY
                    LISQIRAIKPIPLRDGTYTYTGKQRNLSDDVLVALVMAHFLATTQKHTFKKVH"
promoter            129374
                    /note="TATA: TATAAGC"
promoter            complement(129377)
                    /note="TATA: TATAAAG"
misc_feature        129413
                    /note="DONOR: GTGGTAAGT possible donor"
misc_feature        130347
                    /note="polyA signal: ATTAAA"
misc_feature        complement(130359)
                    /note="polyA signal: AATAAA, 3' end of 0.9kb late RNA,
                    2.3kb late RNA and 3.2kb late RNA"
CDS                 complement(130362..131066)
                    /note="BDLF3 late reading frame 9xNXT/S;  NCBI gi: 59140"
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                    /translation="MAHARDKAGAVMAMILICETSLIWTSSGSSTASAGNVTGTTAVT
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                    TTKVTAQNITATEAGTGTSTGVTSNVTTRSSSTTSATTRITNATTLAPTLSSKGTSNA
                    TKTTAELPTVPDERQPSLSYGLPLWTLVFVGLTFLMLILIFAAGLMMSAKNKPLDEAL
                    LTNAVTRDPSLYKGLV"
promoter            complement(131104)
                    /note="TATA: TATAAAA EEL4 late promoter before BDLF3,
                    gives 0.9kb late RNA"
CDS                 complement(131127..132389)
                    /note="BDLF2 late reading frame;  NCBI gi: 59141"
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                    /translation="MVDEQVAVEHGTVSHTISREEDGVVHERRVLASGERVEVFYKAP
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                    GERMRFKEDVYDGEAETLAEPPRCFMLSFVFIYYCCYLAFLALLAFGFNPLFLPSFMP
                    VGAKVLRGKGRDFGVPLSYGCPTNPFCKVYTLIPAVVINNVTYYPNNTDSHGGHGGFE
                    AAALHVAALFESGCPNLQAVTNRNRTFNVTRASGRVERRLVQDMQRVLASAVVVMHHH
                    CHYETYYVFDGVGPEFGTIPTPCFKDVLAFRPSLVTNCTAPLKTSVKGPNWSGAAGGM
                    KRKQCRVDRLTDRSFPAYLEEVMYVMVQ"
promoter            132266
                    /note="TATA: TATAAAA"
CDS                 complement(132400..133305)
                    /note="BDLF1 late reading frame, poor homology to RF 41
                    VZV;  NCBI gi: 59142"
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                    LGQVYSLETVPDYVSMYNYLSDCTLAVLDEVSVDSLILTKIVPGQTYAIKNKYQPFFQ
                    WHGTGSLSVMPPVFGREHATVKLESNDVDIVFPMVLPTPIAEEVLQKILLFNVYSRVV
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                     ASMRLVRGLIRHEHHDLLNLFQEMVPDEIARIDLDDLSVADDLSRMRVMMTYLQSLAS
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                     /note="TATA: TATTTAA before BDLF2, likely promoter for
                     2.3kb late RNA"
     misc_feature    complement(133312)
                     /note="polyA signal: AATAAA, 3' end of 4.5kb late RNA"
     CDS             complement(133321..137466)
                     /note="BcLF1 late reading frame, homologous to RF 40 VZV
                     and major capsid protein of HSV;  NCBI gi: 59143"
                     /codon_start=1
                     /translation="MASNEGVENRPFPYLTVDADLLSNLRQSAAEGLFHSFDLLVGKD
                     AREAGIKFEVLLGVYTNAIQYVRFLETALAVSCVNTEFKDLSRMTDGKIQFRISVPTI
                     AHGDGRRPSKQRTFIVVKNCHKHHISTEMELSMLDLEILHSIPETPVEYAEYVGAVKT
                     VASALQFGVDALERGLINTVLSVKLRHAPPMFILQTLADPTFTERGFSKTVKSDLIAM
                     FKRHLLEHSFFLDRAENMGSGFSQYVRSRLSEMVAAVSGESVLKGVSTYTTAKGGEPV
                     GGVFIVTDNVLRQLLTFLGEEADNQIMGPSSYASFVVRGENLVTAVSYGRVMRTFEHF
                     MARIVDSPEKAGSTKSDLPAVAAGVEDQPRVPISAAVIKLGNHAVAVESLQKMYNDTQ
                     SPYPLNRRMQYSYYFPVGLFMPNPKYTTSAAIKMLDNPTQQLPVEAWIVNKNNLLLAF
                     NLQNALKVLCHPRLHTPAHTLNSLNAAPAPRDRRETYSLQHRRPNHMNVLVIVDEFYD
                     NKYAAPVTDIALKCGLPTEDFLHPSNYDLLRLELHPLYDIYIGRDAGERARHRAVHRL
                     MVGNLPTPLAPAAFQEARGQQFETATSLAHVVDQAVIETVQDTAYDTAYPAFFYVVEA
                     MIHGFEEKFVMNVPLVSLCINTYWERSGRLAFVNSFSMIKFICRHLGNNAISKEAYSM
                     YRKIYGELIALEQALMRLAGSDVVGDESVGQYVCALLDPNLLPPVAYTDIFTHLLTVS
                     DRAPQIIIGNEVYADTLAAPQFIERVGNMDEMAAQFVALYGYRVNGDHDHDFRLHLGP
                     YVDEGHADVLEKIFYYVFLPTCTNAHMCGLGVDFQHVAQTLAYNGPAFSHHFTRDEDI
                     LDNLENGTLRDLLEISDLRPTVGMIRDLSASFMTCPTFTRAVRVSVDNDVTQQLAPNP
                     ADKRTEQTVLVNGLVAFAFSERTRAVTQCLFHAIPFHMFYGDPRVAATMHQDVATFVM
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                     IAQAKLKIHPGVAMTVVRTDEILSENILFSSRASTSMFIGTPNVSRREARVDAVTFEV
                     HHEMASIDTGLSYSSTMTPARVAAITTDMGIHTQDFFSVFPAEAFGNQQVNDYIKAKV
                     GAQRNGTLLRDPRTYLAGMTNVNGAPGLCHGQQATCEIIVTPVTADVAYFQKSNSPRG
                     RAACVVSCENYNQEVAEGLIYDHSRPDAAYEYRSTVNPWASQLGSLGDIMYNSSYRQT
                     AVPGLYSPCRAFFNKEELLRNNRGLYNMVNEYSQRLGGHPATSNTEVQFVVIAGTDVF
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                     /note="TATA: TATTAAA before BDLF1"
     promoter        complement(133386)
                     /note="TATA: TATATAA"
     misc_feature    135178
                     /note="polyA signal: AATAAA"
     promoter        135394
                     /note="TATA: TATAAGT"
     misc_feature    136624
                     /note="polyA signal: AATAAA"
     misc_feature    136868
                     /note="BAM: Bam H1 D/c"
     promoter        complement(137710)
                     /note="TATA: TATTAAA EHL1 promoter before BcLF1, gives
                     4.5kb late RNA"
     promoter        137857
                     /note="TATA: CATAAAC"
     CDS             137862..139718
                     /note="BcRF1 reading frame;  NCBI gi: 583899"
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                     /translation="XRAQCFALSSATCLITNLSAASSSSAAWSRVGFLGTCKRNSAKM
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                     RRLVALLRREDGAPKDPPLGPFGHPRGPGPAKSEDEESERRDAPPPPLDSSFQASRLV
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     misc_feature    138019
                     /note="BAM: Bam H1 c/b"
     misc_feature    139352
                     /note="BAM: Bam H1 b/T"
     CDS             139642..140919
                     /note="BTRF1 reading frame. Northern blots detect 0.95
                     late and 3.8kb early RNA;  NCBI gi: 583900"
                     /codon_start=1
                     /translation="XERLPFSWPTCAKRQPPSTAVMLKCKQPGARFIHGAVHLPSGQI
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                     ASEHPAFSMVESVKRVRVDEGANTRRTIRDILEIPVTVLSSLQLSPTKSILKKAPEPP
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                     LQHLYLKHVVLKSLNLENIVQDFEAIFTSPSDTISEAETKAFEKLVEQAKNTVENIVF
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     misc_feature    complement(140902)
                     /note="polyA signal: AATAAA, 3' end of 2.5kb late RNA"
     CDS             complement(140916..143036)
                     /note="BXLF2 late reading frame, encodes gp85; homologous
                     to RF 37 VZV and glycoprotein H of HSV (gpIII of VZV);
                     NCBI gi: 59146"
                     /codon_start=1
                     /translation="MQLLCVFCLVLLWEVGAASLSEVKLHLDIEGHASHYTIPWTELM
                     AKVPGLSPEALWREANVTEDLASMLNRYKLIYKTSGTLGIALAEPVDIPAVSEGSMQV
                     DASKVHPGVISGLNSPACMLSAPLEKQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVAL
                     SINGDKFQYTGAMTSKFLMGTYKRVTEKGDEHVLSLVFGKTKDLPDLRGPFSYPSLTS
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                     CYGATVKGMQSYGLERLAAMLMATVKMEELGHLTTEKQEYALRLATVGYPKAGVYSGL
                     IGGATSVLLSAYNRHPLFQPLHTVMRETLFIGSHVVLRELRLNVTTQGPNLALYQLLS
                     TALCSALEIGEVLRGLALGTESGLFSPCYLSLRFDLTRDKLLSMAPQEATLDQAAVSN
                     AVDGFLGRLSLEREDRDAWHLPAYKCVDRLDKVLMIIPLINVTFIISSDREVRGSALY
                     EASTTYLSSSLFLSPVIMNKCSQGAVAGEPRQIPKIQNFTRTQKSCIFCGFALLSYDE
                     KEGLETTTYITSQEVQNSILSSNYFDFDNLHVHYLLLTTNGTVMEIAGLYEERAHVVL
                     AIILYFIAFALGIFLVHKIVMFFL"
     misc_feature    140970
                     /note="polyA signal: AATAAA"
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                     /note="polyA signal: AATAAA"
     promoter        142589
                     /note="TATA: GATAAAA"
     misc_feature    142740
                     /note="BAM: Bam H1 T/X"
     CDS             complement(143038..144861)
                     /note="BXLF1 early reading frame, thymidine kinase
                     (Littler et al, 1986). Weak homology to RF 36 VZV and HSV
                     thymidine kinase. 4.0kb early RNA presumably encodes the
                     TK. Also a 2.2kb late RNA here.  NCBI gi: 59148"
                     /codon_start=1
                     /translation="MAGFPGKEAGPPGGWRKCQEDESPENERHENFYAEIDDFAPSVL
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                SRSFMYQKGFEEGLAGLGLDDKSDCESEDESNFRRPSSHSALKQKNGGKGKPSGLFEH
                LAAHGREFSKLSKHAAQLKRLSGSVMNVLNLDDAQDTRQAKAQRKESMRVPIVTHLTN
                HVPVIKPACSLFLEGAPGVGKTTMLNHLKAVFGDLTIVVPEPMRYWTHVYENAIKAMH
                KNVTRARHGREDTSAEVLACQMKFTTPFRVLASRKRSLLVTESGARSVAPLDCWILHD
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                RKHESGLDAGYLKSVNDAYHAVYCAWLLTQYFAPEDIVKVCAGLTTITTVCHQSHTPI
                IRSGVAEKLYKNSIFSVLKEVIQPFRADAVLLEVCLAFTRTLAYLQFVLVDLSEFQDD
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promoter        complement(143310)
                /note="TATA: TATAAGA ECL2 late promoter before BXLF2,
                gives 2.5kb late RNA"
misc_feature    143608
                /note="polyA signal: AATAAA"
misc_feature    144791
                /note="ACCEPT: TCTTTCGTTTTCAGG poss. acceptor before
                BXRF1"
CDS             144860..145606
                /note="BXRF1 late reading frame, homologous to RF 35 VZV.
                Basic (core?) protein.  NCBI gi: 59147"
                /codon_start=1
                /translation="MDPTRGLCALSTHDLAKFHSLPPARKAAGKRAHLRCYSKLLSLK
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                EFPALGQKTLPTSTTGLLNLLSRWQDGALRARLDRPRPTAQGHRPRTHVGPKPSQLTA
                RVPRSARAGRAGGRKGQVGAVGQVCPGAQK"
misc_feature    144862
                /note="BAM: Bam H1 X/V"
misc_feature    144945
                /note="DONOR: CAGGTAAGC possible donor at 3' BXRF1"
promoter        complement(145135)
                /note="TATA: TATAACA before BXLF1"
promoter        145302
                /note="TATA: TATTTAA before BVRF1, potential promoter for
                1.9kb early RNA"
CDS             145416..147128
                /note="BVRF1 early reading frame, homologous to RF 34 VZV;
                 NCBI gi: 59149"
                /codon_start=1
                /translation="MALSGHVLIDPARLPRDTGPELMWAPSLRNSLRVSPEALELAER
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                ADPQASISSLFPGLVLLALELKLMDGQAPSHYAINLTGQKFDTLFEIINQKLLFHDPA
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                VAPS"
misc_feature    complement(146926)
                /note="polyA signal: AATAAA"
misc_feature    147167
                /note="DONOR: AAGGTAAAT possible donor"
misc_feature    147170
                /note="polyA signal: AATAAA, 3' end of 2.4kb late and
                1.9kb early RNAs"
promoter        147721
                /note="TATA: TATTTAT before BVRF2, potential promoter for
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                2.1kb early RNA"
CDS             147927..149744
                /note="BVRF2 early reading frame, N-terminus homologous to
                RF 33 VZV;  NCBI gi: 59150"
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                /translation="MVQAPSVYVCGFVERPDAPPKDACLHLDPLTVKSQLPLKKPLPL
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                WVLKHFSDLEPSIAAQIENDANAAKRESGCPEDHPLPLTKLIAKAIDAGFLRNRVETL
                RQDRGVANIPAESYLKASDAPDLQKPDKALQSPPPASTDPATMLSGNAGEGATACGGS
                AAAGQDLISVPRNTFMTLLQTNLDNKPPRQTPLPYAAPLPPFSHQAIATAPSYGPGAG
                AVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPPPV
                PPYYGSHLRADYVPAPSRSNKRKRDPEEDEEGGGLFPGEDATLYRKDIAGLSKSVNEL
                QHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPRYVPHPPPPPTS
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misc_feature    148007
                /note="BAM: Bam H1 V/d"
promoter        148620
                /note="TATA: TATTTAA ECR1 late promoter before BdRF1,
                gives 1.2kb late RNA"
CDS             148707..149744
                /note="BdRF1 reading frame; this is the C terminus of
                BVRF2;  NCBI gi: 59151"
                /codon_start=1
                /translation="MLSGNAGEGATACGGSAAAGQDLISVPRNTFMTLLQTNLDNKPP
                RQTPLPYAAPLPPFSHQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFL
                AMDAHTYHPHPHPPPAYFGLPGLFGPPPPVPPYYGSHLRADYVPAPSRSNKRKRDPEE
                DEEGGGLFPGEDATLYRKDIAGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPC
                YTHSGPYGFQPHQSYEVPRYVPHPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPE
                AGAAGNSGPREDTNPQQPTTEGHHRGKKLVQASASGVAQSKEPTTPKAKSVSAHLKSI
                FCEELLNKRVA"
misc_feature    149115
                /note="BAM: Bam H1 d/I"
misc_feature    149727
                /note="polyA signal: AATAAA, 3' end of 2.1kb early and
                1.2kb late RNAs"
misc_feature    complement(149758)
                /note="polyA signal: AATAAA, 3' end of 1.0kb late, 1.5kb
                late and 1.8kb late RNAs"
CDS             complement(149779..150525)
                /note="BILF2 late reading frame 11xNXT/S;  NCBI gi: 59152"
                /codon_start=1
                /translation="MTHLVLLLCCCVGSVCAFFSDLVKFENVTAHAGARVNLTCSVPS
                NESVSRIELGRGYTPGDGQLPLAVATSNNGTHITNGGYNYSLTLEWVNDSNTSVSLII
                PNVTLAHAGYYTCNVTLRNCSVASGVHCNYSAGEEDDQYHANRTLTQRMHLTVIPATT
                IAPTTLVSHTTSTSHRPHRRPVSKRPTHKPVTLGPFPIDPWRPKTTWVHWALLLITCA
                VVAPVLLIIIISCLGWLAGWGRRRKGWIPL"
promoter        complement(150571)
                /note="TATA: TATTTAG before BILF2. Potential promoter for
                1.0kb late RNA."
repeat_region   151236..151618
                /note="repetitive sequence 3X"
misc_feature    151767
                /note="polyA signal: AATAAA"
promoter        complement(151780)
                /note="TATA: CATAAAA"
misc_feature    152012..152013
                /note="DEL: B95-8 deletion with respect to Raji"
CDS             complement(152161..153099)
```

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                     /note="BILF1 reading frame, membrane protein, 3xNXS/T;
                     NCBI gi: 59153"
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                     /translation="MLSTMAPGSTVGTLVANMTSVNATEDACTKSYSAFLSGMTSLLL
                     VLLILLTLAGILFIIFVRKLVHRMDVWLIALLIELLLWVLGKMIQEFSSTGLCLLTQN
                     MMFLGLMCSVWTHLGMALEKTLALFSRTPKRTSHRNVCLYLMGVFCLVLLLIIILLIT
                     MGPDANLNRGPNMCREGPTKGMHTAVQGLKAGCYLLAAVLIVLLTVIIIWKLLRTKFG
                     RKPRLICNVTFTGLICAFSWFMLSLPLLFLGEAGSLGFDCTESLVARYYPGPAACLAL
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     promoter        152230
                     /note="TATA: CATAAAA"
     misc_feature    153259
                     /note="polyA signal: AATAAA"
     misc_feature    153637
                     /note="HPN: 22bp 2-fold symmetric"
     misc_feature    complement(153690)
                     /note="DONOR: AAAGTGAGG possible donor"
     CDS             complement(153699..156746)
                     /note="BALF5 DNA polymerase (early), homologous to many
                     DNA polymerases, CMV HFLF2 and RF 28 VZV. 4.5kb early RNA
                     apparently encodes BALF5, RNA ends unknown.  NCBI gi:
                     59154"
                     /codon_start=1
                     /translation="MSGGLFYNPFLRPNKGLLKKPDKEYLRLIPKCFQTPGAAGVVDV
                     RGPQPPLCFYQDSLTVVGGDEDGKGMWWRQRAQEGTARPEADTHGSPLDFHVYDILET
                     VYTHEKCAVIPSDKQGYVVPCGIVIKLLGRRKADGASVCVNVFGQQAYFYASAPQGLD
                     VEFAVLSALKASTFDRRTPCRVSVEKVTRRSIMGYGNHAGDYHKITLSHPNSVCHVAT
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                     RHIYSINPASLGKIRAGGVCEVRRPHDAGKGFLRANTKVRITGLIPIDMYAVCRDKLS
                     LSDYKLDTVARHLLGAKKEDVHYKEIPRLFAAGPEGRRRLGMYCVQDSALVMDLLNHF
                     VIHVEVAEIAKIAHIPCRRVLDDGQQIRVFSCLLAAAQKENFILPMPSASDRDGYQGA
                     TVIQPLSGFYNSPVLVVDFASLYPSIIQAHNLCYSTMITPGEEHRLAGLRPGEDYESF
                     RLTGGVYHFVKKHVHESFLASLLTSWLAKRKAIKKLLAACEDPRQRTILDKQQLAIKC
                     TCNAVYGFTGVANGLFPCLSIAETVTLQGRTMLERAKAFVEALSPANLQALAPSPDAW
                     APLNPEGQLRVIYGDTDSLFIECRGFSESETLRFADALAAHTTRSLFVAPISLEAEKT
                     FSCLMLITKKRYVGVLTDGKTLMKGVELVRKTACKFVQTRCRRVLDLVLADARVKEAA
                     SLLSHRPFQESFTQGLPVGFLPVIDILNQAYTDLREGRVPMGELCFSTELSRKLSAYK
                     STQMPHLAVYQKFVERNEELPQIHDRIQYVFVEPKGGVKGARKTEMAEDPAYAERHGV
                     PVAVDHYFDKLLQGAANILQCLFDNNSGAALSVLQNFTARPPF"
     misc_feature    154747
                     /note="BAM: Bam H1 I/A"
     misc_feature    complement(156707)
                     /note="polyA signal: AATAAA; 3' end of 2.5kb late (gB) RNA
                     and 1.8kb late RNA"
     CDS             complement(156749..159322)
                     /note="BALF4 late reading frame 9xNXT/S homologous to HSV1
                     glycoprotein B (Pellet et al, 1985), CMV HFLF1 and RF 31
                     VZV (gpII);  NCBI gi: 59155"
                     /codon_start=1
                     /translation="MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQT
                     SFPFRVCELSSHGDLFRFSSDIQCPSFGTRENHTEGLLMVFKDNIIPYSFKVRSYTKI
                     VTNILIYNGWYADSVTNRHEEKFSVDSYETDQMDTIYQCYNAVKMTKDGLTRVYVDRD
                     GVNITVNLKPTGGLANGVRRYASQTELYDAPGWLIWTYRTRTTVNCLITDMMAKSNSP
                     FDFFVTTTGQTVEMSPFYDGKNKETFHERADSFHVRTNYKIVDYDNRGTNPQGERRAF
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                     IYGKAVAAKRLGDVISVSQCVPVNQATVTLRKSMRVPGSETMCYSRPLVSFSFINDTK
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                     FISLNTSLIENIDFASLELYSRDEQRASNVFDLEGIFREYNFQAQNIAGLRKDLDNAV
                     SNGRNQFVDGLGELMDSLGSVGQSITNLVSTVGGLFSSLVSGFISFFKNPFGGMLILV
                     LVAGVVILVISLTRRTRQMSQQPVQMLYPGIDELAQQHASGEGPGINPISKTELQAIM
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                     F"
     promoter        158204
                     /note="TATA: TATAAAA"
     CDS             complement(159309..161678)
                     /note="BALF3 reading frame;  NCBI gi: 583901"
                     /codon_start=1
                     /translation="XRRGVLIGPLLRPGGQRPRNPGDHCLQRDRVDGGGRSGLSGGSV
                     GWARGSPGQLYQRGRAGQHRVAGLGRAAAGWRRAGLRGQTQAPSGHRSPRTRGLETPG
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                     NDRACSALSLELVHLLENSREASAALLAPGRKGTRVPPLRTPSVAYSVEFYGGHKVDV
                     SLCLINDIEILMKRINSVFYCMSHTMGLESLERALDLLGRFRGVSPIPDPRLYITSVP
                     CWRCVGELMVLPNHGNPSTAEGTHVSCNHLAVPVNPEPVSGLFENEVRQAGLGHLLEA
                     EEKARPGGPEEGAVPGPGRPEAEGATRALDTYNVFSTVPPEVAELSELLYWNSGGHAI
                     GATGQGEGGGHSRLSALFARERRLALVRGACEEALAGARLTHLFDAVAPGATERLFCG
                     GVYSSSGDAVEALKADCAAAFTAHPQYRAILQKRNELYTRLNRAMQRLGRGEEEASRE
                     SPEVPRPAGAREPGPSGALSDALKRKEQYLRQVATEGLAKLQSCLAQQSETLTETLCL
                     RVWGDVVYWELARMRNHFLYRRAFVSGPWEDRRAGEGAAFENSKYIKTHLFTQTLSSE
                     HLHALTHSLYTFITGPLAEESGLFPPPSNVALARCCDAAGTLPHQKAFLTSLIWPGIE
                     PSDWIETSFNSFYSVPGGSLASSQQILCRALREAVLTVSLYNKTWGRSLILRRADAVS
                     PGQALPPDGLYLTYDSDRPLILLYKGRGWVFKDLYALLYLHLQMRDDSA"
     promoter        complement(159370)
                     /note="TATA: TATTTAA ECL1 late promoter before BALF4,
                     gives 2.5kb late RNA"
     misc_feature    160966
                     /note="polyA signal: AATAAA"
     misc_feature    160990
                     /note="polyA signal: ATTAAA"
     misc_feature    complement(161013)
                     /note="polyA signal: AATAAA, presumed end of 3.9kb early
                     RNA"
     CDS             complement(161384..164770)
                     /note="BALF2 early reading frame, homologous to RF 29 VZV
                     and major DNA binding protein HSV. 3.9kb early RNA;  NCBI
                     gi: 59157"
                     /codon_start=1
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                     FEGPGLEALCGETREVFGYDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKER
                     LYSGNLVAIPSLKQEVAVGQSASVRVPLYDKEVFPEGVPQLRQFYNSDLSRCMHEALY
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                     IFATNSVLYVSGVSKSTGQGKESLFNSFYMTHGLGTLQEGTWDPCRRPCFSGWGGPDV
                     TGTNGPGNYAVEHLVYAASFSPNLLARYAYYLQFCQGQKSSLTPVPETGSYVAGAAAS
                     PMCSLCEGRAPAVCLNTLFFRLRDRFPPVMSTQRRDPYVISGASGSYNETDFLGNFLN
                     FIDKEDDGQRPDDEPRYTYWQLNQNLLERLSRLGIDAEGKLEKEPHGPRDFVKMFKDV
                     DAAVDAEVVQFMNSMAKNNITYKDLVKSCYHVMQYSCNPFAQPACPIFTQLFYRSLLT
                     ILQDISLPICMCYENDNPGLGQSPPEWLKGHYQTLCTNFRSLAIDKGVLTAKEAKVVH
                     GEPTCDLPDLDAALQGRVYGRRLPVRMSKVLMLCPRNIKIKNRVVFTGENAALQNSFI
                     KSTTRRENYIINGPYMKFLNTYHKTLFPDTKLSSLYLWHNFSRRRSVPVPSGASAEEY
                     SDLALFVDGGSRAHEESNVIDVVPGNLVTYAKQRLNNAILKACGQTQFYISLIQGLVP
                     RTQSVPARDYPHVLGTRAVESAAAYAEATSSLTATTVVCAATDCLSQVCKARPVVTLP
                     VTINKYTGVNGNNQIFQAGNLGYFMGRGVDRNLLQAPGAGLRKQAGGSSMRKKFVFAT
                     PTLGLTVKRRTQAATTYEIENIRAGLEAIISQKQEEDCVFDVVCNLVDAMGEACASLT
                     RDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAARDFLEGVWGGPGAAQDNFISV
                     AEPVSTASQASAGLLLGGGGQGSGGRRKRRLATVLPGLEV"
     misc_feature    163978..166635
                     /note="DEL: deletion in Raji"
     promoter        complement(164814)
                     /note="TATA: CATTTAA before BALF2, presumed promoter for
                     3.9kb early RNA"
     misc_feature    complement(164851)
                     /note="polyA signal: AATAAA"
     CDS             complement(164855..165517)
                     /note="BALF1 early reading frame, 0.7kb early RNA;  NCBI
                     gi: 59159"
                     /codon_start=1
                     /translation="MNLAIALDSPHPGLASYTILPRPFYHISLKPVSWPDETMRPAKS
                     TDSVFVRTPVEAWVAPSPPDDKVAESSYLMFRAMYAVFTRDEKDLPLPALVLCRLIKA
                     SLRKDRKLYAELACRTADIGGKDTHVRLIISVLRAVYNDHYDYWSRLRVVLCYTVVFA
                     VRNYLDDHKSAAFVLGAIAHYLALYRRLWFARLGGMPRSLRRQFPVTWALASLTDFLK
                     SL"
     promoter        165442
                     /note="TATA: GATAAAA"
     promoter        165466
                     /note="TATA: TATAAGA EDR1 early promoter before BARF1,
                     gives 0.8kb early RNA"
     CDS             165504..166169
                     /note="BARF1 reading frame;  NCBI gi: 59158"
                     /codon_start=1
                     /translation="MARFIAQLLLLASCVAAGQAVTAFLGERVTLTSYWRRVSLGPEI
                     EVSWFKLGPGEEQVLIGRMHHDVIFIEWPFRGFFDIHRSANTFFLVVTAANISHDGNY
                     LCRMKLGETEVTKQEHLSVVKPLTLSVHSERSQFPDFSVLTVTCTVNAFPHPHVQWLM
                     PEGVEPAPTAANGGVMKEKDGSLSVAVDLSLPKPWHLPVTCVGKNDKEEAHGVYVSGY
                     LSQ"
     promoter        complement(165713)
                     /note="TATA: TATAAAG before BALF1"
     misc_feature    166165
                     /note="polyA signal: AATAAA 3' end of 0.8kb early RNA.
                     Also 1kb late RNA in this region."
     promoter        166469..166475
                     /note="TATA: TTATTTT"
     mRNA            166498..166916
                     /note="Exon 1 of terminal protein RNA"
     misc_feature    166561..166563
                     /note="Likely initiator met of terminal protein"
     misc_feature    166614
                     /note="BAM: Bam H1 A/Nhet"
     misc_feature    complement(166946)
                     /note="polyA signal: AATAAA These 2 polyA sites are 3' end
                     of 0.8kb early, 2.5kb late and 2.5kb latent RNAs"
     misc_feature    complement(166950)
                     /note="polyA signal: AATAAA"
     CDS             complement(166998..167303)
                     /note="BNLF2b reading frame;  NCBI gi: 583902"
                     /codon_start=1
                     /translation="XATMRPGRPLAGFYATLRRSFRRMSKRSKNKAKKERVPVEDRPP
                     TPMPTSQRLIRRNALGGGVRPDAEDCIQRFHPLEPALGVSTKNFDLLSLRCELGWCG"
     CDS             complement(167304..167486)
                     /note="BNLF2a reading frame;  NCBI gi: 59161"
                     /codon_start=1
                     /translation="MVHVLERALLEQQSSACGLPGSSTETRPSHPCPEDPDVSRLRLL
                     LVVLCVLFGLLCLLLI"
     promoter        167320
                     /note="TATA: CATAAAA"
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     promoter        complement(167525)
                     /note="TATA: TATAAAA EDL2 early promoter before BNLF2a,b.
                     Gives 0.8kb RNA"
     mRNA            complement(168163..168965)
                     /note="BNLF1 coding part of exon c of latent membrane
                     protein"
     repeat_region   168399..168574
                     /note="5 x 33bp repeats"
     intron          complement(168966..169041)
                     /note="intervening sequence in BNLF1"
     misc_feature    complement(168966)
                     /note="ACCEPT: TTTTTCAACGCAGT possible acceptor"
     misc_feature    complement(169041)
                     /note="DONOR: TTGGTAAGA donor"
     mRNA            complement(169042..169128)
                     /note="BNLF1 exon b of latent membrane protein mRNA"
     intron          complement(169129..169206)
                     /note="intervening sequence in BNLF1"
     misc_feature    complement(169129)
                     /note="ACCEPT: TCCTCTTTCCCCAGT acceptor"
     promoter        complement(169201)
                     /note="TATA: TATTACA EDL1A late promoter, gives 2.5kb late
                     RNA"
     misc_feature    complement(169206)
                     /note="DONOR: TGAGTAAGT donor"
     mRNA            complement(169207..169474)
                     /note="BNLF1 exon a of latent membrane protein mRNA"
     promoter        complement(169546)
                     /note="TATA: TACATAAGC EDL1 promoter before BNLF1 gives
                     2.5kb latent RNA (LMP)"
     repeat_region   170094..170631
                     /note="terminal repeat 1 538bp"
     repeat_region   170632..171154
                     /note="terminal repeat 2 523bp"
     repeat_region   171155..171692
                     /note="terminal repeat 3 538bp"
     repeat_region   171693..172231
                     /note="terminal repeat 4 538bp"
 BASE COUNT    34054 a  52511 c  50755 g  34961 t
 ORIGIN

Initial Score    =    170  Optimized Score  =    454  Significance = 10.52
Residue Identity =    50%  Matches          =    529  Mismatches   =   418
Gaps             =    105  Conservative Substitutions                =     0

              X       10           20        30        40        50
              CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
              ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
    CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
107030    107040    107050    107060    107070    107080    107090    107100

    60        70          80        90           100       110       120
    CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
     |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
    GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
        107110    107120    107130    107140    107150    107160     107170

       130       140       150       160       170       180        190
    CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
    | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
    CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
           107180    107190    107200      107210    107220    107230

       200       210       220          230        240       250        260
    -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
      ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
    GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
 107240    107250      107260    107270    107280    107290    107300

           270         280           290       300       310       320
    CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
     |   |||| |||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
    GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
 107310    107320    107330    107340    107350          107360    107370

     330       340       350       360       370          380       390
    CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
      ||       ||  | ||||| |  |||  || |  ||||| |||||| |   | |||||| ||||| ||
    GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
     107380    107390     107400      107410    107420    107430    107440

      400        410       420        430       440        450        460
    GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
    |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
    GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      107450    107460    107470    107480      107490    107500    107510

           470          480        490       500       510       520
    GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
     | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
    AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
      107520    107530    107540    107550    107560    107570    107580

   530       540       550       560       570       580       590       600
    CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
      ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
    AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
    107590    107600       107610    107620    107630    107640    107650

           610         620           630       640       650       660
    AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
    || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
    AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
      107660    107670    107680    107690      107700    107710    107720

     670       680        690         700       710       720       730
    AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
    |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
    AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      107730    107740    107750    107760    107770    107780    107790

         740       750        760       770       780           790
    AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
    ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
    AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
    107800     107810    107820    107830      107840    107850    107860

  800       810         820       830        840       850       860
    GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
    || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
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     GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
         107870    107880       107890    107900    107910    107920

    870       880       890       900       910       920        930
     AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
     |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
     AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
 07930    107940    107950        107960    107970    107980    107990

    940       950       960           970       980       X
     GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
     | | | |   | | ||  |   || | |||    || |  | ||   ||.|  |
     GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGAAGTCGT
   108000    108010     108020    108030    108040    108050


11. US-08-162-407-5'  (1-988)
    EBV            Epstein-Barr virus (EBV) genome. The complete sequ

 ID   EBV        standard; circular DNA; VRL; 172281 BP.
 XX
 AC   V01555; J02070; K01729; K01730; V01554; X00498; X00499; X00784;
 XX
 DT   06-DEC-1983 (Rel. 04, Created)
 DT   04-JAN-1995 (Rel. 42, Last updated, Version 51)
 XX
 DE   Epstein-Barr virus (EBV) genome. The complete sequence [1-10] was
 DE   determined from DNA from B95-8 cells cloned by Arrand et al [11].
 DE   B95-8 is a productive marmoset lymphoblastoid cell line
 DE   immortalized with human EBV from a mononucleosis patient.
 XX
 KW   DNA polymerase; EBNA; genome; ribonucleotide reductase;
 KW   tandem repeat; terminal repeat.
 XX
 OS   Epstein-Barr virus (EBV)
 OC   Viridae; ds-DNA enveloped viruses; Herpesviridae;
 OC   Gammaherpesviridae.
 XX
 RN   [1]
 RP   1-172281
 RA   Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L.,
 RA   Farrell P.J., Gibson T.J., Hatfull G.F., Hudson G.S.,
 RA   Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.;
 RT   "DNA sequence and expression of the B95-8 Epstein-Barr virus
 RT   genome";
 RL   Nature 310:207-211(1984).
 XX
 RN   [2]
 RA   Deininger P.L., Bankier A.T., Farrell P.J., Baer R., Barrell B.G.;
 RT   "Sequence analysis and in vitro transcription of portions of the
 RT   Epstein-Barr virus genome";
 RL   J. Cell. Biochem. 19:267-274(1982).
 XX
 RN   [3]
 RA   Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
 RT   "Homologous upstream sequences near Epstein-Barr virus promoters";
 RL   Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
 XX
 RN   [4]
 RA   Farrell P.J., Bankier A.T., Seguin C., Deininger P.L.,
RA   Barrell B.G.;
RT   "Latent and lytic cycle promoters of Epstein-Barr virus";
RL   EMBO J. 2:1331-1338(1983).
XX
RN   [5]
RP   142687-159853
RA   Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
RT   "Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8
RT   Epstein-Barr virus";
RL   Mol. Biol. Med. 1:21-45(1983).
XX
RN   [6]
RP   112620-125316
RA   Seguin C., Farrell P.J., Barrell B.G.;
RT   "DNA sequence and transcription of the BamHI fragment B region of
RT   B95-8 Epstein-Barr virus";
RL   Mol. Biol. Med. 1:369-392(1983).
XX
RN   [7]
RP   159853-172281
RA   Bankier A.T., Deininger P.L., Satchwell S.C., Baer R.,
RA   Farrell P.J., Barrell B.G.;
RT   "DNA sequence analysis of the EcoRI Dhet fragment of B95-8
RT   Epstein-Barr virus containing the terminal repeat sequences";
RL   Mol. Biol. Med. 1:425-446(1983).
XX
RN   [8]
RP   87650-92703
RA   Biggin M.D., Farrell P.J., Barrell B.G.;
RT   "Transcription and DNA sequence analysis of the BamHI L fragment
RT   of B95-8 Epstein-Barr virus";
RL   EMBO J. 3:1083-1090(1984).
XX
RN   [9]
RP   76089-79808
RA   Gibson T.J., Stockwell P., Ginsburg M., Barrell B.G.;
RT   "Homology between two EBV early genes and HSV ribonucleotide
RT   reductase and 38K genes";
RL   Nucleic Acids Res. 12:5087-5099(1984).
XX
RN   [10]
RA   Hatfull G.F., Barrell B.G., Quinn J., McGeoch D.;
RT   ;
RL   Unpublished.
XX
RN   [11]
RA   Arrand J.R., Walsh J.E., Rymo L., Bjoerck E., Lindahl T.,
RA   Griffin B.E.;
RT   "Molecular cloning of the complete Epstein-Barr virus genome as a
RT   set of overlapping restriction endonuclease fragments";
RL   Nucleic Acids Res. 9:2999-3014(1981).
XX
RN   [12]
RA   Kozak M.;
RT   "Possible role of flanking nucleotides in recognition of the AUG
RT   initiator codon by eukaryotic ribosomes";
RL   Nucleic Acids Res. 9:5233-5252(1981).
XX
RN   [13]
RP   7315-9312
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RA   Yates J., Warren N., Reisman D., Sugden B.;
RT   "A cis-acting element from the Epstein-Barr viral genome that
RT   permits stable replication of recombinant plasmids";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).
XX
RN   [14]
RP   45415-52824
RA   Jones M.D., Foster L., Sheedy T., Griffin B.E.;
RT   "The EB virus genome in Daudi Burkitt's lymphoma cells has a
RT   deletion similar to that observed in a non transforming strain
RT   (P3HR-1) of the virus";
RL   EMBO J. 3:813-821(1984).
XX
RN   [15]
RP   45644-52450
RA   Jeang K.T., Hayward S.D.;
RT   "Organisation of the Epstein-Barr virus molecule. III. The
RT   location of the P3HR-1 deletion junction and characterization of
RT   the NotI repeat units that form part of the template for an
RT   abundant 12-0-Tetradecanoylphorbol-13-acetate-induced mRNA
RT   transcript";
RL   J. Virol. 48:135-148(1983).
XX
RN   [16]
RP   1-172281
RA   Farrell P.J., Barrell B.G.;
RT   ;
RL   Submitted (05-JUN-1984) to the EMBL/GenBank/DDBJ databases.
XX
RN   [17]
RA   Bodescot M., Perricaudet M.;
RT   "Clustered alternative splice sites in Epstein-Barr virus RNAs";
RL   Nucleic Acids Res. 15:5887-5887(1987).
XX
RN   [18]
RA   Laux G., Perricaudet M., Farrell P.J.;
RT   "A spliced Epstein-Barr virus gene expressed in immortalized
RT   lymphocytes is created by circularization of the linear viral
RT   genome";
RL   EMBO J. 7:769-774(1988).
XX
RN   [19]
RP   1-172281
RA   Farrell P.J.;
RT   ;
RL   Submitted (18-MAR-1988) to the EMBL/GenBank/DDBJ databases.
RL   Farrell P., Ludwig Institute for Cancer Research, St. Mary's
RL   Hospital Medical School, Norfolk Place London W2 1PG.
XX
DR   EPD; 07138; EBV[DL/R].
DR   EPD; 07139; EBV[BamH1-L] R1.
DR   EPD; 07140; EBV[BamH1-L] R2.
DR   EPD; 07141; EBV[BamH1-L] L2.
DR   EPD; 07142; EBV[BamH1-L] L1.
DR   EPD; 07143; EBV[BamH1-L] L3.
DR   EPD; 07144; EBV[BamH1-K] 2.1 kb.
DR   EPD; 07145; EBV[BamH1-K] 1.3 kb.
DR   EPD; 07146; EBV[EcoR1-H] L1.
DR   EPD; 07147; EBV[EcoR1-C] L1.
DR   EPD; 07148; EBV[EcoR1-D] L1.
DR   EPD; 11192; EBV[EcoR1-D] R1.
DR   EPD; 11193; EBV[EcoR1-D] L2.
DR   EPD; 11194; EBV[EcoR1-D] L1A.
DR   EPD; 16087; EBV[BamHI-N] R1 145K.
DR   EPD; 16088; EBV[BamHI-C] R1 20K.
DR   EPD; 16089; EBV[BamHI-F] R1.
DR   EPD; 16090; EBV[BamHI-F] R2.
DR   EPD; 16091; EBV[BamHI-F] L2.
DR   EPD; 26011; EBV EBNA mRNAs   E1.
DR   EPD; 26012; EBV EBNA mRNAs   E2.
DR   EPD; 26014; EBV[BamH1-Z] L1 1 kb.
DR   SWISS-PROT; P03175; RIR2_EBV.
DR   SWISS-PROT; P03177; KITH_EBV.
DR   SWISS-PROT; P03179; VP14_EBV.
DR   SWISS-PROT; P03180; BCRF_EBV.
DR   SWISS-PROT; P03181; YHL1_EBV.
DR   SWISS-PROT; P03182; EAR_EBV.
DR   SWISS-PROT; P03183; UL31_EBV.
DR   SWISS-PROT; P03184; UL32_EBV.
DR   SWISS-PROT; P03185; UL34_EBV.
DR   SWISS-PROT; P03186; TEGU_EBV.
DR   SWISS-PROT; P03187; VP19_EBV.
DR   SWISS-PROT; P03188; VGLB_EBV.
DR   SWISS-PROT; P03189; UL37_EBV.
DR   SWISS-PROT; P03190; RIR1_EBV.
DR   SWISS-PROT; P03191; EAD_EBV.
DR   SWISS-PROT; P03192; YMR2_EBV.
DR   SWISS-PROT; P03193; UL52_EBV.
DR   SWISS-PROT; P03194; YSR1_EBV.
DR   SWISS-PROT; P03195; DUT_EBV.
DR   SWISS-PROT; P03196; UL73_EBV.
DR   SWISS-PROT; P03197; YLR2_EBV.
DR   SWISS-PROT; P03198; DPOL_EBV.
DR   SWISS-PROT; P03199; YLL2_EBV.
DR   SWISS-PROT; P03200; VGP3_EBV.
DR   SWISS-PROT; P03201; VGP2_EBV.
DR   SWISS-PROT; P03202; YLR3_EBV.
DR   SWISS-PROT; P03203; EBN4_EBV.
DR   SWISS-PROT; P03204; EBN6_EBV.
DR   SWISS-PROT; P03205; YZL2_EBV.
DR   SWISS-PROT; P03206; BZLF_EBV.
DR   SWISS-PROT; P03207; YRR1_EBV.
DR   SWISS-PROT; P03208; VMEM_EBV.
DR   SWISS-PROT; P03209; BRL1_EBV.
DR   SWISS-PROT; P03210; YRR2_EBV.
DR   SWISS-PROT; P03211; EBN1_EBV.
DR   SWISS-PROT; P03212; YKR2_EBV.
DR   SWISS-PROT; P03213; UL06_EBV.
DR   SWISS-PROT; P03214; HELI_EBV.
DR   SWISS-PROT; P03215; VIMP_EBV.
DR   SWISS-PROT; P03216; UL11_EBV.
DR   SWISS-PROT; P03217; EXON_EBV.
DR   SWISS-PROT; P03218; VGL2_EBV.
DR   SWISS-PROT; P03219; VTER_EBV.
DR   SWISS-PROT; P03220; UL95_EBV.
DR   SWISS-PROT; P03221; UL16_EBV.
DR   SWISS-PROT; P03222; UL17_EBV.
DR   SWISS-PROT; P03223; UL92_EBV.
DR   SWISS-PROT; P03224; VGP8_EBV.
DR   SWISS-PROT; P03225; BDL2_EBV.
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DR   SWISS-PROT; P03226; VCAP_EBV.
DR   SWISS-PROT; P03227; DNBI_EBV.
DR   SWISS-PROT; P03228; BRF1_EBV.
DR   SWISS-PROT; P03229; YAL1_EBV.
DR   SWISS-PROT; P03230; LMP1_EBV.
DR   SWISS-PROT; P03231; VGLH_EBV.
DR   SWISS-PROT; P03232; UL24_EBV.
DR   SWISS-PROT; P03233; UL25_EBV.
DR   SWISS-PROT; P03234; VP40_EBV.
DR   SWISS-PROT; P03235; YEC4_EBV.
DR   SWISS-PROT; P12888; UNG_EBV.
DR   SWISS-PROT; P12977; EBN3_EBV.
DR   SWISS-PROT; P12978; EBN2_EBV.
DR   SWISS-PROT; P13285; LMP2_EBV.
DR   SWISS-PROT; P13288; KR2_EBV.
DR   SWISS-PROT; P14347; UL49_EBV.
DR   SWISS-PROT; P14348; VP26_EBV.
DR   SWISS-PROT; P25214; VP23_EBV.
DR   SWISS-PROT; P25215; UL87_EBV.
DR   SWISS-PROT; P25939; IC18_EBV.
DR   SWISS-PROT; P29882; UL07_EBV.
DR   SWISS-PROT; P30117; YKR4_EBV.
DR   SWISS-PROT; P30118; YBL2_EBV.
DR   SWISS-PROT; P30119; YTR1_EBV.
DR   TRANSFAC; 00194; Release Number 1.0.
DR   TRANSFAC; 00195; Release Number 1.0.
DR   TRANSFAC; 00196; Release Number 1.0.
DR   TRANSFAC; 00197; Release Number 1.0.
DR   TRANSFAC; 00198; Release Number 1.0.
DR   TRANSFAC; 00199; Release Number 1.0.
DR   TRANSFAC; 00295; Release Number 1.0.
DR   TRANSFAC; 00296; Release Number 1.0.
DR   TRANSFAC; 00297; Release Number 1.0.
DR   TRANSFAC; 00298; Release Number 1.0.
DR   TRANSFAC; 00299; Release Number 1.0.
DR   TRANSFAC; 00300; Release Number 1.0.
DR   TRANSFAC; 00301; Release Number 1.0.
DR   TRANSFAC; 00302; Release Number 1.0.
DR   TRANSFAC; 00710; Release Number 1.0.
DR   TRANSFAC; 00923; Release Number 1.0.
DR   TRANSFAC; 02818; Release Number 1.0.
DR   TRANSFAC; 03182; Release Number 1.0.
DR   TRANSFAC; 03411; Release Number 1.0.
DR   TRANSFAC; 03412; Release Number 1.0.
XX
CC   CDS
CC
CC   Listed under this feature are all known protein coding regions as
CC   well as all the major open reading frames in the sequence. In
CC   general the term major is taken as the longest frame in a
CC   particular region taking into account the adjacent longest frames
CC   and likely transcription signals. Note that on this basis some long
CC   overlapping frames have been excluded and on the other hand some
CC   small frames have been included which might represent exons or
CC   genes because they occur in a logical combination with other
CC   features or because of some other experimental data. The reading
CC   frames are named according to the Bam H1 fragment in which they
CC   start. eg BALF3 is the third leftward frame starting in Bam H1
CC   fragment A. BORF1 is the first rightward frame in Bam H1 fragment
CC   O. If there is an obvious TATA sequence followed by an in frame Met
CC   codon that satisfies the rules of Kozak [12] in that there is a
CC   purine at -3 and/or a G at +4 then the reading frame is numbered
CC   from the A of the ATG to the base preceding the termination codon.
CC   If there is no obvious initiation codon or there is a substantial
CC   reading frame in phase before the ATG then the reading frame is
CC   numbered from the first base of the first codon.
CC
CC
CC   SITEs of POLYA signals
CC
CC   This feature lists all occurences of the sequence AATAAA which is
CC   found normally approximately 20 bases upstream of the mRNA
CC   processing/polyA addition site. The rarely used homolog ATTAAA is
CC   only listed when it is found in a position close to the end of a
CC   major reading frame.
CC
CC
CC   SITEs of DONOR and ACCEPT sequences
CC
CC   This is not a comprehensive listing of all such sequences and only
CC   the positions of a few have been noted because they occur in
CC   potentially interesting positions. The number quoted in the table
CC   is the position of the terminal base in the intron in each case.
CC
CC
CC   Restriction enzyme SITEs.
CC
CC   Only the positions of the sites Bam HI (BAM) are listed.
CC
CC
CC   RPT
CC
CC   This feature is used to define repetitive sequences.
CC
CC
CC   SITE DEL
CC
CC   This feature defines deletions in B95-8 with respect to other
CC   strains such as RAJI and also to deletions in other strains such as
CC   P3HR1 and DAUDI with respect to B95-8.
CC
CC
CC   SITE HPN
CC
CC   Denotes sequences with twofold symmetry ie could form hairpin
CC   loops. This is not a comprehensive list - only a few occurences
CC   noted.
CC
CC
CC   ORGRPL
CC
CC   Denotes the region that encompasses an origin of replication
CC   (ori P).[13].
CC
CC
CC   NUMBERING
CC
CC   The DNA sequence of B95-8 EBV has been revised [19]. The original
CC   (Baer et al, 1984) base 359 has been deleted so the new sequence
CC   around that position reads TCAGTCTTT. To avoid renumbering the
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CC   entire sequence, position 1 has benn moved 1 base to the left of
CC   the EcoRI site separating EcoRI Dhet from EcoRI I
CC   (ie the first A of AGAATTC)
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..172281
FT                   /organism="Epstein-Barr virus"
FT                   /strain="B95-8"
FT   mRNA            58..272
FT                   /note="exon 2 terminal protein RNA"
FT   mRNA            360..458
FT                   /note="exon 3 terminal protein RNA"
FT   misc_feature    complement(535..535)
FT                   /note="polyA signal: AATAAA"
FT   mRNA            540..788
FT                   /note="exon 4 terminal protein RNA"
FT   mRNA            871..951
FT                   /note="exon 5 terminal protein RNA"
FT   mRNA            1026..1196
FT                   /note="exon 6 terminal protein RNA"
FT   promoter        complement(1192..1192)
FT                   /note="TATA: TATAAAT"
FT   mRNA            1280..1495
FT                   /note="exon 7 terminal protein RNA"
FT   promoter        complement(1383..1383)
FT                   /note="TATA: CATAAAA"
FT   mRNA            1574..1682
FT                   /note="exon 8 terminal protein RNA"
FT   promoter        1676..1676
FT                   /note="TATA: TATAAAG"
FT   promoter        1691..1691
FT                   /note="TATA: TATTAAA BN-R1 late promoter before BNRF1,
FT                   gives 4.1kb late RNA. Probably encodes non glycosylated
FT                   140kd protein in membrane antigen. Also two latent RNAs
FT                   spliced underneath this RNA, lengths 1.8 and 2.0kb (Hudson
FT                   et al, 1985). The longer one encodes terminal protein."
FT   CDS             1736..5692
FT                   /note="BNRF1 reading frame, 5 NXT/S"
FT   misc_feature    complement(1795..1795)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    3955..3955
FT                   /note="BAM: Bam H1 Nhet/h"
FT   misc_feature    3994..3994
FT                   /note="BAM: Bam H1 h/C"
FT   mRNA            5408..5856
FT                   /note="exon 9 terminal protein RNA"
FT   misc_feature    5841..5841
FT                   /note="polyA signal: AATAAA, end of 4.1kb late RNA and TP
FT                   latent RNA."
FT   misc_feature    5863..5863
FT                   /note="alternative end to TP cDNAs"
FT   promoter        6097..6097
FT                   /note="TATA: TATAAGA"
FT   misc_feature    6629..6795
FT                   /note="Pol III RNA EBER 1"
FT   promoter        complement(6823..6823)
FT                   /note="TATA: CATAAAT"
FT   misc_feature    6956..7128
FT                   /note="Pol III RNA EBER 2"
FT   rep_origin      7315..9312
FT                   /note="origin of replication, ori P (Yates et al, 1984,
FT                   1985)"
FT   repeat_region   7421..8042
FT                   /note="21x30bp repeats, binding sites for EBNA-1 (site I,
FT                   Rawlins et al, 1985). Tandem repeat part of oriP (Reisman
FT                   et al, 1985). Also functions as a cell type specific
FT                   enhancer (Reisman et al, 1985; Lupton and Levine, 1985)"
FT   promoter        7738..7738
FT                   /note="TATA: TATAAAT"
FT   promoter        7888..7888
FT                   /note="TATA: TATAAAT"
FT   promoter        8573..8573
FT                   /note="TATA: CATAAAT"
FT   misc_feature    complement(8680..8680)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    complement(8755..8755)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    8962..8962
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    9021..9133
FT                   /note="HPN: dyad symmetry, site II for EBNA-1 binding
FT                   (Rawlins et al, 1985). Dyad symmetry part of oriP (Reisman
FT                   et al, 1985)"
FT   promoter        complement(9398..9398)
FT                   /note="TATA: TATAAAT"
FT   promoter        9631..9631
FT                   /note="TATA: TATAAAT BC-R1 late promoter before BCRF1"
FT   CDS             9675..10187
FT                   /note="BCRF1 reading frame"
FT   promoter        10076..10076
FT                   /note="TATA: GATAAAA"
FT   misc_feature    complement(10148..10148)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    10173..10173
FT                   /note="polyA signal: ATTAAA"
FT   misc_feature    10257..10257
FT                   /note="polyA signal: AATAAA, end of 0.8kb late RNA from
FT                   BCR1 and end of 1.6 kb late RNA, start unknown"
FT   misc_feature    complement(10277..10277)
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(10975..10975)
FT                   /note="TATA: CATAAAT"
FT   promoter        11305..11305
FT                   /note="TATA: TACAAAA; BCR2 promoter for highly spliced EBN
A
 FT                  latent RNAs."
FT   mRNA            11336..11480
FT                   /note="exon C1 of Bodescot et al (1986) RNAs"
FT   promoter        11524..11524
FT                   /note="TATA: TATAATT"
FT   misc_feature    complement(11587..11587)
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(11606..11606)
FT                   /note="TATA: CATAAAT"
FT   mRNA            11626..11657
FT                   /note="exon C2 of Bodescot et al (1986) RNAs"
FT   promoter        11796..11796
FT                   /note="TATA: TATAAGT"
FT   promoter        complement(11799..11799)
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FT                   /note="TATA: TATAAAA"
FT   repeat_region   12001..15072
FT                   /note="3072 repeat 1"
FT   CDS             12541..13689
FT                   /note="BCRF2 3072 repeat, reading frame 1"
FT   misc_feature    13215..13215
FT                   /note="BAM: BamH1 C/W"
FT   promoter        14352..14352
FT                   /note="*TATA: TATAAAG BWR1 one of the promoters for highly
FT                   spliced EBNA and LP RNAs (Sample et al, 1986; Speck et al,
FT                   1986)"
FT   mRNA            14384..14410
FT                   /note="*exon W0 of EBNA/LP RNAs"
FT   mRNA            14554..14619
FT                   /note="*exon W1 (also W66) part of leader protein (LP)
FT                   gene. LP is also called EBNA-5 (Dillner et al, 1986) and
FT                   EBNA-4 (Rowe et al, 1987)."
FT   mRNA            14559..14619
FT                   /note="*exon W1' (also W61) of EBNA/LP RNAs forms initiato
r
 FT                  met when fused to exon W0 or exon C2."
FT   mRNA            14701..14832
FT                   /note="*exon W2 (also W132) part of LP gene"
FT   repeat_region   15073..18144
FT                   /note="3072 repeat 2"
FT   CDS             15613..16761
FT                   /note="BWRF1 reading frame 2"
FT   misc_feature    16287..16287
FT                   /note="BAM: BamH1 W/W"
FT   promoter        17424..17424
FT                   /note="TATA: TATAAAG"
FT   mRNA            17626..17691
FT                   /note="Exon W1"
FT   mRNA            17773..17904
FT                   /note="Exon W2"
FT   repeat_region   18145..21216
FT                   /note="3072 repeat 3"
FT   CDS             18685..19833
FT                   /note="BWRF1 reading frame 3"
FT   misc_feature    19359..19359
FT                   /note="BAM: BamH1 W/W"
FT   promoter        20496..20496
FT                   /note="TATA: TATAAAG"
FT   mRNA            20698..20763
FT                   /note="Exon W1"
FT   mRNA            20845..20976
FT                   /note="Exon W2"
FT   repeat_region   21217..24288
FT                   /note="3072 repeat 4"
FT   CDS             21757..22905
FT                   /note="BWRF1 reading frame 4"
FT   misc_feature    22431..22431
FT                   /note="BAM: BamH1 W/W"
FT   promoter        23568..23568
FT                   /note="TATA: TATAAAG"
FT   mRNA            23771..23835
FT                   /note="Exon W1"
FT   mRNA            23917..24048
FT                   /note="Exon W2"
FT   repeat_region   24289..27360
FT                   /note="3072 repeat 5"
FT   CDS             24829..25977
FT                   /note="BWRF1 reading frame 5"
FT   misc_feature    25503..25503
FT                   /note="BAM: BamH1 W/W"
FT   promoter        26640..26640
FT                   /note="TATA: TATAAAG"
FT   mRNA            26842..26907
FT                   /note="Exon W1"
FT   mRNA            26989..27120
FT                   /note="Exon W2"
FT   repeat_region   27361..30432
FT                   /note="3072 repeat 6"
FT   CDS             27901..29049
FT                   /note="BWRF1 reading frame 6"
FT   misc_feature    28575..28575
FT                   /note="BAM: BamH1 W/W"
FT   promoter        29712..29712
FT                   /note="TATA: TATAAAG"
FT   mRNA            29914..29979
FT                   /note="Exon W1"
FT   mRNA            30061..30192
FT                   /note="Exon W2"
FT   repeat_region   30433..33504
FT                   /note="3072 repeat 7"
FT   CDS             30973..32121
FT                   /note="BWRF1 reading frame 7"
FT   misc_feature    31647..31647
FT                   /note="BAM: BamH1 W/W"
FT   promoter        32784..32784
FT                   /note="TATA: TATAAAG"
FT   mRNA            32986..33051
FT                   /note="Exon W1"
FT   mRNA            33133..33264
FT                   /note="Exon W2"
FT   repeat_region   33505..36576
FT                   /note="3072 repeat 8"
FT   CDS             34045..35193
FT                   /note="BWRF1 reading frame 8"
FT   misc_feature    34719..34719
FT                   /note="BAM: BamH1 W/W"
FT   promoter        35856..35856
FT                   /note="TATA: TATAAAG"
FT   mRNA            36058..36123
FT                   /note="Exon W1"
FT   mRNA            36205..36336
FT                   /note="Exon W2"
FT   repeat_region   36577..39648
FT                   /note="3072 repeat 9"
FT   CDS             37117..38265
FT                   /note="BWRF1 reading frame 9"
FT   misc_feature    37791..37791
FT                   /note="BAM: BamH1 W/W"
FT   promoter        38928..38928
FT                   /note="TATA: TATAAAG"
FT   mRNA            39130..39195
FT                   /note="Exon W1"
FT   mRNA            39277..39408
FT                   /note="Exon W2"
FT   repeat_region   39649..42720
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FT                   /note="3072 repeat 10"
FT   CDS             40189..41337
FT                   /note="BWRF1 reading frame 10"
FT   misc_feature    40863..40863
FT                   /note="BAM: BamH1 W/W"
FT   promoter        42000..42000
FT                   /note="TATA: TATAAAG"
FT   mRNA            42202..42267
FT                   /note="Exon W1"
FT   mRNA            42349..42480
FT                   /note="Exon W2"
FT   repeat_region   42721..45792
FT                   /note="3072 repeat 11"
FT   CDS             43261..44409
FT                   /note="BWRF1 reading frame 11"
FT   misc_feature    43935..43935
FT                   /note="BAM: BamH1 W/W"
FT   promoter        45072..45072
FT                   /note="TATA: TATAAAG"
FT   mRNA            45274..45339
FT                   /note="Exon W1"
FT   misc_feature    45415..52824
FT                   /note="DEL: DAUDI deletion (Jones et al, 1984)"
FT   mRNA            45421..45552
FT                   /note="Exon W2"
FT   misc_feature    45644..52450
FT                   /note="DEL: P3HR1 deletion (Jeang and Hayward, 1983)"
FT   repeat_region   45793..47643
FT                   /note="3072 repeat 12"
FT   CDS             46333..47481
FT                   /note="BWRF1 reading frame 12"
FT   misc_feature    47007..47007
FT                   /note="BAM: BamH1 W/Y"
FT   mRNA            47761..47793
FT                   /note="Exon Y1 Bodescot et al, 1984"
FT   promoter        47831..47831
FT                   /note="TATA: TATAAGT"
FT   mRNA            47878..47999
FT                   /note="Exon Y2 Bodescot et al, 1984 and EBNA-1 (Speck and
FT                   Strominger,1985), last common exon"
FT   misc_feature    complement(48023..48023)
FT                   /note="polyA signal: AATAAA"
FT   CDS             48386..50032
FT                   /note="Coding exon for EBNA-2 (Sample et al,1986)"
FT   mRNA            48386..48444
FT                   /note="exon Bodescot et al, 1984"
FT   CDS             48429..49964
FT                   /note="BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillne
r
FT                   et al, 1984)"
FT   repeat_region   48678..48800
FT                   /note="14 x CCCCCACCA repeats"
FT   misc_feature    48848..48848
FT                   /note="BAM: BamH1 Y/H"
FT   promoter        49350..49350
FT                   /note="TATA: TATAACA"
FT   promoter        complement(49353..49353)
FT                   /note="TATA: TATAAAA"
FT   repeat_region   49525..49578
FT                   /note="9 x GGGGCA repeats"
FT   mRNA            49852..50032
FT                   /note="exon (Bodescot et al 1984)"
FT   misc_feature    50003..50003
FT                   /note="polyA signal: AATAAA, end of Bodescot T1 RNA and
FT                   EBNA-2 RNA (3.0kb latent RNA in IB4 cells)"
FT   promoter        complement(50156..50156)
FT                   /note="TATA: TATAAGT"
FT   misc_feature    complement(50317..50317)
FT                   /note="polyA signal: AATAAA, end of 2.5kb early RNA from
FT                   52817"
FT   repeat_region   50578..52115
FT                   /note="12 x 125bp repeats"
FT   misc_feature    complement(50578..52557)
FT                   /note="BHLF1 early reading frame"
FT   misc_feature    52654..53697
FT                   /note="region homologous to Eco R1 C of Raji"
FT   promoter        complement(52817..52817)
FT                   /note="TATA: GATAAAA promoter for 2.5kb early RNA
FT                   containing BHLF1 (Jeang and Hayward, 1983; Freese et
FT                   al,1983)"
FT   promoter        53759..53759
FT                   /note="TATA: TATTAAC likely promoter for class III and IV
FT                   early RNAs encoding BHRF1 (Pearson et al, 1987)"
FT   misc_feature    53895..53895
FT                   /note="DONOR: CGGGTAACT donor for splice to 54335 in class
FT                   IV early RNAs encoding BHRF1 (Pearson et al, 1987)"
FT   misc_feature    54335..54335
FT                   /note="ACCEPT: TTTTCTAG acceptor from 48444 in class I,
FT                   47999 in class II, and 53895 in class IV early RNAs
FT                   encoding BHRF1 (Pearson et al, 1987)"
FT   misc_feature    54376..54948
FT                   /note="BHRF1 reading frame, limited homolgy to bcl-2 gene.
FT                   Early gene in B95-8 cells and part of restricted EA
FT                   complex."
FT   promoter        54591..54591
FT                   /note="TATA: TATAACA"
FT   promoter        complement(54594..54594)
FT                   /note="TATA: TATAAAT"
FT   misc_feature    54853..54853
FT                   /note="BAM: BamH1 H/F"
FT   misc_feature    complement(54929..54929)
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(54977..54977)
FT                   /note="TATA: TATAAAG"
FT   misc_feature    55518..55518
FT                   /note="polyA signal: AATAAA, 3' end of 2.5kb, 1.9kb, 1.7kb
FT                   and 0.6kb early RNAs"
FT   misc_feature    complement(55990..55990)
FT                   /note="polyA signal: AATAAA, 3' end of 2.3kb and 1.1kb
FT                   early RNAs from 58568 and 57081"
FT   promoter        complement(56132..56132)
FT                   /note="TATA: TATAAAG"
FT   misc_feature    complement(55982..56935)
FT                   /note="BFLF2 reading frame, 4 NXT/S, homologous to RF 27 i
n
FT                   VZV and HFRF2 in CMV"
FT   promoter        complement(57081..57081)
FT                   /note="TATA: TATTTAA before BFLF2; BFL2 promoter gives
FT                   1.1kb early RNA"
FT   promoter        complement(58088..58088)
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FT                   /note="TATA: GATAAAA"
FT   CDS             complement(56951..58525)
FT                   /note="BFLF1 reading frame, 2 NXT/S homologous to RF 26 in
FT                   VZV and HFRF1 in CMV"
FT   promoter        complement(58568..58568)
FT                   /note="TATA: TATTAAA before BFLF1, BFL1 promoter gives
FT                   2.3kb early RNA"
FT   promoter        58832..58832
FT                   /note="TATA: TATAAAA before BFRF1"
FT   CDS             58891..59901
FT                   /note="BFRF1 early reading frame, 1 NXT/S, homologous to
FT                   HFLF4 in CMV"
FT   CDS             59610..61580
FT                   /note="BFRF2 early reading frame, homologous to HFLF5 in
FT                   CMV"
FT   promoter        complement(61062..61062)
FT                   /note="TATA: GATAAAA"
FT   promoter        61344..61344
FT                   /note="TATA: TATTTAA before BFRF3"
FT   CDS             61456..62034
FT                   /note="BFRF3 early reading frame"
FT   misc_feature    complement(62068..62068)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    62069..62069
FT                   /note="polyA signal: AATAAA, 3' end of 10, 6.5, 3.7, 3.4,
FT                   3.1, 2.5 and 0.8kb early RNAs"
FT   misc_feature    62249..62249
FT                   /note="BAM: BamH1 F/Q"
FT   misc_feature    62430..62477
FT                   /note="Site III for EBNA-1 binding (Rawlins et al, 1985)"
FT   misc_feature    66121..66121
FT                   /note="BAM: BamH1 Q/U"
FT   mRNA            67477..67649
FT                   /note="Exon in EBNA-1 RNA (Speck and Strominger,1985) and
FT                   cDNA clone T4 (Bodescot et al, 1986)"
FT   misc_feature    69410..69410
FT                   /note="BAM: BamH1 U/P"
FT   repeat_region   69684..69930
FT                   /note="5 x 51bp repeats"
FT   repeat_region   70387..70521
FT                   /note="9 x 15bp repeat"
FT   promoter        70750..70750
FT                   /note="TATA: CATAAAA"
FT   CDS             complement(62081..71527)
FT                   /note="BPLF1 reading frame, 1 NXT/S, analogous to VZV RF22
"
FT   promoter        complement(72192..72192)
FT                   /note="TATA: TATTAAA before BPLF1"
FT   misc_feature    73468..73468
FT                   /note="BAM: BamH1 P/O"
FT   promoter        75017..75017
FT                   /note="TATA: TATTTAA BO-R1 late promoter before BORF1,
FT                   gives 3.9kb late RNA"
FT   CDS             75238..76332
FT                   /note="BORF1 late reading frame, 2 NXT/S homologous to VZV
FT                   RF20"
FT   CDS             complement(71523..75239)
FT                   /note="BOLF1 reading frame, 1 NXT/S analogous to VZV RF 21
"
FT   promoter        complement(75322..75322)
FT                   /note="TATA: TATTTAG before BOLF1"
FT   promoter        75819..75819
FT                   /note="TATA: TATAAAG"
FT   misc_feature    75838..75838
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    complement(76126..76126)
FT                   /note="polyA signal: AATAAA"
FT   promoter        76169..76169
FT                   /note="TATA: TACATAT BO-R2 early promoter before BORF2,
FT                   gives 2.8kb RNA"
FT   misc_feature    complement(76300..76300)
FT                   /note="polyA signal: AATAAA"
FT   CDS             76407..78887
FT                   /note="BORF2 early reading frame, 2 NXT/S. Homology HSV
FT                   140K ribonucleotide reductase (Gibson et al, 1984) and RF
FT                   19 VZV"
FT   misc_feature    77835..77835
FT                   /note="BAM: Bam H1 O/a"
FT   promoter        78804..78804
FT                   /note="TATA: TATAAGT Ba-R1 early promoter before BaRF1,
FT                   gives 3.5kb RNA"
FT   misc_feature    78883..78883
FT                   /note="polyA signal: AATAAA, end of 3.9kb late RNA from
FT                   75017 and 2.8kb early RNA from 76169"
FT   misc_feature    complement(78896..78896)
FT                   /note="polyA signal: AATAAA"
FT   CDS             78900..79808
FT                   /note="BaRF1 early reading frame, homologous to HSV 38K
FT                   ribonucleotide reductase (Gibson et al, 1984) and RF 18
FT                   VZV"
FT   promoter        complement(79495..79495)
FT                   /note="TATA: TATAACA"
FT   misc_feature    79537..79537
FT                   /note="BAM: Bam H1 a/M"
FT   promoter        79840..79840
FT                   /note="TATA: CATAAAT BM-R1 early promoter before BMRF1,
FT                   gives 2.5kb RNA"
FT   CDS             79899..81113
FT                   /note="BMRF1 early reading frame. Early antigen protein
FT                   recognised by R3 monoclonal (Pearson et al 1983; Cho et al
'
FT                   1985a)"
FT   promoter        80779..80779
FT                   /note="TATA: TATTTAA BM-R2 late promoter before BMRF2"
FT   misc_feature    complement(80782..80782)
FT                   /note="polyA signal: AATAAA"
FT   promoter        80832..80832
FT                   /note="TATA: GATAAAA, possible promoter for 1.4kb late RNA
FT                   encoding BMRF2"
FT   CDS             81118..82191
FT                   /note="BMRF2 early reading frame"
FT   promoter        81751..81751
FT                   /note="TATA: CATAAAT"
FT   misc_feature    82180..82180
FT                   /note="polyA signal: ATTAAA, end of 3.5kb early RNA from
FT                   78804, 2.5kb early RNA from 79840 and 1.4kb late RNA"
FT   promoter        complement(82311..82311)
FT                   /note="TATA: CATAAAT"
FT   repeat_region   82319..82461
FT                   /note="2x71bp repeats"
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FT   misc_feature    complement(82747..82747)
FT                   /note="polyA signal: AATAAA"
FT   repeat_region   83640..83729
FT                   /note="10x9bp repeats"
FT   misc_feature    complement(84122..84122)
FT                   /note="ACCEPT: CTCCCCTCTGCAG acceptor in spliced form of
FT                   BMLF1 RNA"
FT   CDS             complement(82746..84122)
FT                   /note="BMLF1 early reading frame. Diffuse early antigen
FT                   (Cho et al, 1985b). Also homologous to RF 4 VZV and IE63 o
f
FT                   HSV.(BSLF2 + BMLF1) is also called EB2 (Chevallier-Greco e
t
FT                   al, 1986). General transactivator of transcription
FT                   (Lieberman et al, 1986)."
FT   misc_feature    complement(84227..84227)
FT                   /note="DONOR: CAGGTAAGA donor in spliced form of BMLF1 RNA
"
FT   misc_feature    84233..84233
FT                   /note="BAM: Bam H1 M/S"
FT   CDS             complement(84229..84288)
FT                   /note="BSLF2 early reading frame in 5' exon of spliced RNA
FT                   encoding BMLF1"
FT   promoter        complement(84356..84356)
FT                   /note="TATA: CATAAAT before BSLF2 and BMLF1. Two RNAs star
t
FT                   here; one is spliced and the other is unspliced, both
FT                   traverse BMLF1."
FT   CDS             complement(84260..86881)
FT                   /note="BSLF1 reading frame, homologous to RF 6 VZV"
FT   promoter        86882..86882
FT                   /note="TATA: TATTTAA BS-R1 late promoter before BSRF1"
FT   CDS             86924..87580
FT                   /note="BSRF1 reading frame"
FT   misc_feature    complement(87134..87134)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    87599..87599
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    complement(87613..87613)
FT                   /note="polyA signal: AATAAA, end 1.0kb early RNA from BLL3
"
FT   misc_feature    87650..87650
FT                   /note="BAM: Bam H1 S/L"
FT   CDS             complement(87641..88474)
FT                   /note="BLLF3 early reading frame (BLLF2 in Baer et al,
FT                   1984). Homologous to RF 8 VZV and dUTPase HSV."
FT   promoter        88507..88507
FT                   /note="TATA: TATATAT BL-R1 late promoter before BLRF1,
FT                   gives 1.0kb late RNA"
FT   promoter        88511..88511
FT                   /note="TATA: TATAAGA"
FT   promoter        complement(88514..88514)
FT                   /note="TATA: TATATAT BL-L3 early promoter before BLLF3,
FT                   gives 1.0kb early RNA"
FT   CDS             88547..88855
FT                   /note="BLRF1 late reading frame"
FT   promoter        88863..88863
FT                   /note="TATA: TATTTAA BL-R2 late promoter before BLRF2,
FT                   gives 0.6kb late RNA"
FT   CDS             88925..89413
FT                   /note="BLRF2 late reading frame, 2 NXS/T"
FT   misc_feature    89412..89412
FT                   /note="polyA signal: AATAAA, end of 1.0kb and 0.6kb late
FT                   RNAs"
FT   misc_feature    complement(89425..89425)
FT                   /note="polyA signal: AATAAA, end of 0.7kb early, 2.2kb lat
e
FT                   and 2.8kb late RNA"
FT   promoter        complement(89434..89434)
FT                   /note="TATA: TATAAAG"
FT   CDS             complement(89569..90013)
FT                   /note="BLLF2 early reading frame (BLLF3 in Baer et al,
FT                   1984)"
FT   promoter        complement(90051..90051)
FT                   /note="TATA: TATAACA BL-L2 early promoter before BLLF2,
FT                   gives 0.7kb early RNA"
FT   repeat_region   90177..90639
FT                   /note="21 copies of 21bp approximate repeat"
FT   intron          complement(90062..90652)
FT                   /note="intervening sequence in gp220 gene"
FT   CDS             complement(89433..92153)
FT                   /note="BLLF1b, late reading frame gp220 membrane antigen,
FT                   spliced form of BLLF1a (Hummel et al, 1984; Biggin et al,
FT                   1984; Beisel et al, 1985)"
FT   CDS             complement(89433..92153)
FT                   /note="BLLF1a, late reading frame, gp350 membrane antigen,
FT                   36 NXT/S (Hummel et al, 1984; Biggin et al, 1984; Beisel e
t
FT                   al, 1985)"
FT   promoter        complement(92192..92192)
FT                   /note="TATA: TATTAAA BL-L1 late promoter before BLLF1a,b.
FT                   Gives 2.8 and 2.2kb late RNAs"
FT   mRNA            92238..92581
FT                   /note="Exon in Bodescot et al (1986) RNA (spliced from
FT                   20763 to 92670)"
FT   CDS             92243..92581
FT                   /note="BLRF3 reading frame"
FT   mRNA            92670..95248
FT                   /note="Exon in (Bodescot et al, 1986) RNA from 92581, to 3
'
FT                   end"
FT   CDS             92670..95162
FT                   /note="BERF1 frame, homology with BERF2b and BERF4. A
FT                   fusion of BLRF3 with BERF1 encodes EBNA-3A, latent cycle
FT                   gene. (Hennessy et al, 1986, Joab et al, 1987)"
FT   misc_feature    92703..92703
FT                   /note="BAM: Bam H1 L/E"
FT   promoter        complement(93161..93161)
FT                   /note="TATA: CATAAAT"
FT   promoter        93479..93479
FT                   /note="TATA: TATAAGA"
FT   promoter        complement(93482..93482)
FT                   /note="TATA: TATAAAT"
FT   repeat_region   94208..94277
FT                   /note="repeat type A"
FT   repeat_region   94281..94306
FT                   /note="repeat type B"
FT   repeat_region   94307..94381
FT                   /note="repeat type C"
FT   repeat_region   94386..94411
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FT                   /note="repeat type B"
FT   repeat_region   94412..94489
FT                   /note="repeat type C"
FT   repeat_region   94490..94560
FT                   /note="repeat type A"
FT   repeat_region   94571..94648
FT                   /note="repeat type C"
FT   repeat_region   94649..94719
FT                   /note="repeat type A"
FT   repeat_region   94896..94982
FT                   /note="repeat type D"
FT   repeat_region   94983..95069
FT                   /note="repeat type D"
FT   misc_feature    95221..95221
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    complement(95272..95272)
FT                   /note="polyA signal: AATAAA"
FT   CDS             95353..95724
FT                   /note="BERF2a reading frame"
FT   CDS             95725..98244
FT                   /note="BERF2b frame, homology with BERF1 and BERF4. BERF2a
FT                   and BERF2b are spliced together to make EBNA3B (EBNA4A)
FT                   latent protein."
FT   misc_feature    complement(95819..95819)
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(95853..95853)
FT                   /note="TATA: TATAAAT"
FT   misc_feature    complement(96276..96276)
FT                   /note="polyA signal: AATAAA"
FT   repeat_region   97522..97698
FT                   /note="3x60bp repeat"
FT   CDS             98323..98769
FT                   /note="BERF3 reading frame"
FT   mRNA            98364..98730
FT                   /note="Exon in EBNA-1 RNA (Speck and Strominger, 1985)"
FT   misc_feature    98731..98731
FT                   /note="DONOR: AAGGTGAGT donor"
FT   CDS             98805..101420
FT                   /note="BERF4 frame, homology with BERF1 and BERF2b. BERF3
FT                   and BERF4 are spliced together to make the EBNA3C (EBNA 4B
)
FT                   latent protein."
FT   mRNA            98805..99050
FT                   /note="Exon in T4 cDNA (Bodescot et al 1986). 99050 is not
FT                   the end of the RNA."
FT   misc_feature    99126..102118
FT                   /note="DEL: Deletion in Raji"
FT   promoter        99443..99443
FT                   /note="TATA: CATAAAA"
FT   misc_feature    100104..100104
FT                   /note="DONOR: ACCGTGAGT possible donor before repeat."
FT   repeat_region   100122..100304
FT                   /note="10 x 15bp repeat"
FT   misc_feature    100528..100528
FT                   /note="DONOR: CTGGTAAGG possible donor"
FT   misc_feature    100613..100613
FT                   /note="BAM: Bam H1 E/e1"
FT   repeat_region   100665..100781
FT                   /note="3x39bp repeat"
FT   promoter        complement(100860..100860)
FT                   /note="TATA: TATAACA"
FT   misc_feature    100919..100919
FT                   /note="BAM: Bam H1 e1/e2"
FT   misc_feature    101426..101426
FT                   /note="BAM: Bam H1 e2/e3"
FT   promoter        101690..101690
FT                   /note="TATA: CATAAAA"
FT   misc_feature    101765..101765
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(101786..101786)
FT                   /note="TATA: TATAAAG"
FT   misc_feature    101947..101947
FT                   /note="BAM: Bam H1 e3/Z"
FT   misc_feature    complement(102098..102098)
FT                   /note="DONOR: CAGGTGAGG possible donor"
FT   CDS             complement(101448..102116)
FT                   /note="BZLF2 reading frame 3x NXT/S. 2.5kb late RNA
FT                   traverses BZLF2, ends unknown."
FT   promoter        102153..102153
FT                   /note="TATA: TATTAAT"
FT   misc_feature    complement(102156..102156)
FT                   /note="polyA signal: AATAAA 3' end of 0.9kb and 2.8kb RNAs
FT                   encoding BZLF1 and BRLF1"
FT   promoter        complement(102160..102160)
FT                   /note="TATA: TATTAAT"
FT   mRNA            complement(102126..102341)
FT                   /note="3' terminal exon of 0.9kb and 2.8kb early RNAs"
FT   promoter        complement(102380..102380)
FT                   /note="TATA: CATAAAT"
FT   promoter        102415..102415
FT                   /note="TATA:TATATAC"
FT   promoter        complement(102420..102420)
FT                   /note="TATA: TATATAC"
FT   misc_feature    complement(102504..102504)
FT                   /note="polyA signal: AATAAA, apparently not functional"
FT   mRNA            complement(102426..102530)
FT                   /note="Exon of 0.9kb and 2.8kb early RNAs"
FT   repeat_region   102581..102652
FT                   /note="semi-repetitive sequence, homologous to human c-fos
FT                   3' sequence"
FT   misc_feature    complement(102918..102918)
FT                   /note="splice acceptor used in RZ fusion gene (Sargeant)"
FT   CDS             complement(102213..103155)
FT                   /note="BZLF1 reading frame, modified from Baer et al, 1984
.
 FT                  Has two splices within frame. 2xNXT/S. Immediate early gen
e
 FT                  which disrupts latency (Countryman and Miller, 1985),
 FT                  called EB1 by Chevallier-Greco et al, 1986 and ZEBRA by
 FT                  Miller."
 FT  mRNA            complement(102655..103194)
 FT                  /note="First exon of 0.9kb early RNA encoding BZLF1"
 FT  promoter        complement(103231..103231)
 FT                  /note="TATA: TTTAAA of BZL1 immediate early promoter gives
 FT                  0.9kb RNA"
 FT  misc_feature    complement(103256..103311)
 FT                  /note="Upstream of BZL1, homology to 106243 to 106188"
 FT  misc_feature    complement(103453..103462)
 FT                  /note="TAATGAAATC sequence"
 FT  misc_feature    103741..103741
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FT                   /note="BAM: Bam H1 Z/g"
FT   misc_feature    103816..103816
FT                   /note="BAM: Bam H1 g/R"
FT   mRNA            complement(104927..104989)
FT                   /note="BRLF2 poss. small 5' exon"
FT   promoter        105016..105016
FT                   /note="TATA: TATAAAT before BRRF1, possible promoter for
FT                   1.1 kb early RNA encoding BRRF1"
FT   promoter        complement(105019..105019)
FT                   /note="TATA: TATAAAT before BRLF2"
FT   CDS             105182..106114
FT                   /note="BRRF1 early reading frame"
FT   CDS             complement(103369..105183)
FT                   /note="BRLF1 reading frame, (immediate?) early gene, acts
FT                   as transcription activator."
FT   misc_feature    complement(105185..105185)
FT                   /note="ACCEPT: splice acceptor in 2.8kb early RNA encoding
FT                   BRLF1 and RZ fusion gene (Sargeant)"
FT   mRNA            complement(104926..105185)
FT                   /note="exon in RZ fusion gene (Sargeant)"
FT   promoter        105213..105213
FT                   /note="TATA: CATTAAA"
FT   misc_feature    106110..106110
FT                   /note="polyA signal: AATAAA, 3' end of early 1.1kb RNA
FT                   encoding BRRF1"
FT   misc_feature    complement(106125..106125)
FT                   /note="DONOR: CAGGTAAGA possible donor"
FT   promoter        complement(106213..106213)
FT                   /note="TATA: CATAAAA"
FT   promoter        106243..106243
FT                   /note="TATA: TATAAAA before BRRF2, possible promoter for
FT                   1.8 kb RNA encoding BRRF2"
FT   misc_feature    complement(106188..106243)
FT                   /note="Homology to upstream region of BZL1"
FT   CDS             106302..107915
FT                   /note="BRRF2 reading frame"
FT   promoter        complement(106385..106385)
FT                   /note="TATA: GATAAAA"
FT   misc_feature    complement(106973..106973)
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(107124..107124)
FT                   /note="TATA: GATAAAA"
FT   misc_feature    107457..107457
FT                   /note="BAM: Bam H1 R/f"
FT   misc_feature    107565..107565
FT                   /note="BAM: Bam H1 f/K"
FT   misc_feature    107914..107914
FT                   /note="polyA signal: AATAAA, 3' end of 1.8kb RNA encoding
FT                   BBRF2"
FT   misc_feature    107942..107942
FT                   /note="ACCEPT: splice acceptor for EBNA-1 RNA (from 98730)
"
FT   CDS             107950..109875
FT                   /note="BKRF1 encodes EBNA-1 protein, latent cycle gene."
FT   repeat_region   108217..108924
FT                   /note="EBNA triplet repeat GGA,GCA,GGG."
FT   misc_feature    109856..109856
FT                   /note="DONOR: AGGGTGAGG possible donor at end BKRF1"
FT   promoter        109905..109905
FT                   /note="TATA: TATTAAA before BKRF2, possible start for 2.3k
```

```
b
FT                   late RNA"
FT   misc_feature    109906..109906
FT                   /note="polyA signal: ATTAAA"
FT   misc_feature    109937..109937
FT                   /note="polyA signal: AATAAA 3' end of EBNA-1 RNA"
FT   CDS             109958..110371
FT                   /note="BKRF2 reading frame"
FT   misc_feature    110271..110271
FT                   /note="DONOR: TCCGTGAGT possible donor at end of BKRF2"
FT   CDS             110275..111117
FT                   /note="BKRF3 reading frame, homologous to RF 59 VZV"
FT   misc_feature    111098..111098
FT                   /note="DONOR: TCGGTGAGA possible donor at end BKRF3"
FT   CDS             111107..111784
FT                   /note="BKRF4 reading frame, contains complex repetitive
FT                   sequence"
FT   misc_feature    111272..111272
FT                   /note="DONOR: GACGTGAGT poss.donor before rpt.seq. in
FT                   BKRF4"
FT   misc_feature    111719..111719
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    111787..111787
FT                   /note="polyA signal: AATAAA : currently unknown which is 3
'
FT                   end of the 2.3kb late and 1.1kb early RNAs"
FT   misc_feature    complement(111830..111830)
FT                   /note="polyA signal: AATAAA"
FT   promoter        112471..112471
FT                   /note="TATA: TATATAT"
FT   promoter        complement(112476..112476)
FT                   /note="TATA: TATATAA"
FT   misc_feature    112620..112620
FT                   /note="BAM: Bam H1 K/B"
FT   promoter        113876..113876
FT                   /note="TATA: TATTTAT before BBRF1"
FT   promoter        complement(113885..113885)
FT                   /note="TATA: CATAAAT"
FT   CDS             114204..116045
FT                   /note="BBRF1 late reading frame, homologous to RF 54 VZV"
FT   CDS             complement(111833..114259)
FT                   /note="BBLF4 early reading frame, very good homology to
FT                   RF55 VZV"
FT   CDS             115843..116781
FT                   /note="BBRF2 late reading frame, homologous to RF 53 VZV"
FT   promoter        complement(116683..116683)
FT                   /note="TATA: GATAAAA"
FT   misc_feature    complement(116696..116696)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    116785..116785
FT                   /note="polyA signal: AATAAA"
FT   CDS             complement(116784..117386)
FT                   /note="BBLF3 early reading frame, spliced to BBLF2. BBLF3
FT                   contains a consensus nucleotide binding site"
FT   intron          complement(117386..117515)
FT                   /note="intron spliced out in RNA linking BBLF2 and BBLF3"
FT   promoter        118981..118981
FT                   /note="TATA: TATAAAA BBR1 late promoter before BBRF3"
FT   promoter        119067..119067
FT                   /note="TATA: TTTAAAA BBR2 late promoter ?"
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FT   CDS             complement(117515..119080)
FT                   /note="BBLF2 early reading frame, spliced to BBLF3"
FT   promoter        119098..119098
FT                   /note="TATA: TATTTAA BBR3 late promoter before BBRF3"
FT   misc_feature    119108..119108
FT                   /note="DONOR: AAGGTGAAT possible donor"
FT   CDS             119137..120354
FT                   /note="BBRF3 late reading frame"
FT   misc_feature    120260..120260
FT                   /note="ACCEPT: ATCTTCCTCCAGGT possible acceptor"
FT   misc_feature    120358..120358
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    complement(120764..120764)
FT                   /note="polyA signal: AATAAA, 3' end of 0.6kb late, 1.6kb
FT                   early, 3.0kb early RNAs"
FT   CDS             complement(120750..120974)
FT                   /note="BBLF1 late reading frame, possibly homologous to RF
FT                   49 VZV"
FT   promoter        complement(121331..121331)
FT                   /note="TATA: TATTAAA BBL1 late promoter before BBLF1"
FT   promoter        121669..121669
FT                   /note="TATA: CATAAAT"
FT   promoter        121697..121697
FT                   /note="TATA: TATAAAG"
FT   promoter        121772..121772
FT                   /note="TATA: CATAAAG"
FT   misc_feature    122313..122313
FT                   /note="BAM: Bam H1 B/G"
FT   CDS             complement(120932..122341)
FT                   /note="BGLF5 early reading frame, homologous to RF 48 VZV
FT                   and alkaline exonuclease of HSV"
FT   misc_feature    complement(123506..123506)
FT                   /note="DONOR: AAGGTGACT possible donor"
FT   CDS             complement(122328..123692)
FT                   /note="BGLF4 early reading frame, homologous to RF 47 VZV"
FT   promoter        complement(124117..124117)
FT                   /note="TATA: TATAAAA"
FT   misc_feature    complement(124219..124219)
FT                   /note="polyA signal: AATAAA"
FT   CDS             124938..125915
FT                   /note="BGRF1 reading frame, homologous to RF 45 VZV and
FT                   spliced HSV gene (Costa et al, 1985). Spliced to BDRF1.
FT                   Northern blots in BGRF1 detect 2.7, 2.6, 2.1kb late and
FT                   1.9kb early RNAs. 2.6, 2.1kb RNAs very weak."
FT   CDS             complement(123944..124939)
FT                   /note="BGLF3 reading frame"
FT   promoter        complement(125113..125113)
FT                   /note="TATA: TATAAAT before BGLF3"
FT   misc_feature    complement(125484..125484)
FT                   /note="polyA signal: AATAAA, 3' end of 1.6kb late, 1.8kb
FT                   late, 3.0kb late and 3.7kb early RNAs"
FT   promoter        126277..126277
FT                   /note="TATA: GATAAAA"
FT   CDS             complement(125866..126873)
FT                   /note="BGLF2 late reading frame, poor homology to RF 44
FT                   VZV"
FT   promoter        complement(126929..126929)
FT                   /note="TATA: TATTAAA EEL8 late promoter before BGLF2, give
s
FT                   1.6kb late RNA"
FT   promoter        complement(127237..127237)
FT                   /note="TATA: TATAAAA, potential promoter for 1.8kb late
FT                   RNA"
FT   misc_feature    128029..128029
FT                   /note="polyA signal: AATAAA"
FT   CDS             complement(126854..128374)
FT                   /note="BGLF1 late reading frame"
FT   promoter        complement(128432..128432)
FT                   /note="TATA: TATTTAA before BGLF1, potential promoter for
FT                   3.0kb late RNA"
FT   misc_feature    128848..128848
FT                   /note="BAM: Bam H1 G/D"
FT   CDS             complement(128347..129021)
FT                   /note="BDLF4 early reading frame"
FT   promoter        complement(129054..129054)
FT                   /note="TATA: TATTTGC before BDLF4, potential promoter for
FT                   3.7kb early RNA"
FT   CDS             129188..130348
FT                   /note="BDRF1 reading frame, homologous to RF 42 VZV and
FT                   spliced gene in HSV (Costa et al, 1985). Spliced from
FT                   BGRF1. Northern blots in BDRF1 detect 2.7, 2.6 kb late and
FT                   1.9kb early RNAs. Possibly also 1.8kb early RNA."
FT   promoter        129374..129374
FT                   /note="TATA: TATAAGC"
FT   promoter        complement(129377..129377)
FT                   /note="TATA: TATAAAG"
FT   misc_feature    129413..129413
FT                   /note="DONOR: GTGGTAAGT possible donor"
FT   misc_feature    130347..130347
FT                   /note="polyA signal: ATTAAA"
FT   misc_feature    complement(130359..130359)
FT                   /note="polyA signal: AATAAA, 3' end of 0.9kb late RNA,
FT                   2.3kb late RNA and 3.2kb late RNA"
FT   CDS             complement(130365..131066)
FT                   /note="BDLF3 late reading frame 9xNXT/S"
FT   promoter        complement(131104..131104)
FT                   /note="TATA: TATAAAA EEL4 late promoter before BDLF3, give
s
FT                   0.9kb late RNA"
FT   promoter        132266..132266
FT                   /note="TATA: TATAAAA"
FT   CDS             complement(131130..132389)
FT                   /note="BDLF2 late reading frame"
FT   promoter        complement(132476..132476)
FT                   /note="TATA: TATTTAA before BDLF2, likely promoter for
FT                   2.3kb late RNA"
FT   CDS             complement(132403..133305)
FT                   /note="BDLF1 late reading frame, poor homology to RF 41
FT                   VZV"
FT   misc_feature    complement(133312..133312)
FT                   /note="polyA signal: AATAAA, 3' end of 4.5kb late RNA"
FT   misc_feature    complement(133332..133332)
FT                   /note="DONOR: AAGGTGGTT possible donor"
FT   promoter        complement(133352..133352)
FT                   /note="TATA: TATTAAA before BDLF1"
FT   promoter        complement(133386..133386)
FT                   /note="TATA: TATATAA"
FT   misc_feature    135178..135178
FT                   /note="polyA signal: AATAAA"
FT   promoter        135394..135394
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FT                   /note="TATA: TATAAGT"
FT   misc_feature    136624..136624
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    136868..136868
FT                   /note="BAM: Bam H1 D/c"
FT   CDS             complement(133324..137466)
FT                   /note="BcLF1 late reading frame, homologous to RF 40 VZV
FT                   and major capsid protein of HSV"
FT   promoter        complement(137710..137710)
FT                   /note="TATA: TATTAAA EHL1 promoter before BcLF1, gives
FT                   4.5kb late RNA"
FT   promoter        137857..137857
FT                   /note="TATA: CATAAAC"
FT   CDS             137862..139715
FT                   /note="BcRF1 reading frame"
FT   misc_feature    138019..138019
FT                   /note="BAM: Bam H1 c/b"
FT   misc_feature    139352..139352
FT                   /note="BAM: Bam H1 b/T"
FT   CDS             139642..140916
FT                   /note="BTRF1 reading frame. Northern blots detect 0.95 lat
e
FT                   and 3.8kb early RNA"
FT   misc_feature    complement(140902..140902)
FT                   /note="polyA signal: AATAAA, 3' end of 2.5kb late RNA"
FT   misc_feature    140970..140970
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    complement(141286..141286)
FT                   /note="polyA signal: AATAAA"
FT   promoter        142589..142589
FT                   /note="TATA: GATAAAA"
FT   misc_feature    142740..142740
FT                   /note="BAM: Bam H1 T/X"
FT   CDS             complement(140919..143036)
FT                   /note="BXLF2 late reading frame, encodes gp85; homologous
FT                   to RF 37 VZV and glycoprotein H of HSV (gpIII of VZV)"
FT   promoter        complement(143310..143310)
FT                   /note="TATA: TATAAGA ECL2 late promoter before BXLF2, give
s
FT                   2.5kb late RNA"
FT   misc_feature    143608..143608
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    144791..144791
FT                   /note="ACCEPT: TCTTTCGTTTTCAGG poss. acceptor before BXRF1
"
FT   CDS             144860..145606
FT                   /note="BXRF1 late reading frame, homologous to RF 35 VZV.
FT                   Basic (core?) protein."
FT   CDS             complement(143041..144861)
FT                   /note="BXLF1 early reading frame, thymidine kinase (Little
r
FT                   et al, 1986). Weak homology to RF 36 VZV and HSV thymidine
FT                   kinase. 4.0kb early RNA presumably encodes the TK. Also a
FT                   2.2kb late RNA here."
FT   misc_feature    144862..144862
FT                   /note="BAM: Bam H1 X/V"
FT   misc_feature    144945..144945
FT                   /note="DONOR: CAGGTAAGC possible donor at 3' BXRF1"
FT   promoter        complement(145135..145135)
FT                   /note="TATA: TATAACA before BXLF1"
FT   promoter        145302..145302
FT                   /note="TATA: TATTTAA before BVRF1, potential promoter for
FT                   1.9kb early RNA"
FT   CDS             145416..147128
FT                   /note="BVRF1 early reading frame, homologous to RF 34 VZV"
FT   misc_feature    complement(146926..146926)
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    147167..147167
FT                   /note="DONOR: AAGGTAAAT possible donor"
FT   misc_feature    147170..147170
FT                   /note="polyA signal: AATAAA, 3' end of 2.4kb late and 1.9k
b
FT                   early RNAs"
FT   promoter        147721..147721
FT                   /note="TATA: TATTTAT before BVRF2, potential promoter for
FT                   2.1kb early RNA"
FT   CDS             147927..149744
FT                   /note="BVRF2 early reading frame, N-terminus homologous to
FT                   RF 33 VZV"
FT   misc_feature    148007..148007
FT                   /note="BAM: Bam H1 V/d"
FT   promoter        148620..148620
FT                   /note="TATA: TATTTAA ECR1 late promoter before BdRF1, give
s
FT                   1.2kb late RNA"
FT   CDS             148707..149741
FT                   /note="BdRF1 reading frame; this is the C terminus of
FT                   BVRF2"
FT   misc_feature    149115..149115
FT                   /note="BAM: Bam H1 d/I"
FT   misc_feature    149727..149727
FT                   /note="polyA signal: AATAAA, 3' end of 2.1kb early and
FT                   1.2kb late RNAs"
FT   misc_feature    complement(149758..149758)
FT                   /note="polyA signal: AATAAA, 3' end of 1.0kb late, 1.5kb
FT                   late and 1.8kb late RNAs"
FT   CDS             complement(149782..150525)
FT                   /note="BILF2 late reading frame 11xNXT/S"
FT   promoter        complement(150571..150571)
FT                   /note="TATA: TATTTAG before BILF2. Potential promoter for
FT                   1.0kb late RNA."
FT   repeat_region   151236..151618
FT                   /note="repetitive sequence 3X"
FT   misc_feature    151767..151767
FT                   /note="polyA signal: AATAAA"
FT   promoter        complement(151780..151780)
FT                   /note="TATA: CATAAAA"
FT   misc_feature    152012..152013
FT                   /note="DEL: B95-8 deletion with respect to Raji"
FT   promoter        152230..152230
FT                   /note="TATA: CATAAAA"
FT   CDS             complement(152164..153099)
FT                   /note="BILF1 reading frame, membrane protein, 3xNXS/T"
FT   misc_feature    153259..153259
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    153637..153637
FT                   /note="HPN: 22bp 2-fold symmetric"
FT   misc_feature    complement(153690..153690)
FT                   /note="DONOR: AAAGTGAGG possible donor"
FT   misc_feature    154747..154747
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FT                   /note="BAM: Bam H1 I/A"
FT   misc_feature    complement(156707..156707)
FT                   /note="polyA signal: AATAAA; 3' end of 2.5kb late (gB) RNA
FT                   and 1.8kb late RNA"
FT   CDS             complement(153702..156746)
FT                   /note="BALF5 DNA polymerase (early), homologous to many DN
A
FT                   polymerases, CMV HFLF2 and RF 28 VZV. 4.5kb early RNA
FT                   apparently encodes BALF5, RNA ends unknown."
FT   promoter        158204..158204
FT                   /note="TATA: TATAAAA"
FT   CDS             complement(156752..159322)
FT                   /note="BALF4 late reading frame 9xNXT/S homologous to HSV1
FT                   glycoprotein B (Pellet et al, 1985), CMV HFLF1 and RF 31
FT                   VZV (gpII)"
FT   promoter        complement(159370..159370)
FT                   /note="TATA: TATTTAA ECL1 late promoter before BALF4, give
s
FT                   2.5kb late RNA"
FT   misc_feature    160966..160966
FT                   /note="polyA signal: AATAAA"
FT   misc_feature    160990..160990
FT                   /note="polyA signal: ATTAAA"
FT   misc_feature    complement(161013..161013)
FT                   /note="polyA signal: AATAAA, presumed end of 3.9kb early
FT                   RNA"
FT   CDS             complement(159312..161678)
FT                   /note="BALF3 reading frame"
FT   misc_feature    163978..166635
FT                   /note="DEL: deletion in Raji"
FT   CDS             complement(161387..164770)
FT                   /note="BALF2 early reading frame, homologous to RF 29 VZV
FT                   and major DNA binding protein HSV. 3.9kb early RNA"
FT   promoter        complement(164814..164814)
FT                   /note="TATA: CATTTAA before BALF2, presumed promoter for
FT                   3.9kb early RNA"
FT   misc_feature    complement(164851..164851)
FT                   /note="polyA signal: AATAAA"
FT   promoter        165442..165442
FT                   /note="TATA: GATAAAA"
FT   promoter        165466..165466
FT                   /note="TATA: TATAAGA EDR1 early promoter before BARF1,
FT                   gives 0.8kb early RNA"
FT   CDS             165504..166169
FT                   /note="BARF1 reading frame"
FT   CDS             complement(164858..165517)
FT                   /note="BALF1 early reading frame, 0.7kb early RNA"
FT   promoter        complement(165713..165713)
FT                   /note="TATA: TATAAAG before BALF1"
FT   misc_feature    166165..166165
FT                   /note="polyA signal: AATAAA 3' end of 0.8kb early RNA. Als
o
FT                   1kb late RNA in this region."
FT   promoter        166469..166475
FT                   /note="TATA: TTATTTT"
FT   mRNA            166498..166916
FT                   /note="Exon 1 of terminal protein RNA"
FT   misc_feature    166561..166563
FT                   /note="Likely initiator met of terminal protein"
FT   misc_feature    166614..166614
FT                   /note="BAM: Bam H1 A/Nhet"
FT   misc_feature    complement(166946..166946)
FT                   /note="polyA signal: AATAAA These 2 polyA sites are 3' end
FT                   of 0.8kb early, 2.5kb late and 2.5kb latent RNAs"
FT   misc_feature    complement(166950..166950)
FT                   /note="polyA signal: AATAAA"
FT   CDS             complement(167001..167303)
FT                   /note="BNLF2b reading frame"
FT   promoter        167320..167320
FT                   /note="TATA: CATAAAA"
FT   CDS             complement(167307..167486)
FT                   /note="BNLF2a reading frame"
FT   promoter        complement(167525..167525)
FT                   /note="TATA: TATAAAA EDL2 early promoter before BNLF2a,b.
FT                   Gives 0.8kb RNA"
FT   repeat_region   168399..168574
FT                   /note="5 x 33bp repeats"
FT   mRNA            complement(168163..168965)
FT                   /note="BNLF1 coding part of exon c of latent membrane
FT                   protein"
FT   misc_feature    complement(168966..168966)
FT                   /note="ACCEPT: TTTTTTCAACGCAGT possible acceptor"
FT   misc_feature    complement(169041..169041)
FT                   /note="DONOR: TTGGTAAGA donor"
FT   intron          complement(168966..169041)
FT                   /note="intervening sequence in BNLF1"
FT   mRNA            complement(169042..169128)
FT                   /note="BNLF1 exon b of latent membrane protein mRNA"
FT   misc_feature    complement(169129..169129)
FT                   /note="ACCEPT: TCCTCTTTCCCCAGT acceptor"
FT   promoter        complement(169201..169201)
FT                   /note="TATA: TATTACA EDL1A late promoter, gives 2.5kb late
FT                   RNA"
FT   misc_feature    complement(169206..169206)
FT                   /note="DONOR: TGAGTAAGT donor"
FT   intron          complement(169129..169206)
FT                   /note="intervening sequence in BNLF1"
FT   mRNA            complement(169207..169474)
FT                   /note="BNLF1 exon a of latent membrane protein mRNA"
FT   promoter        complement(169546..169546)
FT                   /note="TATA: TACATAAGC EDL1 promoter before BNLF1 gives
FT                   2.5kb latent RNA (LMP)"
FT   repeat_region   170094..170631
FT                   /note="terminal repeat 1 538bp"
FT   repeat_region   170632..171154
FT                   /note="terminal repeat 2 523bp"
FT   repeat_region   171155..171692
FT                   /note="terminal repeat 3 538bp"
FT   repeat_region   171693..172231
FT                   /note="terminal repeat 4 538bp"
XX
SQ   Sequence 172281 BP; 34054 A; 52511 C; 50755 G; 34961 T; 0 other;

Initial Score    =   170  Optimized Score   =   454  Significance = 10.52
Residue Identity =   50%  Matches           =   529  Mismatches   =   418
Gaps             =   105  Conservative Substitutions            =     0

                X       10           20        30        40        50
                CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
                ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
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     CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
 107030    107040    107050    107060    107070    107080    107090    107100

     60        70          80        90           100       110       120
     CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
      |    | ||||| | | ||  ||| ||||  ||  |    ||| | |   | || ||      |  |||||
     GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
         107110    107120    107130    107140    107150    107160     107170

        130       140       150       160       170       180        190
     CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
     | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
     CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
            107180    107190    107200      107210    107220    107230

        200       210       220          230        240       250         260
     -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
       ||  |   |     |   |  |    |||  |    |||||| || || |  |  ||||   ||  ||
     GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
  107240    107250      107260    107270    107280    107290    107300

            270         280           290       300       310       320
     CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
      |   ||||.|||  | |  ||| | ||    ||| | ||||||   |     ||| | || | | |    |
     GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
  107310    107320    107330    107340    107350          107360    107370

      330       340       350       360       370          380       390
     CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
       ||       ||  | ||||| |  |||  || |  ||||| ||||||  |   | |||||| ||||| ||
     GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
      107380    107390     107400      107410    107420    107430    107440

       400        410       420        430       440        450         460
     GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
     |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
     GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
       107450    107460    107470    107480      107490    107500    107510

            470          480        490       500       510       520
     GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
      | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
     AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
       107520    107530    107540    107550    107560    107570    107580

    530       540       550       560       570       580       590       600
     CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
       ||||   || | ||  ||| |   |  || |    |||||||| |||  | |  || | ||| |    |
     AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
     107590    107600       107610    107620    107630    107640    107650

            610         620           630       640       650       660
     AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
     || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
     AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
       107660    107670    107680    107690      107700    107710    107720

      670       680        690         700       710       720       730
     AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
     |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
    AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      107730    107740    107750    107760    107770    107780    107790

         740       750        760       770       780           790
    AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
    ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
    AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
    107800     107810    107820    107830       107840    107850    107860

  800       810         820       830        840       850       860
    GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
    || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
    GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
        107870    107880       107890    107900    107910    107920

   870       880       890       900       910       920        930
    AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
    |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
    AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
07930    107940     107950       107960    107970    107980     107990

  940       950       960           970        980        X
    GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
    | | | |   | | ||  |   || | |||    || |  | ||   || |  |
    GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGGAAGTCGT
  108000    108010     108020    108030    108040    108050


12. US-08-162-407-5'  (1-988)
    HUMLSPRO     Human lymphocyte surface protein exons 1-5, comple

 LOCUS       HUMLSPRO      2622 bp ss-mRNA            PRI       25-JAN-1993
 DEFINITION  Human lymphocyte surface protein exons 1-5, complete cds.
 ACCESSION   M99578
 KEYWORDS    lymphocyte surface protein.
 SOURCE      Homo sapiens (library: lambda gt11) neonate placenta cDNA to mRNA.
   ORGANISM  Homo sapiens
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
 REFERENCE   1  (bases 1 to 2622)
   AUTHORS   Voland,J.R., Wyzykowski,R.J., Mark,H. and Dutton,R.W.
   TITLE     Cloning and sequencing of a trophoblast- endothelial- activated
             lymphocyte surface protein: cDNA sequence and genomic structure
   JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89, 10425-10429 (1992)
   STANDARD  full automatic
 COMMENT     NCBI gi: 187241
 FEATURES             Location/Qualifiers
      source          1..2622
                      /organism="Homo sapiens"
                      /cell_type="trophoblast"
                      /dev_stage="neonate"
                      /sequenced_mol="cDNA to mRNA"
                      /tissue_type="placenta"
                      /tissue_lib="lambda gt11"
      mRNA            join(1..153,153..933,934..1082,1083..1323,1324..2622)
      exon            1..153
                      /note="codes the 5' UTR; intron between exon 1 and exon 2
                      is 2.7Kb"
                      /number=1
      5'UTR           1..171
```

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                      /note="84% GC in 5'UTR"
      exon            153..933
                      /note="codes the extracellular domain; intron between exon
                      2 and exon 3 is 0.7Kb"
                      /number=2
      CDS             170..1822
                      /note="550 amino acids MW=61kDa, glycosylated=75 kDa;
                      expressed on endothelium, activated lymphocytes and
                      syncytiotrophoblast, contains leucine zipper and basic
                      region homologous to myc; 721P;  NCBI gi: 187242"
                      /codon_start=1
                      /translation="MAAATIVHDTSEAVELCPAYGLYLKPITKMTISVALPQLKQPGK
                      SISNWEVMERLKGMVQNHQFSTLRISKSTMDFIRFEGEVENKSLVKSFLACLDGKTIK
                      LSGFSDILKVRAAEFKIDFPTRHDWDSFFRDAKDMNETLPGERPDTIHLEGLPCKWFA
                      LKESGSEKPSEDVLVKVFEKFGEIRNVDIPMLDPYREEMTGRNFHTFSFGGHLNFEAY
                      VQYREYMGFIQAMSALRGMKLMYKGEDGKAVACNIKVSFDSTKHLSDASIKKRQLERQ
                      KLQELEQQREEQKRREKEAEERQRAEERKQKELEELERERKREEKLRKREQKQRDREL
                      RRNQKKLEKLQAEEQKQLQEKIKLEERKLLLAQRNLQSIRLIAELLSRAKAVKLREQE
                      QKEEKLRLQQQEERRRLQEAELRRVEEEKERALGLQRKERELRERLLSILQSKKPDDS
                      HTHDELGVAHGPAAARPGHPADRVVRLCERHHAAPPRGPAPGRCPQGEPGPPRGRRRS
                      QKRERERGRGGPMQGGSELLSCGPRGWLSREEVPGRRPLLHS"
      misc_feature    172..232
                      /note="codes for protein leader sequence"
      exon            934..1082
                      /note="codes the putative basic region; intron between
                      exon 3 and exon 4 is 3.5Kb"
                      /number=3
      exon            1083..1323
                      /note="codes the leucine zipper region; the intron between
                      exon 4 and exon 5 is 1.3Kb"
                      /number=4
      misc_feature    1199..1263
                      /note="codes for leucine zipper, homologous to myc"
      exon            1324..2622
                      /note="codes the serine phosphorylation site and the
                      3'UTR"
                      /number=5
 BASE COUNT      589 a    792 c    898 g    343 t
 ORIGIN

Initial Score    =    167  Optimized Score    =     464  Significance = 10.29
Residue Identity =    51%  Matches            =     546  Mismatches   =   399
Gaps             =    107  Conservative Substitutions            =     0

              X       10        20        30        40          50
              CGGGGGCTTTGTTCAGAGTTGGGTAAATGGGGCCGGTGCTGG--ATTCTGGCGTTGC-CTCC
               ||    | ||        || ||| |||||     | | ||  ||    ||  ||| |
    TTGAACTTCGAGGCCTATGTGCAGTACCGTGAGTACATGGGCTTCATCCAGGCCATGAGCGCCCTGCGCGGG
      810     X 820       830       840       850       860       870

   60        70         80          90        100       110       120
    ATTCTGGGGAGGGA-ATGAGAGGGGCC--CAAGGAAGGGACCGGCCTCTAGCCAACTTCCTCTGTGTCCAGG
    ||       | | | | | | | || |  |||||  | | || ||  | | | |  || || | ||    |
    ATGAAACTCATGTACAAGGGCGAGGACGGCAAGGCCGTGGCCTGCAAC-ATCAAGGTTTCT-TTTGATTCGA
    880       890       900       910       920        930        940

   130       140       150       160         170          180         190
    CTATACATCCTCTGGCTGGTGACTCCCCTCTG-TGTG-CCTCAGTA---TCCTCCCCTGTA--AAATGG-GA
    | | ||| |||  |  || || |||   |  |  | | |  | | |    |     ||  |  || ||| |
    CCAAACA-CCT--GAGTGATGCCTCAATTAAGAAGCGGCAGCTGGAGAGGCAGAAGCTTCAGGAACTGGAGC
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  950          960       970       980       990      1000      1010

        200       210        220       230       240         250       260
  TG-ATAGATGTCTGTCTCACTGCGTTG-TTTAAGGCTCCGCAGGATGAGGCCTTG-GC-CAGGTCAGTGCTC
   | | ||| |     |  |  |||  |    ||||   || |||| |||||   | ||  |||  || |
  AGCAAAGA-GAAGAAC-AAAAGCGCAGAGAGAAGGAAGCGGAGGA-GAGGCAGCGAGCGGAGGAAAG-GAAA
  1020       1030       1040      1050       1060      1070      1080

         270            280           290       300       310       320
  CACAAGCAGC---AGGTCCTG--GGGACTGGGGA----CGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCT
  || ||| |||   | |  |||  | ||  | |||     |  | | | || | |   |||| |  |   |
  CAAAAGGAGCTGGAAGAGCTGGAGCGAGAGAGGAAAAGAGAAGAGAAGCTTCGCAAGAGGGAGCAGAAGCAG
    1090      1100      1110      1120      1130      1140      1150

      330       340       350         360       370       380       390
  CCGCCGCGTCCTCTGCCAGTGCAGGCACCAG--GCAGCGGCCAGCAGCAGGAGGCCCACGGGCAGCAGCAGT
    |   |||   ||||    || || | |||  | ||| |  || ||| | ||||  | | |||| |||||
  AGGGACCGTGAGCTGC----GCCGGAATCAGAAGAAGCTG-GAGAAGCTGCAGGCGGAGGAGCAGAAGCAGC
  1160      1170          1180      1190       1200      1210      1220

      400       410        420       430        440       450       460
  AGGAGGAGCAGAGGGGGCT-GCGGGGCTGTCGGGGCTG-TGGCCTCCAGGGGCCGGGGACTCCATGGGG---
   | ||||| |||    ||| | || ||    |  |||| |||||   |||  ||  | | |||||  ||
  TGCAGGAGAAGATCAAGCTGGAGGAGCGCAAGCTGCTGCTGGCCCAGAGGAACC-TGCAGTCCATCCGGCTC
     1230      1240      1250      1260      1270       1280      1290

         470       480         490       500       510       520       530
  GTGGCAGGGTTGAGGAGTCGGGC--TGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATCCA
   | || | | ||   ||  | ||   | |  || |||| | || | | |||| ||    || | | ||  |
  ATCGCCGAGCTGCTCAGCAGAGCCAAGGCTGTGAAGCTAC-GGGAACAGGAGCAG--AAGGAG-GAGAAGCT
    1300      1310      1320      1330       1340        1350       1360

          540       550       560       570       580        590       600
  G-GGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTG-GTCTGGACGAAGCGA
  | |||| ||||  ||  ||  |  ||| || |  |||||||||||  ||| ||  | |  |||| || | ||
  GAGGCTCCAGCAGCAGGAG--GAGCGGCGG-CGGCTGCAGGAGGC-CGAGCTGCGGCGCGTGGAGGAGGAGA
      1370      1380        1390       1400       1410      1420      1430

          610       620       630        640       650       660       670
  AGACAGC-TGGGGGGGGGCTGAAAGGCACATTTGGTGA-CAAAGTGTATCTCCGTGTTCACGCGCTCCAGCA
  ||  |||  | |  ||| ||| |  | | |    | || |   | | | |  | || | | ||  ||| |||
  AG-GAGCGCGCGCTGGGCCTGCAGCGGAAAGAGCGGGAGCTGCGCG-AGCGGC-TGCTGA-GC-ATCCTGCA
         1440      1450      1460      1470       1480         1490

         680        690       700       710       720        730
  AGCCTTGCATCTTGGAC-CCAGCGACAGTCTTGAGCCGCTCCATCCAGCGC-TGTGCCAGGACCAG-CCGCC
     |  | | |  ||||  |||| |||  |  ||   |||       || |  |  || |   ||| ||| |
  GAGCAAGAAGC-CGGACGACAGCCACACACACGACGAGCTGGGCGTGGCACACGGACCTGCTGCAGCCCGTC
 1500       1510      1520      1530      1540      1550      1560

740        750       760       770       780       790        800
  AGAGGC-CCCCGCAGAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGACTGGGTAATCT-TGAAGCAGGTA
     | |  || ||||| |   |||||| || |  ||   |||||   | |||      ||  |  ||  |
  CTGGACATCCTGCAGACCGTGTCGTCCGGCTGTGTGAGCGCCACCACG-CTGCACCCCCTCGGGGGCCAGCC
1570      1580      1590      1600      1610       1620      1630

810       820       830          840        850              860       870
  GTCAGACAGCTCACGGATTTTGA---CAGCGAAGTCGGAGG-AGATGGGGCT-------GTGTTGGAAGGAG
    | | | |  | |  |    ||   | ||     | ||||  || || |||       | ||  ||| | |
  CCCGGCCGGTGCCCCCAAGGAGAGCCCGGCCCCCCCAGAGGCCGACGGCGCTCCCAAAAGCGT--GAACG-G
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1640      1650      1660      1670      1680      1690      1700

          880       890       900       910       920        930        940
   CAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGATAGGTTGT-TGGGCTCC-AGG
    || | |||  || |  ||| ||| |   ||  || ||   || |||    |  || || ||| | || |||
   GAG-CGTGG--CCGA-GGAGGCCCCA-TGCA--AGGAGGTTCA-GAGCTCCT--GTCGTGTGGTCCCCGAGG
 1710         1720       1730         1740       1750        1760      1770

            950        960       970          980       X
   CTGG--CGCCAGCACTGTCAT-TTCGGCCGGGGGCC---CCGGAATTCCGGCCG
    |||  | ||||    |   |   ||| ||| | ||   || | ||||| | |
   ATGGCTCTCCAGAGAAGAGGTGCCCGGGCGGCGTCCTCTCCTGCATTCCTGACAACAACCAACA
         1780      1790      1800      1810      1820   X  1830
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13. US-08-162-407-5' (1-988)
    STMCARA       Streptomyces thermotolerans carbomycin-resistance

 LOCUS        STMCARA       2393 bp ds-DNA              BCT       11-SEP-1992
 DEFINITION   Streptomyces thermotolerans carbomycin-resistance protein (carA)
              gene, complete cds.
 ACCESSION    M80346
 KEYWORDS     carA gene; carbomycin resistance protein.
 SOURCE       Streptomyces thermotolerans DNA.
   ORGANISM   Streptomyces thermotolerans
              Prokaryotae; Firmicutes; Streptomycetaceae.
 REFERENCE    1  (bases 1 to 2393)
   AUTHORS    Schoner,B.E., Geistlich,M., Rosteck,P., Rao,R.N., Seno,E.,
              Reynolds,P., Cox,K., Burgett,S. and Hershberger,C.L.
   TITLE      Sequence similarity between macrolide resistance determinants and
              ATP-binding transport proteins
   JOURNAL    Gene 115, 93-96 (1992)
   STANDARD   full automatic
 COMMENT      NCBI gi: 153197
 FEATURES              Location/Qualifiers
      source           1..2393
                       /organism="Streptomyces thermotolerans"
                       /sequenced_mol="DNA"
      CDS              411..2066
                       /gene="carA"
                       /note="NCBI gi: 153198"
                       /codon_start=1
                       /product="carbomycin resistance protein"
                       /translation="MSTAQLALHDITKRYQDHVVLDRIGFTIKPGEKVGVIGDNGSGK
                       STLIKLIAGREQPDNGAVTVVAPGGVGYLAQTLELPLEATVQDAVDLALADLRELEEG
                       MRRTEAELAERPYQTGQDPELAGLLESYAALVDRYQARGGYEADSRVEIALHGLGLPG
                       LERGRRLGTLSGGERSRLALAATLASEPELLLLDEPTNDLDDRAVDWLEEHLRKHKGT
                       VVAVTHDRLFLDRLTTTILEIDSGKVMRYGNGYEGYLAAKAAERQRRLLEYEQWRAEL
                       DRSRDLIASNVARLDAIPRKLPFAVFGAGQFRMRGRGHGAMVRIRNAKERVARLTENP
                       VAPPPEPLTFTAEITTEAAQSRETVAELTGVRVGDRLSVDSLHLGPGERLLVTGPNGA
                       GKTTLLRVLSGELEPDSGSLLVSGRVGHLRQEQTPWRPGMTVLQAFSSGRAGDIDEHT
                       EALLSLGLFSPDDLRQRVQDLSYGQRRRIELARLVTEPVDLLLLDEPTNHLSPALVEE
                       LEEALTGYQGTVVVVTHDRRMRSRFNGAHLTLQDGRVAEFTAA"
 BASE COUNT      379 a    823 c    878 g    313 t
 ORIGIN

Initial Score     =    164  Optimized Score    =    448  Significance = 10.07
Residue Identity  =    50%  Matches            =    540  Mismatches   =   398
Gaps              =    131  Conservative Substitutions                 =     0
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```
            X       10        20          30         40             50
            CGGGGGCTTTGTTCAGAGTTGGGTA--AATGGGGC-CGGTGCTG---GA--TTCTGGCGTTG
            ||  ||    | || |    |   |  || | | | ||  ||||   ||    | ||    |
  GGCCATGGTGCGATGGTGCGGATCCGCAACGCCAAGGAACGCGTCGCGCGGCTGACCGAAAACCCGGTCGCG
  1350      1360      1370      1380      1390      1400      1410

      60        70             80        90       100       110       120
  CCTCCATTCTGGGGAGGGAA---TGA--GAGGGGCCCAAGGAAGGGACCGGCCTCTAGCCAACTTCCTCTGT
  || ||   | | |  |   |   | |  | || |  ||     | | |||  |   || |        | ||
  CCGCC-GCCCGAGCCGCTCACCTTCACCGCGGAGATCACCACCGAGGCCGCGC---AGTCCCGGGAGACGGT
1420       1430      1440      1450      1460      1470         1480

        130       140        150       160        170           180
  GTCCAGGCTATACATCCTCTGGCT-GGTGACTCCCCTCTGTGT-GCCTCAGT-ATCCTC---CCCTGTAAAA
  | ||   ||   |  | || || | || ||| |  ||| | || | |||  |   ||||   ||| || ||
  GGCCGAACTCACCGGCGTCCGGGTCGGCGAC-CGGCTCAGCGTCGACTCCCTGCACCTCGGGCCCGGTGAA-
  1490      1500      1510       1520      1530      1540      1550

  190       200       210       220       230       240       250
  TGGGATGATAGATGTCTGTCTCACTGCGTTGTTTAAGGCTCCGCAGGATGAGGCCTTGGCCAGGTCAGTGCT
    || || | |    | | | ||  | |  |   ||| |  ||| |     ||   |  || ||    ||
  -CGGCTGCTGGTCACCGGCCCCAACGGGGCGGGCAAGACGACGCTGCTGCGGGTGCTCTCCGGGGAGCTGGA
   1560      1570      1580      1590      1600      1610      1620

260       270         280       290         300       310       320
  CCACAAGCAGCAGGT-CCTG-GGGACTGGGGACGG--GGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCGC
   | | | |||| | | ||||  ||  | ||| |||  ||| ||||||      |||  ||      | ||
  ACCCGA-CAGCGGATCCCTGCTGGTGTCGGGCCGGGTGGGACACCTG------AGGCAGGAACAGACACCAT
 1630       1640      1650      1660      1670            1680      1690

  330          340          350       360       370         380       390
  CGCGTCC---TCTGCCAGTG---CAGGCACCAGGCAGCGGCCAGCAGCAGGAGGC--CCACGGGCAGCAGCA
   ||| ||   | || | |||   |||||     ||||||| | |  || || | |  | ||| ||| || |
  GGCGGCCGGGTATGACGGTGCTTCAGGCGTTCAGCAGCGGACGG--GCCGGTGACATCGACGAGCA-CACC-
      1700      1710      1720      1730        1740      1750       1760

        400       410       420        430           440        450
  GTAGGAGGAGCAGAGGGGGCTGCGGGGCTG-TCGGGGCTGTGG-CCT---CCAG-GGGCCGGGGACTCCATG
      |||| || |      || || ||||| || |  | |  | |||   |||| | |    |||| |  |
  ----GAGGCGCTGCTCTCCCT-CG-GGCTGTTCAGCCCGGACGACCTCCGCCAGCGTGTGCAGGAC-CTGTC
            1770        1780      1790      1800      1810      1820

  460       470       480       490       500       510         520
  GGGGTGGCAGGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTG--GC-GAGTGA
  |    ||||| |  |  |  ||| |||  | | || | |   ||  ||||  ||  | |||  || |   ||
  GTACGGGCAGCGGCGCCGCATCGAGCTTGCCCGGCTGGTGACGGAGCCGGTCGACCTGCTGCTGCTGGACGA
   1830      1840      1850      1860      1870      1880      1890

   530       540        550         560       570        580       590
  TCCAGGGCTTCAGCGC-CACCAGCTGCTCG--GAGGTCTCCTGCAGGAGGCG-GGAGATGTTGGTCTGGACG
   ||       || | | | || || |||||  ||||    ||| ||||||||  ||   |||  || || |
  ACCCACCAACCACCTCTCGCCCGC-GCTCGTCGAGG--AACTGGAGGAGGCGCTGACCGGTT-ATCAGGGC-
 1900      1910      1920       1930        1940      1950       1960

     600       610       620       630       640       650        660
  AAGCGAAGACAGCTGGGGGGGGGCTGAAAGGCACATTTGGTGACAAAGTGTATCTCCG-TGTTCACGCGCTC
  | | |  | |   | |       | ||  ||| |||  |||  |    |  | |  ||    ||   ||||
  ACG-GTCGTC--GTCGTCACCCAC-GACCGGCGCATGCGGT--CCCGCTTCAACGGCGCCCATCTGACGCTG
     1970        1980       1990      2000        2010      2020      2030
```

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  670       680         690       700       710       720       730
CAGCAAGCCTTGCATCTTGGA-CCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CCA
||| | |    || ||   ||   || || | | | |||  ||| | |   ||||  || | ||||    |
CAGGACG-GGCGCGTCGCCGAGTTCACCG-CCGCC-TGA-TCGC-CGA---AGCG--GTACGAGGAGGGACG
       2040      2050       2060        2070            2080      2090

    740             750           760       770           780       790
GCCGCCAGAGGCCC------CCGCAGAGCTC----CTCGTCCTGCAG----GTTGGAGGCCACGGTGACTGG
|  ||||| |||||      |||||  | ||       | || ||||     |  || ||||| |   | ||
GGTGCCAGGGGCCCGTCCCTCCGCA-CGGTCAGAGACGGACCGGCAGACTCTTCAGACGCCAC-GCACCCGG
    2100      2110       2120      2130      2140      2150       2160

      800       810        820         830          840       850
GTAATCTTGAAGCAGGTAGTCAGACAGC-TCACG--GATTTTGA--CA-GCGAAGTCGGAGGAGATGGGGCT
| |    ||  |      | | ||| ||  ||||  ||    ||  |  | ||||  |  | ||| || |
GAAGGGCTGCCGTTCCAGGGCGGACGGCGGCACGGCGAGGGCGAGGCTGGGGAAGCGGTCGAAGAGGGTGTC
    2170      2180      2190      2200      2210      2220      2230

860       870        880       890        900       910       920
GTGTTGGAAGGAGCAGTCCTGG-GTCCCACTGAGTC-CCGAGCTCAGCAGCAGCAGCAGGAGGAGATAG--G
| |   ||  | |   |||||| || |||  | | | || ||  ||| ||     || | ||  || ||  |
GAGGGCGATCGCGGTCTCCTGGTGTGCCAGGGCGGCGCCCAG-GCAGTAGTGCGGGCCGAAGCCGA-AGCCG
  2240      2250      2260      2270       2280      2290       2300

  930        940        950          960          970       980       X
TTGTTGGGCTCCAG-GCTG-GCGCCAG---CACTGTCATTTCG-GCCG--GGGGCCCCGGAATTCCGGCCG
  ||  | |||  | | || |||   |   |   || || |||  |||   |||  | || |  | | |||
ACGTGTGCCTCGTGCGGTGCGCGGTGGTTTCCGGGTGATGTCGAACCGCTCGGGGTCGGGGAACCGGTCCG
  2310      2320      2330      2340      2350      2360      2370    X

GATCGTGTC
2380
```

```
14. US-08-162-407-5' (1-988)
    GORINVOLUB   Gorilla gorilla involucrin gene medium allele, com

 LOCUS       GORINVOLUB   1818 bp ds-DNA             PRI       08-SEP-1994
 DEFINITION  Gorilla gorilla involucrin gene medium allele, complete cds.
 ACCESSION   M23604 J04499
 KEYWORDS    epidermal protein; involucrin.
 SOURCE      Gorilla gorilla (individual_isolate Gorilla K) (library: vagina)
             DNA.
   ORGANISM  Gorilla gorilla
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Pongidae.
 REFERENCE   1  (bases 1 to 1818)
   AUTHORS   Teumer,J. and Green,H.
   TITLE     Divergent evolution of part of the involucrin gene in the
             hominoids: Unique intragenic duplications in the gorilla and human
   JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 1283-1286 (1989)
   STANDARD  full automatic
 COMMENT     Draft entry and computer readable copy of sequence [1] kindly
             provided by J.K. Teumer (03-31-89).

             NCBI gi: 340978
 FEATURES             Location/Qualifiers
      source          1..1818
                      /organism="Gorilla gorilla"
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BASE COUNT     531 a    454 c    657 g    176 t
ORIGIN

Initial Score    =    160  Optimized Score =    462  Significance =  9.76
Residue Identity =    51%  Matches         =    555  Mismatches   =   379
Gaps             =    134  Conservative Substitutions           =     0

           X          10        20        30        40        50
           CGGGG--GCT-TTGTTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTGCCTCC
            ||||  |||   | ||  ||    | |   |||||    ||||||  ||  |   | | |
 GAGCAGCAGGAGGGGCAGCTGGAGCTCCCAGAGCAGCAGGAGGGGC---AGCTGGA-GCTCCCAGAG-CAGC
710       720       730       740       750          760        770

60        70          80        90           100       110
 ATTCTGGGGAG-GGAATGA-GAGGGGCCCAAGGAAGGG-ACC---GGCCTCTAGCCAAC-------TTCCTC
 |    ||  ||  |||  |   || ||   |||| ||| | |    || ||| |  |||         |  |
 AGGAGGGACAGCTGAAGCACCTGGAGCAGCAGGAGGGGCAGCTGAAGCATCTGGAGAACCAGGAGGGGCAGC
   780       790       800       810       820       830       840

120         130       140       150           160         170       180
 TG--TGTCCAGGCTATACATCCTCTGGCTGGTGACTCCCCT----CTG--TGTGCCTCAGTATCCTCCCCTG
 ||   ||||  |     ||   |  ||| | |||    |||    | |   | |   |||      | ||||
 TGGAGGTCCCAGAGGAGCA-GGTGGGGCAGCTGAAGTACCTGGAACAGCAGGAGGGGCAGCTGAAGCACCTG
 850       860        870       880       890       900       910

      190       200        210       220       230       240         250
 TAAAATGGGATGATAGATGTCTG-TCTCACTGCGTTGTTTAAGGCTCCGCAGGATGAGGC-CTTGG-CCAG-
  |  |   |  || ||  | | |  ||| | | |  |    |||    ||| | ||| || | |||  |||
 GATCAGCAGGAGA-AGCAGCCGGAGCTCCCAGAGCAG---CAGGTGGGGCA-GCTGAAGCACCTGGAGCAGC
920       930        940       950          960        970       980

         260       270       280       290       300       310
 -GTCAGTGCTCCACAAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGG-GC-GGGGTG
  |   | ||  |  ||||| | ||  | |  |   ||| |   || |||||||      ||| || || | |
 AGGAGGGGCAGCCTAAGCATCTGGAGCAGCAGGAGGGGCAACTGGAGCACCTG-----GAGGAGCAGGAGGG
   990      1000      1010      1020      1030           1040      1050

320      330       340       350       360       370          380
 TCCTCCGCCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCA
  |  | |  ||  |||    ||  |||||     |||||| |  |||| | ||||  ||   | |||||||
 GCAGCTGAAGC-ACCTGGAGCA--GCAGG--AGGGGCAGCTG-GAGCACCTGGAGCACCAGGAAGGGCAGCT
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     1060       1070          1080       1090      1100      1110

390       400       410       420        430        440       450
 GCAGTAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGGGGCT-GTG-GCCTCCAGGGGCCGGGGACTC-CATG
 |  |      ||||||  || || ||   ||||  |  ||| | |       |||||| |   |  | | ||
 GGGGCTCCCAGAGCAGCAGGTGCGGC--AGCTGAAGCAGCTAGAGAAGGAGGAGGGGCAGCCAAAGCACCTG
1120     1130      1140        1150      1160      1170      1180

 460       470       480        490         500       510       520
 GGGGTGGCAGGGTTGAGGAGTCG-GGCTGACACTGCAGCTCCA--GGCACCGGGAGAAGTTCTGGCGAGTGA
 | || || || |  | | ||| |  ||      ||||||   |  |||||  |||| |   |||| |    |
 GAGGAGG-AG-GAGGGGCAGTTGAAGCACCTGGTGCAGCAGGAGGGGCACGTGGAGCA--CCTGGTGCAGCA
1190       1200      1210      1220      1230      1240        1250

  530       540       550          560       570       580       590
 TCCAGGGCTTCAGCGCCACCAGCTGC--TCGGA-GGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGA
     ||||  | |   || | | |||    ||| || |  ||| || | || ||||  |  ||  ||||  |
 GGAGGGGCAGCTGGAGCATCTGGTGCAGCAGGAGGGGCAGCTGGAGCA-GCAGGAGGGGCAGG--TGGAGCA
 1260      1270      1280      1290      1300       1310        1320

   600       610        620       630         640       650       660
 AGCGAAGACAGCTGG-GGGGGGGCTGAAAGGCACAT-TTGGTG-ACAAAGTGTATCTCCGTGTTCACGCGCT
    | || |||| || ||||  ||||||  |||| |   || | |  | | | | ||      ||  | ||
 CCTGGAG-CAGCAGGTGGGGCAGCTGAA--GCACCTAGAGGAGCAGGAGGGGCAACTGAAGCATCTGGAGCA
  1330       1340      1350        1360      1370      1380      1390

    670         680       690       700        710       720         730
 CCAGCAAGCCTTGCA--TCTTGGACCCAGCGACAGTCTTGAGCCGC-TCCATCCAGCGCTGTGC--CAGGAC
  ||||| |    |||  |   || ||||| | ||| |  | |  ||  |||  || |   | ||   ||||
 GCAGCAGG---GGCAGTTGGGGGTCCCAGAG-CAG-CAGGTGGGGCAGCCAAACAACCTGGAGCAGGAGGAG
   1400         1410      1420        1430      1440      1450      1460

       740         750           760             770         780
 CAGCCGCCAGAGGCCCC--CGCA----GAGCTCCTCGT------CCTGCAG--GTTGGAGGCCACGGTGACT
  ||| ||  |||  |||   |||    |||  ||   |      |||| ||  |  ||||| ||| |   ||
 AAGCAGCTGGAGCTCCCAGAGCAGCAAGAGGGCCAGCTGAAGCACCTGAAGAAGCAGGAGG-CACAG---CT
      1470      1480      1490      1500      1510      1520

790      800         810       820       830        840       850
 GGGTAATCTTGA--AGCAGGTAGTCAGACAGCTCACGGATTTTGA-CAGCGAAGTCGGAGGAGATGGGGCTG
 ||     |  ||  |||||||||   ||||||  | | |  | || ||||  ||    || || | | ||
 GGAGCTCCCAGAGCAGCAGGTAG---GACAGCCAAAGCACCTGGAGCAGC--AGGAAAAGCAGCTAGAGC--
1530    1540      1550         1560      1570        1580      1590

860       870       880       890        900       910       920
 TGTTGGAAGGAGCAGTCCTGGGTCCCACTGAGTCCCGAGC-TCAGCAGCAGCAGCAGGAGGAGATAG-GTTG
      || | |||||  | |    | |     ||  ||||  ||| ||  ||||| | ||||  | | |  |
 ACCCAGA-GCAGCAGGACGGACAACTAAAACATCTGGAGCAGCAGGAGGGGCAGCTGAAGGACCTGGAGCAG
   1600       1610      1620      1630      1640      1650      1660

930        940       950       960               970        980       X
 TTG-GGCTCCAGGCTGGCGCCAGCACTGTCATTTC-----GGCCGGG---GGCCCCGGA-ATTCCGGCCG
   |  |   || ||||| | |||| ||||  || |       || ||   || ||  || ||||   | |
 CAGAAGGGGCA-GCTGGAG-CAGC-CTGTGTTTGCCCCAGCTCCAGGCCAGGTCCAAGACATTCAACCAGCC
  1670       1680        1690      1700      1710      1720      1730 X

 CTGCCCAC
   1740
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15. US-08-162-407-5' (1-988)
    GORINVOLUA   Gorilla gorilla involucrin gene large allele, comp

 LOCUS       GORINVOLUA   1908 bp ds-DNA             PRI       07-SEP-1994
 DEFINITION  Gorilla gorilla involucrin gene large allele, complete cds.
 ACCESSION   M23603 J04499
 KEYWORDS    epidermal protein; involucrin.
 SOURCE      Gorilla gorilla (individual_isolate Gorilla F) DNA.
   ORGANISM  Gorilla gorilla
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Primates; Haplorhini; Catarrhini; Pongidae.
 REFERENCE   1  (bases 1 to 1908)
   AUTHORS   Teumer,J. and Green,H.
   TITLE     Divergent evolution of part of the involucrin gene in the
             hominoids: Unique intragenic duplications in the gorilla and human
   JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86, 1283-1286 (1989)
   STANDARD  full automatic
 COMMENT     Draft entry and computer readable copy of sequence [1] kindly
             provided by J.K. Teumer (03-31-89).

             NCBI gi: 340977
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                      GELKHLEQQKGQLELPEQQEGQLELPEQQEGQLKHLEQQKGQLELPEQQEGQLELPEQ
                      QEGQLELPEQQEGQLKHLEQQEGQLELPEQQEGQLKHLEQQKGQLELPEQQEGQLELP
                      EQQEGQLELPEQQEGQLKHLEQQEGQLKHLENQEGQLEVPEEQVGQLNYLEQQEGQLK
                      HLDQQEKQPELPEQQVGQLKHLEKQEGQPKHLEQQEGQLEHLEEQEGQLKHLEQQEGQ
                      LEHLEHQEGQLGLPEQQVRQLKQLEKEEGQPKHLEEEEGQLKHLVQQEGQLEHLVQQE
                      GQLEHLVQQEGQLEQQEGQVEHLEQQVGQLKHLEEQEGQLKHLEQQQGQLGVPEQQVG
                      QPNNLEQEEKQLELPEQQEGQLKHLEKQEAQLELPEQQVGQPKHLEQQEKQLEHPEQQ
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                      KQEVQWPPKHK"
 BASE COUNT      554 a    476 c    696 g    182 t
 ORIGIN

Initial Score    =    160  Optimized Score  =    462  Significance =  9.76
Residue Identity =    52%  Matches          =    556  Mismatches   =   377
Gaps             =    136  Conservative Substitutions          =     0

              X       10        20        30        40        50
              CGGGG--GCT-TTGTTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTGCCTCC
               ||||  |||   | ||  ||    | |   |||||    ||||||  ||  |   | |  |
    GAGCAGCAGGAGGGGCAGCTGGAGCTCCCAGAGCAGCAGGAGGGGC---AGCTGGA-GCTCCCAGAG-CAGC
   800       810       820       830       840          850        860

   60        70          80        90            100       110
    ATTCTGGGGAG-GGAATGA-GAGGGGCCCAAGGAAGGG-ACC---GGCCTCTAGCCAAC-------TTCCTC
```

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  |    ||  ||  |||  |   || ||   |||| ||| | |    || ||| |  |||         |  |
  AGGAGGGACAGCTGAAGCACCTGGAGCAGCAGGAGGGGCAGCTGAAGCATCTGGAGAACCAGGAGGGGCAGC
     870       880       890       900       910       920       930

 120         130       140       150           160         170       180
  TG--TGTCCAGGCTATACATCCTCTGGCTGGTGACTCCCCT----CTG--TGTGCCTCAGTATCCTCCCCTG
  ||   ||||  |     ||   |  ||| | ||| |  |||    | |   | |   |||      | ||||
  TGGAGGTCCCAGAGGAGCA-GGTGGGGCAGCTGAATTACCTGGAACAGCAGGAGGGGCAGCTGAAGCACCTG
  940        950       960       970       980       990      1000

      190       200         210       220       230       240
  TAAAATGGGATGATAGATGTCTG-TCTCACTGCGTTGTTTAAGGCTCCGCAGGATGAGGC-CTTGG----CC
   |  |   |  || ||  | | |  ||| | | |  |    |||    ||| | ||| || | |||     |
  GATCAGCAGGAGA-AGCAGCCGGAGCTCCCAGAGCAG---CAGGTGGGGCA-GCTGAAGCACCTGGAGAAGC
 1010      1020        1030      1040          1050      1060      1070

 250       260       270       280       290       300       310
  AGGTCAGTGCTCCACAAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGG-GC-GGGGT
  |||   | ||  |  ||||| | ||  | |  |   ||| |   || |||||||      ||| || || |
  AGG-AGGGGCAGCCTAAGCATCTGGAGCAGCAGGAGGGGCAACTGGAGCACCTG-----GAGGAGCAGGAGG
     1080      1090      1100      1110      1120            1130      1140

 320       330       340       350       360       370        380
  GTCCTCCGCCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGC
  | |  | |  ||  |||    ||  |||||     |||||| |  |||| | ||||  ||   | |||||||
  GGCAGCTGAAGC-ACCTGGAGCA--GCAGG--AGGGGCAGCTG-GAGCACCTGGAGCACCAGGAAGGGCAGC
      1150      1160          1170      1180      1190      1200

  390       400       410       420        430       440       450
  AGCAGTAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGGGGCT-GTG-GCCTCCAGGGGCCGGGGACTC-CAT
   |  |      ||||||  || || ||   ||||  |  ||| | |       |||||| |   |  | | |
  TGGGGCTCCCAGAGCAGCAGGTGCGGC--AGCTGAAGCAGCTAGAGAAGGAGGAGGGGCAGCCAAAGCACCT
 1210      1220      1230        1240      1250      1260      1270

   460       470       480        490          500       510       520
  GGGGGTGGCAGGGTTGAGGAGTCG-GGCTGACACTGCAGCTCCA--GGCACCGGGAGAAGTTCTGGCGAGTG
  || || || || |  | | ||| |  ||      ||||||   |  |||| | |||| |   |||| |
  GGAGGAGG-AG-GAGGGGCAGTTGAAGCACCTGGTGCAGCAGGAGGGGCAGCTGGAGCA--CCTGGTGCAGC
 1280        1290      1300      1310      1320      1330        1340

    530       540       550           560       570       580       590
  ATCCAGGGCTTCAGCGCCACCAGCTGC--TCGGA-GGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACG
  |    ||||  | |   || | | |||    ||| || |  ||| || | || ||||  |  ||  ||||
  AGGAGGGGCAGCTGGAGCATCTGGTGCAGCAGGAGGGGCAGCTGGAGCA-GCAGGAGGGGCAGG--TGGAGC
   1350      1360      1370      1380      1390       1400       1410

     600       610        620       630         640       650       660
  AAGCGAAGACAGCTGG-GGGGGGGCTGAAAGGCACAT-TTGGTG-ACAAAGTGTATCTCCGTGTTCACGCGC
  |   | || |||| || ||||  ||||||  |||| |   || | | | | | ||      ||  | ||
  ACCTGGAG-CAGCAGGTGGGGCAGCTGAA--GCACCTAGAGGAGCAGGAGGGGCAACTGAAGCATCTGGAGC
    1420      1430      1440        1450      1460      1470      1480

      670         680       690       700        710       720        730
  TCCAGCAAGCCTTGCA--TCTTGGACCCAGCGACAGTCTTGAGCCGC-TCCATCCAGCGCTGTGC--CAGGA
    ||||| |    |||  |   || ||||| | ||| |  | |  ||  |||  || |   | ||   ||||
  AGCAGCAGG---GGCAGTTGGGGGTCCCAGAG-CAG-CAGGTGGGGCAGCCAAACAACCTGGAGCAGGAGGA
    1490         1500      1510        1520      1530      1540       1550

         740        750         760               770        780
  CCAGCCGCCAGAGGCCCC--CGCA----GAGCTCCTCGT------CCTGCAG--GTTGGAGGCCACGGTGAC
```

```
      ||| ||  |||  |||   |||    |||  ||   |      |||| ||  |  ||||| ||| |   |
    GAAGCAGCTGGAGCTCCCAGAGCAGCAAGAGGGCCAGCTGAAGCACCTGGAGAAGCAGGAGG-CACAG---C
          1560      1570      1580      1590      1600      1610

   790       800         810       820       830        840       850
    TGGGTAATCTTGA--AGCAGGTAGTCAGACAGCTCACGGATTTTGA-CAGCGAAGTCGGAGGAGATGGGGCT
    |||     |  ||  |||||||||   ||||||  | | |  | || ||||  ||    || || | | ||
    TGGAGCTCCCAGAGCAGCAGGTAG---GACAGCCAAAGCACCTGGAGCAGC--AGGAAAAGCAGCTAGAGC-
  1620      1630      1640         1650      1660        1670      1680

    860       870       880       890        900       910       920
    GTGTTGGAAGGAGCAGTCCTGGGTCCCACTGAGTCCCGAGC-TCAGCAGCAGCAGCAGGAGGAGATAG-GTT
          || | |||||  | |    | |     ||  ||||  ||| ||  ||||| | ||||  | | |
    -ACCCAGA-GCAGCAGGACGGACAACTAAAACATCTGGAGCAGCAGGAGGGGCAGCTGAAGGACCTGGAGCA
       1690       1700      1710      1720      1730      1740      1750

    930        940       950       960               970        980       X
    GTTG-GGCTCCAGGCTGGCGCCAGCACTGTCATTTC-----GGCCGGG---GGCCCCGGA-ATTCCGGCCG
    |  |  |   || ||||| | |||| ||||  || |       || ||   || ||  || ||||   | |
    GCAGAAGGGGCA-GCTGGAG-CAGC-CTGTGTTTGCCCCAGCTCCAGGCCAGGTCCAAGACATTCAACCAGC
      1760       1770        1780      1790      1800      1810      1820 X

    CCTGCCCAC
       1830
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq5nsq.res made by  on Wed 5 Apr 95 20:58:10-PDT.


Query sequence being compared:US-08-162-407-5 (1-988)
Number of sequences searched:                57621
Number of scores above cutoff:                4402

      Results of the initial comparison of US-08-162-407-5 (1-988) with:
   Data bank : N-GeneSeq 17, all entries

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U50000-
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U     -    *
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N     -         **
C     -           *
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E     -            *
S 1000-             *
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      -
      -                   **
      -                     **
      -                       *
      -
      -                        **
   100-                          *
      -                           *
      -
    50-                            ***
      -                               *
      -                                 *     *
      *                                *   *
      -                                             *
      -                                   *
      -                                  *  *
    10-
      -                                      *
      -                                         *
     5-                                        *   * * *
      -
      -
      -
      -
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      |   |  | |    |    | |  |   | |    |    | |  |   ||     |      |
SCORE 0   | 21 |   43    |64  |  86 |  107    129  | 150|   172    193
STDEV     0    1    2    3    4     5    6    7    8    9

                             PARAMETERS

Similarity matrix      Unitary     K-tuple                         4
Mismatch penalty             1     Joining penalty                30
Gap penalty               1.00     Window size                    32
Gap size penalty          0.33
Cutoff score                 2
Randomization group          0

Initial scores to save      45     Alignments to save          15
Optimized scores to save     0     Display context             10

                             SEARCH STATISTICS

Scores:                  Mean       Median     Standard Deviation
                           19          14        15.41

Times:                   CPU                   Total Elapsed
                     00:04:04.07               00:04:05.00

Number of residues:              24347505
Number of sequences searched:       57621
Number of scores above cutoff:       4402
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Cut-off raised to 11.
Cut-off raised to 18.
Cut-off raised to 26.
Cut-off raised to 32.
Cut-off raised to 38.
Cut-off raised to 42.
Cut-off raised to 47.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                     Init. Opt.
Sequence Name    Description                 Length Score Score   Sig. Frame
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                   **** 11 standard deviations above mean ****
  1. Q41760        Oxytocin receptor coding sequ   1167   193   455  11.29   0
                   ****  8 standard deviations above mean ****
  2. Q14645        Clone associated with biochem   2702   155   453   8.83   0
  3. Q05536        Sequence enoding purified sol   1443   150   453   8.50   0
  4. Q21171        Clone encoding Intercellular    1846   149   454   8.44   0
  5. N90611        Intercellular adhesion molecu   1846   149   454   8.44   0
  6. Q04049        Sequence of clone HL-60 encod   3024   149   454   8.44   0
  7. N80995        HL-cDNA clone encoding human    3113   149   451   8.44   0
  8. Q06583        Sequence encoding bovine meta   1045   143   326   8.05   0
  9. Q55132        Sequence encoding enzyme whic   5535   143   449   8.05   0
                   ****  7 standard deviations above mean ****
 10. Q38735        Human OP-2.                     1723   142   393   7.98   0
 11. Q01758        cDNA sequence of rat C kinase   2909   142   428   7.98   0
 12. Q55131        Sequence encoding enzymes whi   5533   142   450   7.98   0
 13. Q55342        tICAM(452) cysteine mutant.     1359   141   453   7.92   0
 14. Q55340        tICAM(453)IgG immunoadhesin.    2043   141   454   7.92   0
 15. Q57016        PKC delta.                      2891   141   431   7.92   0
 16. Q57397        Human ICAM-1.                   3024   141   454   7.92   0
 17. Q45164        Human OP-2.                     1723   140   394   7.85   0
 18. Q65393        Osteogenic protein hOP2-PP.     1723   140   392   7.85   0
 19. Q45118        Human OP-2.                     1723   140   394   7.85   0
 20. Q67313        Human OP-2.                     1723   140   394   7.85   0
 21. Q57917        Human osteogenic protein hOP2   1723   140   393   7.85   0
 22. Q56233        hOP2 cDNA.                      1723   140   393   7.85   0
 23. Q56200        hOP2 cDNA.                      1723   140   393   7.85   0
 24. Q53155        Sequence encoding human osteo   1723   140   393   7.85   0
 25. Q38859        Morphogen hOP2 coding sequenc   1723   140   392   7.85   0
 26. Q38946        Human osteogenic protein 2 (h   1723   140   393   7.85   0
 27. Q28737        Human osteogenic protein hOP2   1723   140   393   7.85   0
 28. Q56106        DNA encoding a lipase gene an   2417   140   464   7.85   0
 29. Q13288        P.denitrificans genes cob q,   13144   140   451   7.85   0
 30. N70753        Sequence of segment of Xantho  16079   140   434   7.85   0
 31. Q06069        Sequence encoding H20B recept   1179   138   442   7.72   0
 32. Q06070        Sequence encoding H20A recept   1251   138   442   7.72   0
 33. Q11140        Cellular Receptor 2 ligand ge   2208   136   450   7.59   0
 34. N70938        DNA fragment contg. streptomy   3830   136   453   7.59   0
 35. Q24522        cDNA encoding prepro human os   1941   134   450   7.46   0
 36. N50498        Angiotensin.                    1762   132   447   7.33   0
 37. Q25752        Non-A, Non-B Hepatitis Virus     561   129   230   7.14   0
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 38. Q47954        Calf IAP DNA.                   5399   129   445   7.14   0
 39. Q47065        tie truncated receptor kinase   3713   128   455   7.07   0
 40. Q47064        tie receptor kinase cDNA.       3845   128   455   7.07   0
 41. Q46081        Sequence derived from human c   2726   127   449   7.01   0
 42. Q53993        Myotonic dystrophy (DM) gene    3407   127   449   7.01   0
                    ****  6 standard deviations above mean ****
 43. Q06845        Sequence encoding tumour grow   2530   126   422   6.94   0
 44. Q03259        Pseudorabies virus glycoprote   4897   126   424   6.94   0
 45. Q42383        TGF-beta1 receptor type II (c   2090   125   270   6.88   0

1. US-08-162-407-5 (1-988)
  Q41760        Oxytocin receptor coding sequence.

 ID     Q41760 standard; DNA; 1167 BP.
 AC     Q41760;
 DT     02-SEP-1993  (first entry)
 DE     Oxytocin receptor coding sequence.
 KW     Human uterine myometrium tissue; labour; hypertonic uterine
 KW     dysfunction; ss.
 OS     Homo sapiens.
 PN     EP-542424-A.
 PD     19-MAY-1993.
 PF     09-OCT-1992; 309239.
 PR     09-OCT-1991; JP-262167.
 PR     27-MAR-1992; JP-071258.
 PA     (ROHT ) ROHTO PHARM CO LTD.
 PI     Azuma C,  Kimura T,  Okayama H,  Saji F,  Tanizawa O;
 DR     WPI; 93-160903/20.
 DR     P-PSDB; R37264.
 PT     Isolated oxytocin receptor and DNA encoding it - obtd. from human
 PT     uterine myometrium tissue, used in study and treatments during
 PT     labour
 PS     Claim 8; Page 9-11; 15pp; English.
 CC     RNA was isolated from human myometrium tissue and used to prep. a
 CC     cDNA library in E. coli DH5 cells.  Plasmid DNA was isolated,
 CC     linearised and used to synthesise mRNA transcripts.  The mRNA was
 CC     injected into Xenopus oocytes and membrane currents after perfusion
 CC     with oxytocin were examined.  Positive pools were selected and the
 CC     cDNA encoding the oxytocin receptor isolated.  The oxytocin receptor
 CC     can be used to determine oxytocin receptor levels, partic. in
 CC     uterine endometrium cells.  This can be used to e.g. infer labour
 CC     time, predict whether or not relief of labour pains of patients with
 CC     preterm labour is possible or for prevention of hypertonic uterine
 CC     dysfunction or determination of the time of inducing labour pains.
 SQ     Sequence   1167 BP;    178 A;    404 C;    363 G;    222 T;

Initial Score     =    193  Optimized Score   =    455  Significance = 11.29
Residue Identity  =    51%  Matches           =    539  Mismatches   =   394
Gaps              =    120  Conservative Substitutions                 =     0

            X       10        20        30        40        50          60
            CGGCCGGAATTCCGGGGCCCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAG--CCCAA
            |  ||| |   ||||  ||||  || || ||  |  |  |||||||  || |||||    |
  GGGCCGAGGGCAACCGCACCGCCGGACCCCCGGGGCGCAACCA-GGCCCTGGCGC--GCGTGGAGGTGGCGG
      70    X   80         90       100        110         120       130

          70        80        90       100        110        120       130
  CAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTC-AGTGGGACCCAGG-ACTGCTCCTTCCAACA
       | |||| ||||||| |||  |||||||  || || |  ||| |   | ||  |||| |    ||
   TGCTGTGTCTCATCCTGCTCCTGGCGCTGAGC-GGGAACGCGTGTGTGCTGCTGGCGCTGCGCACCACACGC
       140       150       160        170       180       190       200

          140       150       160        170       180       190       200
   CAGCCCCATCTCCTCCGACTTCGCTGTCA-AAATC-CGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCA
   |||   || |||   |  ||||    |||  || | | | |||  || | | ||||| |    | |  |
   CAGAAGCA-CTCGCGCCTCTTCTTCTTCATGAAGCACCTAAGC-ATC-GCCGACCTGGT----GGTGGCAGT
      210        220       230       240         250       260

          210        220       230       240       250       260       270
   GTCACCGTGGCCTCC-AACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCG
   ||  | |  ||  ||  |  ||| |     |||  ||  |    || |||   |||  | ||||   | | |
   GTTTCAGGTGCTGCCGCAGTTGCTG---TGGGACATCACCTTCCGCTTCTACGGGCCCGACCTG---CTGTG
 270       280       290          300       310       320       330

         280       290         300        310             320       330
   CTGGATGGAGCGGCTCAAG-AC-TGTCGCTGG-GTCCAAGAT-GC--AAGGCT---TGCTGGAGCGCGTGAA
   | |  |||      ||||| || ||  | ||| |  || | | ||      ||   |||||  || | ||
   CCGCGTGG------TCAAGTACTTGCAGGTGGTGGGCATGTTCGCCTCCACCTACCTGCTGCTGCTCATGTC
     340             350       360       370       380       390       400

      340       350       360       370       380       390       400
   CACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAA
   |  |||    | ||   |  ||  || ||||   |    | | | | || | |  |||  || || | |
   CCTGGA---CCGCTGCCTGGCC--ATCTGCCAGCCGCTGCGCTCGCTGC-GCCGCCGCACCGACC-GCCTGG
            410       420         430       440        450       460

    410       420         430        440       450       460        470
   CATCTCCCGCCTCCTG--CAGGAGACCT-CCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTC-GCCAGA
   ||   | |||| | ||    ||   |||   |  ||||  | | ||| |  || |    || ||| ||  ||
   CAGTGCTCGCCACGTGGCTCGGCTGCCTGGTGGCCAGC--GCGCCGCAGGTGCACATCTTCTCTCTGCGCGA
    470       480       490       500         510       520       530

       480       490       500       510         520       530       540
   ACT-TCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGAC-TCCTC-AACCCTGCCACCCCCATGGAGTCCCC
     |  ||  ||| | ||    |||| |     | ||| | || || | |||||     |||| ||  |   |
   GGTGGCTGACGGCGTCTTCGACTGCTG-----GGCCGTCTTCATCCAGCCCTG-GGGACCCAAGGCCT--AC
    540       550       560            570       580        590        600

       550        560          570         580        590        600
   GGCCCCTGGAGGCCAC-AGC-CCCGACA--GCCCCG--CAGCCCCCTCTGCT-CCTCCTACTG-CTGCTGCC
     | | ||||   | | |||   | |||  |  |||  || |   ||| ||| ||| |||| | ||  |
   ATCACATGGATCACGCTAGCTGTCTACATCGTGCCGGTCATCGTGCTC-GCTACCTGCTACGGCCTTATCAG
          610       620       630       640        650       660       670

   610       620         630       640       650       660          670
   CGTGGGCCTCCTGCTG--CTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCG---GAGGACAC--
   | |     ||  || |  || || ||| |  |    |||||  ||| | || || ||||   |||| | |
   CTTCAAGATCTGGCAGAACTTGCGGCT-CAAGACCGCTGCAGCGGCGGCGGCCGAGGCGCCAGAGGGCGCGG
         680       690        700       710       720       730       740

           680       690       700       710        720       730
   ---CCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAG-GACCTGCTGCTTGTGGA--GCACTGA-
      |  ||  ||||| ||  |||  ||| | | |  |||  ||| | |  ||| | | |  |  ||   ||
   CGGCTGGCGATGGGGGGCGCGTG-GCCCTGGCGCGTGTCAGCAGCGTCAAGCT-CATCTCCAAGGCCAAGAT
        750       760        770       780       790        800       810

      740         750            760       770        780       790
   ---CCTGGCCAAG--GCC-----TCATCCTGCGGAGCCTTAAAC-AACGCAGTGAGACAGACATCTATCATC
      |  || ||||  | |     ||||| ||| | ||||| | |    || |   | |   | ||| || |
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   CCGCACGGTCAAGATGACTTTCATCATCGTGCTG-GCCTTCATCGTGTGCTGGACGCCTTTCTTCT-TCGTG
        820       830       840        850       860       870        880

  800       810         820       830       840       850          860
   CCATTTTACAGGG--GAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGAT-GT-AT-AGCCTGG
   |   | |  || |    |||| |  | || | || || | || | |   |   |  || || ||   |||||
   CAGATGTGGAGCGTCTGGGATGCCAACGCGCCCA-AG-GAAGCCTCGGCCTTCATCATCGTCATGCTCCTGG
        890       900       910         920       930       940       950

      870       880       890       900        910       920       930
   ACA-CAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCT-TGGCCCCCTCTCATTCCCTCCCCAGAATGGAGGC
    || |      || ||     |  || |   || | |   |  | |   |   | || |   |||     ||
   CCAGCCTCAACAGCTGCTGCAACCCCTGGATCTACATGCTGTTCACGGGCCACCTCTTCGACGAACTCGTGC
        960       970       980       990      1000      1010      1020

     940         950       960       970       980      X
   AACGCCAGAATCC--AGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCG
   | |||     |||   ||  |  | |||  ||||  |    |  || |  || |
   AGCGC----TTCCTGTGCTGCTCCGCCAGCTACCTGA---AGGGCAGACGCCTGGAGAGACGAG
         1030      1040      1050         1060     1070 X     1080

2. US-08-162-407-5 (1-988)
   Q14645         Clone associated with biochemical pathway involvin

 ID   Q14645 standard; DNA; 2702 BP.
 AC   Q14645;
 DT   30-JAN-1992  (first entry)
 DE   Clone associated with biochemical pathway involving cAMP.
 KW   RAS; oncogene; cancer; cyclic nucleotide phosphodiesterase; ss.
 OS   Homo sapiens.
 FH   Key               Location/Qualifiers
 FT   CDS               2..2701
 FT   /*tag=  a
 PN   WO9116457-A.
 PD   31-OCT-1991.
 PF   19-APR-1991; U02714.
 PR   20-APR-1990; US-511715.
 PA   (COLD-) COLD SPRING HARBOR.
 PI   Wigler MH, Colicelli JJ;
 DR   WPI; 91-339841/46.
 DR   P-PSDB; R14854.
 PT   Complementary screening for genes and prods. - e.g. RAS protein
 PT   and cAMP, that modify, complement or suppress genetic defect and
 PT   correct associated phenotypic alteration
 PS   Disclosure; Page 141; 169pp; English.
 CC   In the specification this sequence is given the SEQ ID NO. 1 and
 CC   is additional to SEQ ID NO.s 1-55, i.e. the specification contains
 CC   two sequences denoted as SEQ ID NO.1 ! The only reference to SEQ ID
 CC   NO.1 in the text is to a 10 base pair linker. The origin and
 CC   identity of Q14645 is therefore obscure. Other sequences
 CC   in the specification were isolated from human glioblastoma cells
 CC   and encode cyclic nucleotide PDEs and RAS-related polypeptides.
 CC   (They were isolated by their ability to complement or suppress
 CC   genetic defects in a biochemical pathway involving cAMP or which is
 CC   controlled by a RAS protein).
 SQ   Sequence   2702 BP;    568 A;    899 C;    747 G;    488 T;

Initial Score    =    155  Optimized Score  =    453  Significance =  8.83
Residue Identity =    51%  Matches          =    554  Mismatches   =   367
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Gaps              =     153  Conservative Substitutions             =     0

              X       10        20        30        40            50
              CGGCCGGAATTCCGGGGCCCCCGGCCGAAATGACAGTGCTGGC----GCCAGCCT---GGA-
              | || |   | | |  | || |   || | || | |  |  ||    |||| |||   |||
    AGCCTGCACGCAGCTGACGTGCTGCAGTCCACCCACGTACTG-CTGGCCACGCCTTGGCCAACCTTAAGGAA
        1230  X   1240      1250      1260       1270      1280      1290

              60             70          80        90       100         110
    -GC-----CCAACAACCT----AT-CT--CCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGG--GACCC
     ||      ||   ||||    || ||  || ||  || | || ||||   ||   ||   ||||   ||||
    TGCAGTGTTCACGGACCTGGAGATTCTCGCCGCCCTCTTC-GCGGCTGCCATC--CACGATGTGGATCACCC
       1300      1310      1320      1330       1340        1350      1360

          120       130         140       150          160       170
    AGGACTGCTCCTTCCAACACAG--CCCCATCTCCTCCGACTTC---GCTGTCAAAATCCGTGAGCTGTCTGA
     ||   | ||  |||||| |||  || ||||  | || | |||   |||| |    ||    |      |||
    TGG---GGTC--TCCAAC-CAGTTCCTCATCAACACC-AATTCGGAGCTGGC--GCTCATGTACAACGATGA
             1370       1380      1390       1400        1410      1420

   180       190       200       210       220       230       240       250
    CTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTG
     |   ||||  |  || |||   |  |||||| || ||| |||| | | |||||   ||||   | | |||
    GTCGGTGCTCGAGAATCACCACCTGGCCGTGGGCTTCAAGCTGCTGCAGGAGGACAACTGC---GACATCTT
     1430      1440      1450      1460      1470      1480         1490

           260       270       280          290           300       310
    GCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCT---CAAGACTGTC----GCTGGGTCCAAGATGCAAG
     | |    ||   ||| |||||  |  | || | ||   |||||  |||     |  ||| |  |   || |
    CCAGAACCTC--AGCA-AGCGCCAGCGGCAGAGCCTACGCAAGATGGTCATCGACATGGTGCTGG--CCACG
      1500         1510      1520      1530      1540      1550        1560

       320       330       340       350       360        370       380
    G-CTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTC-AGCCCCCCCCCAGCT-
    | | ||    ||| | ||| |     |    || |    ||| |  |||     | ||       ||||||
    GACATGTCCAAGCACATGACCCTCCTGGCTGACCTGAAGACC-ATGGTGGAGACCAAGAAAGTGACCAGCTC
         1570      1580      1590      1600       1610      1620      1630

        390       400       410       420       430       440       450
    -GTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAG
     |   || || |  | |||  |||  ||||  || | | |||  | |||||| | |  |||| || |||  |
    AGGGGTC-CTCCTGCTAGA-TAACTACTCCGACCGCATCCAG--GTCCTCCG-GAACATGGT-GCACTG-TG
         1640      1650       1660      1670        1680        1690

      460       470       480       490       500       510         520
    CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGAC--TCCTCAACCCTGC
    ||   || | |  ||   |||  | ||  |   ||||||||| |  | |||   |||   || || |   ||
    CC---GACCTC-AGC---AACCCCACCAAGCCGCTGGAGCTGTACCGCCAG-TGGACAGACCGCATCATGGC
      1700          1710      1720      1730      1740       1750      1760

      530       540       550       560       570       580       590
    CACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTGCTCC--TCCT
    |     | |  || |   |   ||  || ||   |||   |   |     ||||||| | ||   |   |
    CGAGTTCTTCCAG-CAGGGTGACCGAGA-GCGCGAGCGTGGCATGGAAATCAGCCCCATGTGTGACAAGCAC
         1770       1780       1790      1800      1810      1820      1830

      600       610              620       630       640       650       660
    ACTGCTGCTGCCCGTGG----GCCTC---CTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGC
    |||||  ||  ||||||    | |||     | |  |     || | | ||||   || ||   |||  |
    ACTGC--CT--CCGTGGAGAAGTCTCAGGTGGGTTTTATTGACTACATTGTGCACCCATTGTGGGAGACCTG
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             1840      1850      1860      1870      1880      1890

               670             680       690       700       710       720
    GGCGGA----GGACACCC------CGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTG
    ||||||    |  |||||      |||| |  |  ||| | ||||  |  | |||  ||| ||||   | |
    GGCGGACCTTGTCCACCCATACAGCGCCATCCG--GCA-GAGCCCATCTCCGCCA--CCCGAGGAGGAG-TC
 1900      1910      1920      1930         1940      1950        1960

           730           740          750       760        770        780
    CTTGTGG--AG--CACTGA--CCTG---GCCAAGGCCTCATCCTGCGGAG-CCTTAAACAACGCAG-TGAGA
       | ||  ||  |||  |  ||||   | ||||  | ||   || |  | |  |  |  | | ||  |||
    AAGGGGGCCAGGCCACCCACCCCTGCCTGACAAGTTC-CAGTTTGAGCTGACGCTGGAGGAGGAAGAGGAGG
     1970      1980      1990      2000       2010      2020      2030

        790          800       810        820         830           840
    CAGACATCTATCA---TCCCATTTTACAGGGGA-GGATACTGAGGCA--CACAGAG--GGGA--GTCACCAG
     ||| |  |||||    ||||   ||| | | |  |     ||||||   || |||  ||||  ||||  ||
    AAGAAA--TATCAATGGCCCA-GATACCGTGCACAGCCCAAGAGGCATTGACTGAGCAGGGATTGTCAGGAG
    2040        2050       2060      2070      2080      2090      2100

      850       860        870       880        890       900       910
    CCAGAGGATGTATAGC-CTGGACACAGAGGAAGTTGGCT-AGAGGCCGGTCCCTTCCTTGGGCCCCTCTCAT
     | |||||     ||| |||||  || |  |  | | ||  |||||    ||   ||  | | |  |   |
    TC-GAGGA-----AGCTCTGGATGCA-ACCA--TAGCCTGGGAGGCATCCCCGGCCCAGGAGTCGTTGGAAG
      2110           2120         2130      2140      2150      2160

      920       930       940       950       960        970         980
    TCCCTCCCCAGAATGGAGGCAACGCCAGAATCCAGCACCGGCCCCA-TTTACCCAACTCTGAA--CAAAGCC
    |     | ||    ||| ||| | || | |  | |  | ||   || | ||    || | | |  || || |
    TTATGGCACA----GGAAGCATC-CCTGGAGGCCGAGCTGGAGGCAGTGTATTTGACACAGCAGGCACAGTC
  2170          2180       2190      2200      2210      2220      2230

       X
    CCCG
    | |
    CACAGGCAGTGCAC
     2240


3. US-08-162-407-5 (1-988)
   Q05536          Sequence enoding purified soluble intercellular ad

 ID   Q05536 standard; DNA; 1443 BP.
 AC   Q05536;
 DT   07-DEC-1990  (first entry)
 DE   Sequence enoding purified soluble intercellular adhesion molecle-1
 DE   (sICAM-1).
 KW   Soluble intercellular adhesion molecule-1; HeLa; LFA-1; rhinovirus;
 KW   Coxsackie A virus; ds;
 OS   Homo sapiens.
 PN   EP-379904-A.
 PD   01-AUG-1990.
 PF   12-JAN-1990; 100557.
 PR   24-JAN-1989; US-301192.
 PR   13-DEC-1989; US-445951.
 PA   (MOLE-) MOLECULAR THERAPEUT.
 PI   Greve J, Mcclelland A;
 DR   WPI; 90-232770/31.
 DR   P-PSDB; R06240.
 PT   Human soluble inter-cellular adhesion molecule-1 - which inhibits
PT    lymphocyte function associated with LFA-1 and ICAM-1 interaction
PS    Claim 2; Fig 1; 16pp; English.
CC    sICAM can inhibit lymphocyte function associated with antigen
CC    LFA-1 and ICAM-1 interaction, useful in treating inflamation,
CC    graft rejection, and for LFA-1 expressing tumour cells. Can also
CC    inhibit infection by rhinovirus and Coxsackie A virus, increase
CC    cell adhesion and reverse immune dysfunction due to excess sICAM-1.
SQ    Sequence   1443 BP;    306 A;    453 C;    433 G;    251 T;

Initial Score     =    150  Optimized Score  =    453  Significance =  8.50
Residue Identity  =    50%  Matches          =    542  Mismatches   =   395
Gaps              =    126  Conservative Substitutions                =     0

              X         10           20        30         40         50
              CGGCCGGAA--TTCCG---GGGCCCCCGGCCGAAATGACAGTG-CTGGCGCCAG-CCTGGAG
              |  | || |   ||||    ||   |  || | |    | ||| |  || | ||   | | |
    AGTCATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGG
       110    X  120       130       140       150       160       170

        60        70          80        90         100       110         120
    CCCA-ACAACCTATCTCCT--CCTGCTGCTGCTGCTGAGCTCGGGAC--TCAGTGGGACCCAGGACT--GCT
    |  | | | ||  |  |||     |  | |||| |||  || || ||   | |  ||     | |||  ||
    CATAGAGACCCCGTTGCCTAAAAAGGAGTTGCTCCTG-CCTGGGAACAACCGGAAGGTGTATGAACTGAGCA
     180       190       200       210        220       230       240

           130       140       150        160        170       180       190
    CCTTCCAACACAGCCCCATCTCCTCCGACTTCGCT-GTCAAAAT-CCGTGAGCTGTCTGACTACCTGCTTCA
       | ||| | ||    ||  ||  | | |  |||  ||||| | || |||   | | | | | | |||  |
    ATGTGCAAGA-AG----ATAGCCAACCAATGTGCTATTCAAACTGCCCTGA-TGGGCAGTC-AACAGCTAAA
    250            260       270       280       290        300        310

           200         210        220        230             240       250
    AGATTACCCA--GTCACCGTGGCCTCCA-ACCTGCAGG-ACGAGGAGCTCTGC------GGGGGCCTCTGGC
    |  || | ||  ||   | ||| ||||| | | |  || ||  | | | || |      ||  |||  |||
    ACCTTCCTCACCGTGTAC-TGGACTCCAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGG-
             320       330        340       350       360       370       380

         260       270       280       290       300       310       320
    GGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGG
    |   |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |   |||||
    GCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGGTGCTGC
             390       400       410       420         430        440       450

       330       340        350       360              370       380
    AGCGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAGCTGTCT
      || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  ||| | ||
    TCCGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-CGGTGC
              460       470         480       490       500       510        520

   390       400       410       420       430        440         450
    TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCTGAAGCC
    | | |  |   ||| || ||   |   |||   | |  | | | | | || | |  |  | ||| |  |||
    T-GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CCCAAGGG
                530         540       550       560       570       580

    460       470       480       490        500        510       520
    CTGGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACCCTGCCA
    ||||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  | || |  |||
    CTGGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACTCCCCCA
   590       600       610        620       630       640        650
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    530       540       550        560       570        580           590
    CCCCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-CTCCTC
    |  |     || ||||||  ||| ||||   |||  |  |  | |   | | |  ||||   | | ||  ||
    CAACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTC
    660       670       680       690       700       710       720

        600       610       620       630       640       650       660
    CTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCGG
    | | |   |  | ||  || || ||||   ||||  |   ||  | |  || ||   || | | | |  |
    CCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGG--GGGACC-AGAGGTTGAAC-CCCACA-GTCAC--CTA
  730       740       750       760         770       780         790

      670       680       690       700        710         720       730
    AGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTC-CCCAGTCCCC--AGGACCTGCTGCTTGTGGAGCAC
     ||  ||  | || |   |  || | | || | |||     | || |  |||||  |  ||     | |  |
    TGGCAACGACTCCTTCTCGGCCAAG-G-CCTCAGTCAGTGTGACCGCAGAGGACGAG-GGCACCCAGCG-GC
       800       810        820        830       840        850       860

       740       750       760       770         780       790        800
    TGACCTGGCCAAGGCCTCATCCTGCGGAGCCTTAAACA--ACGCAGTGAGACAGACATCTATCATC-CCATT
    |||| ||  ||     | || ||| ||| ||  |  ||  |  || ||   ||||||   | ||||  ||
    TGACGTGTGCA----GTAATACTGGGGAACCAGAGCCAGGAGACACTG---CAGACAGTGACCATCTACAGC
         870           880       890       900          910       920

        810             820       830            840           850
    TTACAGGGG----AGG--ATACTGAGGCACACAGAGG-----GGAGTCACC-AG---CCAGAGGA-TGTATA
    || | || |    | |  || |||| | |  ||||||     | ||  ||| ||    ||| | | |||
    TTTCCGGCGCCCAACGTGATTCTGACGAAGCCAGAGGTCTGAGAAGGGACCGAGGTGACAGTGAAGTGTGAG
    930       940       950       960       970       980       990

  860        870        880         890           900       910       920
    GCCTGGACAC-AGAG-GAAGTTG--GCTAGAGGCCGGT----CCCTTCCTTGGGCCCCTCTCATTCCCTCCC
    |||   || | ||||  ||| ||  |||  | |  | |    |||  ||   || |||       ||  | |
    GCC--CACCCTAGAGCCAAGGTGACGCTGAATGGGGTTCCAGCCCAGCCACTGGGCCC-GAGGGCCCAGCTC
 1000        1010      1020      1030      1040      1050       1060

        930       940       950       960       970       980       X
    CAGAATGGAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
    | |  || |||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
    CTG-CTGAAGGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGC
  1070       1080      1090        1100      1110        1120        1130

    CGG


4. US-08-162-407-5 (1-988)
   Q21171        Clone encoding Intercellular Adhesion Molecule-1.

   ID    Q21171 standard; DNA; 1846 BP.
   AC    Q21171;
   DT    21-MAY-1992  (first entry)
   DE    Clone encoding Intercellular Adhesion Molecule-1.
   KW    cloning technique; cell surface antigen; immunodiagnosis; ICAM-1;
   KW    integrin; lymphocyte function associated antigen; LFA-1; ss.
   OS    Homo sapiens.
   FH    Key             Location/Qualifiers
   FT    sig_peptide     13..87
   FT    /*tag=  a
FT   mat_peptide      88..1608
FT   /*tag=  b
FT   /product= ICAM-1
PN   WO9201049-A.
PD   23-JAN-1992.
PF   15-JUL-1990; U04986.
PR   13-JUL-1990; US-553759.
PA   (GEHO-) GEN HOSPITAL CORP.
PI   Seed B, Aruffo A, Amiot M;
DR   WPI; 92-056864/07.
DR   P-PSDB; R20809.
PT   New CD53 cell surface antigen and DNA encoding it - for
PT   immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
PS   Example 7; Fig 11; 160pp; English.
CC   A cDNA library was constructed using RNA prepared from HL60 cells
CC   induced with PMA. The library was transfected into COS cells  and
CC   cells expressing surface antigens were recovered by panning with
CC   the anti-ICAM MAbs 8F5 and 84H10. Episomal DNA was recovered from
CC   the panned cells and the expression-panning cycle repeated twice
CC   more to obtain a cDNA clone designated pICAM-1. The availability of
CC   a functional ICAM-1 cDNA will allow a better assessment of the role
CC   of ICAM-1/LFA-1 mediated adhesion in antigen-specific leukocyte
CC   function, including T-cell mediated killing, T-helper responses and
CC   antibody-dependent cell mediated killing.
SQ   Sequence   1846 BP;    416 A;    580 C;    531 G;    319 T;

Initial Score     =    149  Optimized Score  =    454  Significance =  8.44
Residue Identity  =    50%  Matches          =    535  Mismatches   =   409
Gaps              =    112  Conservative Substitutions             =     0

            X         10           20        30         40         50
            CGGCCGGAA--TTCCG---GGGCCCCGGCCGAAATGACAGTG-CTGGCGCCAG-CCTGGAG
            |  | || |   ||||    ||   |  || | |    | ||| |  || | ||   | | |
  AGTCATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGG
   120       130       140       150       160       170       180

      60        70          80        90         100       110         120
  CCCA-ACAACCTATCTCCT--CCTGCTGCTGCTGCTGAGCTCGGGAC--TCAGTGGGACCCAGGACT--GCT
  |  | | | ||  |  |||     |  | |||| |||  || || ||   | |  ||     | |||  ||
  CATAGAGACCCCGTTGCCTAAAAAGGAGTTGCTCCTG-CCTGGGAACAACCGGAAGGTGTATGAACTGAGCA
 190       200       210       220        230       240       250

         130       140       150        160        170       180       190
  CCTTCCAACACAGCCCCATCTCCTCCGACTTCGCT-GTCAAAAT-CCGTGAGCTGTCTGACTACCTGCTTCA
     | ||| | ||    ||  ||  | | |  |||  ||||| | || |||   | | | | | | |||  |
  ATGTGCAAGA-AG----ATAGCCAACCAATGTGCTATTCAAACTGCCCTGA-TGGGCAGTC-AACAGCTAAA
260        270           280       290       300        310        320

         200         210        220        230             240       250
  AGATTACCCA--GTCACCGTGGCCTCCA-ACCTGCAGG-ACGAGGAGCTCTGC------GGGGGCCTCTGGC
  |  || | ||  ||   | ||| ||||| | | |  || ||  | | | || |      ||  |||  |||
  ACCTTCCTCACCGTGTAC-TGGACTCCAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGG-
     330       340        350       360       370       380       390

       260       270       280       290       300       310       320
  GGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGG
  |   |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |   |||||
  GCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGGTGCTGC
     400       410       420       430         440        450       460
```

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     330       340        350       360              370       380
  AGCGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAGCTGTCT
    || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  ||| | ||
  TCCGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-CGGTGC
      470       480         490       500       510       520        530

 390       400       410       420       430        440         450
  TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCTGAAGCC
  | | |  |   ||| || ||  |   |||   | |  | | | | | || | |  |  | ||| |  |||
  T-GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CCCAAGGG
        540       550         560       570       580       590        600

  460       470       480       490        500        510       520
  CTGGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACCCTGCCA
  ||||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  | || |  |||
  CTGGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACTCCCCCA
         610        620        630       640       650        660

  530       540       550        560       570        580           590
  CCCCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-CTCCTC
  |  |     || ||||||  ||| ||||   |||  |  |  | |   | | |  ||||   | | ||  ||
  CAACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTC
670       680       690       700       710       720       730       740

      600       610       620           630       640       650       660
  CTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGG----CCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCG
  | | | - |  | ||  || || ||||   ||||    ||   |  ||   ||  ||| | ||      ||
  CCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCC--CACAGTCACCTATGGCA
        750       760       770       780       790         800       810

        670       680            690        700         710       720
  GCGGAGGACACCCCGCCCTGGG---GAG-CAG-GTGCCCCCCG-TCCCCAG--TCCCCAGGACCTGCTG-CT
   | ||   |  | || ||  ||    || ||| ||| || | |    | ||    |||||   | |||| |
  AC-GACTCCTTCTCGGCCAAGGCCTCAGTCAGTGTGACCGCAGAGGACGAGGGCACCCAG---CGGCTGACG
         820       830       840       850       860       870

     730       740       750       760        770       780       790
  TGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCT-TAAACAACGCAGTGAGACAGACATCTATC
  |||| || | | || |||  ||  ||  | || |  ||  ||  | |||  |       ||||   ||   |
  TGTGCAGTAAT-AC-TGGGGAA--CCAGAGCCAGGAGACACTGCAGACAGTGACCATCTACAGCTTTCCGGC
880       890           900       910       920       930       940

    800       810       820       830       840       850        860
  ATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGA-TGTATAGCCTGGA
    || |  | |    |  | |  | ||||  | |||| ||||   |   | ||| | | |||   |||   |
  GCCCAACGTGATTCTGACGAAGCCAGAGG-TCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCC--CA
  950       960       970        980       990      1000      1010

    870        880         890           900       910       920       930
  CAC-AGAG-GAAGTTG--GCTAGAGGCCGGT----CCCTTCCTTGGGCCCCTCTCATTCCCTCCCCAGAATG
  | | ||||  ||| ||  |||  | |  | |    |||  ||   || |||       ||  | || |  ||
  CCCTAGAGCCAAGGTGACGCTGAATGGGGTTCCAGCCCAGCCACTGGGCCC-GAGGGCCCAGCTCCTG-CTG
  1020      1030      1040      1050      1060       1070      1080

         940       950       960       970       980       X
  GAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
   |||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
  AAGGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGCCGG
  1090      1100        1110      1120        1130        1140
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5. US-08-162-407-5 (1-988)
   N90611       Intercellular adhesion molecule-1 (ICAM-1) cDNA.

 ID   N90611 standard; cDNA; 1846 BP.
 AC   N90611;
 DT   20-DEC-1989  (first entry).
 DE   Intercellular adhesion molecule-1 (ICAM-1) cDNA.
 KW   Tyrosine suppressor gene; ASV LTR; human cytomegalovirus AD169 enhancer;
 KW   HIV box; immunoselection; immune deficiency diseases;  vasculitis;
 KW   systemic lupus erythematosus; rheumatoid arthritis; neoplasms;
 FH   Key             Location/Qualifiers
 FT   CDS             13..1608
 FT   /*tag= a
 PN   EP-330191-A.
 PD   30-AUG-1989.
 PF   23-FEB-1989; 103127.
 PR   25-FEB-1988; US-160416.
 PA   (GEHO) Gen. Hospital Corp.
 PI   Seed B, Allen J, Aruffo A, Camerini D, Lauffer L, Oquendo CP,
 PI   Simmons D, Stamenkovic I, Stengelin S;
 DR   WPI; 89-250302/35.
 DR   P-PSDB; P91357.
 PT   Rapid immuno:selection cloning - used to clone genes encoding
 PT   cell surface antigens associated with mammalian T lymphocytes.
 PS   Disclosure; fig. 11; 69pp; English.
 CC   ICAM-1 is a ligand for LFA-1 (a major receptor of T and B cells
 CC   and grnulocytes). ICAM contains no RGD motifs and is instead
 CC   homologous to the neural cell adhesion molecule (NCAM). COS cells
 CC   transfected with ICAM cDNA clone bind myeloid cells by a specific
 CC   interaction which can be blocked by monoclonal antibodies directed
 CC   against either ICAM-1 or LFA-1.
 SQ   Sequence   1846 BP;   416 A;   580 C;   531 G;   319 T;

Initial Score     =    149  Optimized Score  =    454  Significance =  8.44
Residue Identity  =    50%  Matches          =    535  Mismatches   =   409
Gaps              =    112  Conservative Substitutions             =     0

            X         10           20        30         40         50
            CGGCCGGAA--TTCCG---GGGCCCCCGGCCGAAATGACAGTG-CTGGCGCCAG-CCTGGAG
            |  | || |   ||||    ||   |  || | |    | ||| |  || | ||   | | |
  AGTCATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGG
   120       130       140       150       160       170       180

      60        70          80        90         100       110         120
  CCCA-ACAACCTATCTCCT--CCTGCTGCTGCTGCTGAGCTCGGGAC--TCAGTGGACCCAGGACT--GCT
  |  | | | ||  |  |||     |  | |||| |||  || || ||   | |  ||     | |||  ||
  CATAGAGACCCCGTTGCCTAAAAAGGAGTTGCTCCTG-CCTGGGAACAACCGGAAGGTGTATGAACTGAGCA
 190       200       210       220        230       240       250

         130       140       150        160        170       180       190
  CCTTCCAACACAGCCCCATCTCCTCCGACTTCGCT-GTCAAAAT-CCGTGAGCTGTCTGACTACCTGCTTCA
     | ||| | ||    ||  ||  | | |  |||  ||||| | || |||   | | | | | | |||  |
  ATGTGCAAGA-AG----ATAGCCAACCAATGTGCTATTCAAACTGCCCTGA-TGGGCAGTC-AACAGCTAAA
260        270           280       290       300        310        320

         200         210        220        230             240       250
  AGATTACCCA--GTCACCGTGGCCTCCA-ACCTGCAGG-ACGAGGAGCTCTGC------GGGGGCCTCTGGC
  |  || | ||  ||   | ||| ||||| | | |  || ||  | | | || |      ||  |||  |||
  ACCTTCCTCACCGTGTAC-TGGACTCCAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGG-
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      330        340         350        360        370        380        390

       260       270       280       290       300       310       320
  GGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGG
  |   |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |   |||||
  GCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGGTGCTGC
     400       410       420       430         440        450       460

     330       340        350       360              370       380
  AGCGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAGCTGTCT
    || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  ||| | ||
  TCCGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-CGGTGC
      470       480         490       500       510       520        530

 390       400       410       420       430        440         450
  TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCTGAAGCC
  | | |  |   ||| || ||  |   |||   | |  | | | | | || | |  |  | ||| |  |||
  T-GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CCCAAGGG
        540       550         560       570       580       590        600

  460       470       480       490        500        510       520
  CTGGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACCCTGCCA
  ||||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  |||  |  |||
  CTGGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACTCCCCCA
         610        620        630       640       650        660

  530       540       550        560       570        580           590
  CCCCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-CTCCTC
  |  |     || ||||||  ||| ||||   |||  |  |  | |   | | |  ||||   | | ||  ||
  CAACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTC
670       680       690       700       710       720       730       740

      600       610       620           630       640       650       660
  CTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGG----CCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCG
  | | |   |  | ||  || ||  ||||   ||||    ||   |  ||   ||  ||| | ||      ||
  CCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCC--CACAGTCACCTATGGCA
        750       760       770       780       790         800       810

        670       680            690        700         710       720
  GCGGAGGACACCCCGCCCTGGG---GAG-CAG-GTGCCCCCCG-TCCCCAG--TCCCCAGGACCTGCTG-CT
   | ||   |  | || ||  ||    || ||| ||| || | |    | ||    |||||   | |||| |
  AC-GACTCCTTCTCGGCCAAGGCCTCAGTCAGTGTGACCGCAGAGGACGAGGGCACCCAG---CGGCTGACG
         820       830       840       850       860       870

     730       740       750       760        770       780       790
  TGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCT-TAAACAACGCAGTGAGACAGACATCTATC
  |||| || | | || |||  ||  ||  | || |  ||  ||  | |||  |       ||||   ||   |
  TGTGCAGTAAT-AC-TGGGGAA--CCAGAGCCAGGAGACACTGCAGACAGTGACCATCTACAGCTTTCCGGC
880       890           900       910       920       930       940

    800       810       820       830       840       850        860
  ATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGA-TGTATAGCCTGGA
    || |  | |    |  | |  | ||||  | |||| ||||   |   | ||| | | |||   |||   |
  GCCCAACGTGATTCTGACGAAGCCAGAGG-TCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCC--CA
  950       960       970        980       990      1000      1010

    870        880         890           900       910       920       930
  CAC-AGAG-GAAGTTG--GCTAGAGGCCGGT----CCCTTCCTTGGGCCCCTCTCATTCCCTCCCCAGAATG
  | | ||||  ||| ||  |||  | |  | |    |||  ||   || |||       ||  | || |  ||
  CCCTAGAGCCAAGGTGACGCTGAATGGGGTTCCAGCCCAGCCACTGGGCCC-GAGGGCCCAGCTCCTG-CTG
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    1020      1030      1040      1050      1060       1070      1080

           940       950       960       970       980       X
    GAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
     |||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
    AAGGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGCCGG
    1090      1100        1110      1120        1130        1140

6. US-08-162-407-5 (1-988)
   Q04049         Sequence of clone HL-60 encoding inter-cellular ad

 ID    Q04049 standard; cDNA; 3024 BP.
 AC    Q04049;
 DT    11-SEP-1990  (first entry)
 DE    Sequence of clone HL-60 encoding inter-cellular adhesion molecule
 DE    (ICAM-1).
 KW    Inter-cellular adhesion molecule; ICAM-1; Cancer;
 KW    metastasis; dexamethazone; azathioprine; cyclosporin A; ds.
 OS    Homo sapiens.
 FH    Key              Location/Qualifiers
 FT    CDS              58..1653
 FT    /*tag=  a
 PN    WO9003400-A.
 PD    5-APR-1990.
 PF    28-SEP-1989; 004242.
 PR    28-SEP-1988; US-250446.
 PR    30-JUN-1989; US-373882.
 PA    (DANA-) Dana-Farber Cancer.
 PI    Springer T, Rothlein R, Marlin SD, Dustin ML;
 DR    WPI; 90-132247/17.
 DR    P-PSDB; R04165.
 PT    Inter-cellular adhesion molecules and binding ligands -
 PT    used for treating inflamation and tumour cells, etc.
 PS    Claim 1; Fig 8; 158pp; English.
 CC    Gene product may be used in treatment of inflamation caused by
 CC    deffence system response, and in supression of metastasis and
 CC    tumour growth. The product may also be used in conjunction with an
 CC    immunosuppressant selected from dexamethazone, azathioprine and
 CC    cyclosporin A.
 SQ    Sequence   3024 BP;    722 A;    874 C;    802 G;    626 T;    0 Others;

Initial Score    =    149  Optimized Score  =    454  Significance =  8.44
Residue Identity =    50%  Matches          =    534  Mismatches   =   412
Gaps             =    108  Conservative Substitutions         =     0

              X         10           20         30          40          50
              CGGCCGGAA--TTCCG---GGGCCCCCGGCCGAAATGACAGTG-CTGGCGCCAG-CCTGGAG
              |  | || |   ||||    ||   |  || | |    | ||| |  || | ||   | | |
    AGTCATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGG
          170 X     180       190       200       210       220       230

        60        70          80        90       100       110       120
    CCCA-ACAACCTATCTCCT--CCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGGACCCAGGACTGCTCCTT
    |  | | | ||  |  |||     |  | |||| |||  || ||||  ||   |||    | | ||  | |
    CATAGAGACCCCGTTGCCTAAAAAGGAGTTGCTCCTG-CCT-GGGA-ACAACCGGAAGGTGTA-TGAACTTA
        240       250       260       270         280        290         300

         130       140       150        160        170       180       190
    CCAA--CACAGCCCCATCTCCTCCGACTTCGCT-GTCAAAAT-CCGTGAGCTGTCTGACTACCTGCTTCAAG
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   |||    ||     ||  ||  | | |  |||  ||||| | || |||   | | | | | | |||  ||
  GCAATGTGCAAGAAGATAGCCAACCAATGTGCTATTCAAACTGCCCTGA-TGGGCAGTC-AACAGCTAAAAC
       310       320       330        340       350         360       370

       200         210       220        230              240       250
  ATTACCCA--GTCACCGTGGCCTCCA-ACCTGCAGG-ACGAGGAGCTCTGC------GGGGGCCTCTGGCGG
   || | ||  ||   | ||| ||||| | | |  || ||  | | | || |      ||  |||  ||| |
  CTTCCTCACCGTGTAC-TGGACTCCAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGG-GC
        380        390       400       410       420       430        440

     260       270       280       290       300        310      320
  CTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAG
    |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |   |||||
  AAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGGTGCTGCTC
        450       460       470         480        490       500        510

   330       340        350       360              370       380      390
  CGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAGCTGTCTTC
  || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  ||| | ||  |
  CGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-CGGTGCT-
         520       530         540       550       560       570

         400       410       420       430       440          450
  GCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCTGAAGCCCT
  | |  |   ||| || ||  |   |||   | |  | | | | | || | |  |  | ||| |  |||  ||
  GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CCCAAGGGCT
 580       590          600       610       620       630        640

460       470       480       490        500       510       520
  GGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACCCTGCCACC
  ||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  | || |  ||||
  GGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACTCCCCCACA
  650       660       670       680       690       700        710

530       540       550        560       570       580           590
  CCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-CTCCTCCT
   |     || ||||||  ||| ||||   |||  |  |  | |   | | |  ||||   | | ||  |||
  ACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTCCC
   720       730       740       750       760       770       780

    600       610       620           630       640       650       660
  ACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGG----CCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGC
  | |   |  | ||  || || ||||   ||||    ||   |  ||   ||  ||| | ||      ||  |
  AGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCC--CACAGTCACCTATGGCAAC
 790       800       810       820       830        840       850

      670       680           690         700        710       720
  GGAGGACACCCCGCCCTGGG---GAG-CAG-GTGCCCCCCG-TCCCCAG--TCCCCAGGACCTGCTG-CTTG
   ||   |  | || ||  ||    || ||| ||| || | |    | ||    |||||   | |||| | ||
  -GACTCCTTCTCGGCCAAGGCCTCAGTCAGTGTGACCGCAGAGGACGAGGGCACCCAG---CGGCTGACGTG
  860       870       880       890       900       910        920

   730       740       750       760          770       780       790
  TGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCT-TAAACAACGCAGTGAGACAGACATCTATCAT
  || || | | || |||  ||  ||  | || |  ||  ||  | |||  |       ||||   ||   |
  TGCAGTAAT-AC-TGGGGAA--CCAGAGCCAGGAGACACTGCAGACAGTGACCATCTACAGCTTTCCGGCGC
   930         940         950       960       970       980       990

  800       810       820       830       840       850        860
  CCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGA-TGTATAGCCTGGACA
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|| |  | |    |  | |  | ||||  | |||| ||||   |   | ||| | | |||   |||   ||
CCAACGTGATTCTGACGAAGCCAGAGG-TCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCC--CACC
  1000      1010      1020       1030      1040      1050        1060

870        880         890       900           910       920       930
C-AGAG-GAAGTTG--GCTAGAGGCCGGTCCCTTCCTTG----GGCCCCTCTCATTCCCTCCCCAGAATGGA
| ||||  ||| ||  ||| ||    ||| ||  ||  |     || || |     |||  | |    || |
CTAGAGCCAAGGTGACGCT-GAATGGGGTTCCAGCCCAGCCACTGCGCC-CGAGGGCCCAGCTCCTGCTGAA
   1070      1080       1090      1100      1110       1120      1130

     940       950       960       970       980       X
GGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
GGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGCCGG
   1140      1150        1160      1170          1180  X   1190


7. US-08-162-407-5 (1-988)
   N80995        HL-cDNA clone encoding human intercellular adhesio

 ID   N80995 standard; cDNA; 3113 BP.
 AC   N80995;
 DT   28-DEC-1990  (first entry)
 DE   HL-cDNA clone encoding human intercellular adhesion molecule-1
 DE   (ICAM-1)
 KW   Lymphocyte recognition; antiinflammatory agent;
 KW   lymphocyte function associated antigen 1 (LFA-1); ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   sig_peptide     58..138
 FT   /*tag=  a
 FT   mat_peptide     139..1746
 FT   /*tag=  b
 FT   polyA_signal    2976..2981
 FT   /*tag=  c
 PN   AU8815518-A.
 PD   10-NOV-1988.
 PF   29-APR-1988; 106901.
 PR   04-MAY-1987; US-045963.
 PA   (DANA-) Dana Farber Cancer.
 PI   Springer TA, Rothlein R, Marlin SD, Dustin ML;
 DR   WPI; 89-033081/05.
 DR   P-PSDB; P80458.
 PT   New inter-cellular adhesion molecule-7, derived antibodies etc. -
 PT   are used for diagnosis and treatment of inflammation and
 PT   tumours, and for new DNA coding sequences
 PS   Claim 8; Fig 8; 74pp; English.
 CC   ICAM-1 and functional derivs. are new. Also new are recombinant DNA
 CC   able to express ICAM-1 or derivs. ICAM-1 is able to bind to a molecule
 CC   present on the surface of lymphocytes and contains at least one of 17
 CC   specified AA sequences (p80441 to p80457). ICAM-1 is a 76-97kD
 CC   glycoprotein which is a binding partner for LFA-1, and is involved in
 CC   lymphocyte recognition and adhering to cell surfaces. ICAM-1 contains
 CC   5 Ig-like domains.
 SQ   Sequence   3113 BP;   735 A;   905 C;   833 G;   640 T;

Initial Score     =    149  Optimized Score  =    451  Significance =  8.44
Residue Identity  =    51%  Matches          =    542  Mismatches   =   390
Gaps              =    130  Conservative Substitutions          =     0
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           X         10        20        30         40        50
           CGGCC--GGAATTCCGGGGCCCCCGGCCGAAATGA-CAGTGCTGGCGCCAGCCTGGAGCCCA
           | |||  ||||   |  ||     |   ||| ||| || || ||   | ||     |||| |
 GGAGTTGCTCCTGCCTGGGAACAAC-CGGAAGGTGTATGAACTGAGCAATG-TG---CAAGAAGATAGCCAA
 260       270       280        290       300           310       320

60           70          80              90           100              110
 ACAA---CCTATCTCCTCCTG--CTGCTGCTGCTG-----AGCT----CGGGACTCA--GTG----GGAC-C
  |||    |||| ||   |||  ||| ||  || |     ||||    |    ||||  |||    |||| |
 CCAATGTGCTAT-TCAAACTGCCCTGATG-GGCAGTCAACAGCTAAAACCTTCCTCACCGTGTACTGGACTC
    330        340       350        360       370       380       390

        120       130        140       150       160       170       180
 CAGGACTGCTCCTTCCAACACAGC-CCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTA
 ||| || | |    |   |||  | ||| |||   | | |   |  | ||| | || | | |  |  | ||
 CAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCC--AGTGGGCAAGAACC-TTACC-CTACG-CTG
    400       410       420       430         440        450         460

       190       200       210       220       230              240
 CCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCT-CTGC------GGGGGCC
 || | |  | | |    ||  | ||| |||   |||||| ||   || || ||| || |      ||  |||
 CCAGGTGGAGGGTGGGGCA--CCCCG-GGC---CAACCT-CA--CCGTGGTGCTGCTCCCCTCTTGGCAGCC
       470       480             490          500       510       520

  250       260       270       280       290       300       310
 TCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCT
   ||| |   |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |
 AGTGG-GCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGG
     530       540       550       560         570        580       590

320       330       340        350       360              370       380
 TGCTGGAGCGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAG
 |||||   || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  |||
 TGCTGCTCCGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-
      600       610       620         630       640       650       660

      390       400       410       420       430        440         450
 CTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCT
 | ||  | | |  |   ||| || ||  |   |||   | |  | | | | | || | |  |  | ||| |
 CGGTGCT-GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CC
        670       680         690       700       710       720

       460       470       480       490        500        510       520
 GAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACC
  |||  ||||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  | ||
 CAAGGGCTGGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACT
730      740        750        760       770       780       790

       530       540       550        560       570        580
 CTGCCACCCCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-
 |  ||||  |     || ||||||  ||| ||||   |||  |  |  | |   | | |  ||||   | |
 CCCCCACAACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGG
800       810       820       830       840       850       860       870

 590       600       610       620           630       640       650
 CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGG----CCGCTGCCTGGTGCCTGCACTGGCAGAG
 ||  ||| | |   |  | ||  || || ||||   ||||    ||   |  ||   ||  ||| | ||
 CTGTTCCCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCC--CACAGTCACCT
        880       890       900       910       920         930       940
    660       670       680            690        700         710
  GACGCGGCGGAGGACACCCCGCCCTGGG---GAG-CAG-GTGCCCCCCG-TCCCCAG--TCCCCAGGACCTG
     ||  | ||   |  | || ||  ||    || ||| ||| || | |    | ||    |||||   | |
  ATGGCAAC-GACTCCTTCTCGGCCAAGGCCTCAGTCAGTGTGACCGCAGAGGACGAGGGCACCCAG---CGG
          950       960       970       980       990      1000

720        730       740       750       760        770       780
  CTG-CTTGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCT-TAAACAACGCAGTGAGACAGACA
  ||| | |||| || | | || |||  ||  ||  | || |  ||  ||  | |||  |       ||||
  CTGACGTGTGCAGTAAT-AC-TGGGGAA--CCAGAGCCAGGAGACACTGCAGACAGTGACCATCTACAGCTT
1010      1020       1030        1040      1050      1060      1070

790       800       810       820       830       840       850        860
  TCTATCATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGA-TGTATAG
  ||   |  || |  | |    |  | |  | ||||  | |||| ||||   |   | ||| | | |||   |
  TCCGGCGCCCAACGTGATTCTGACGAAGCCAGAGG-TCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGG
  1080      1090      1100      1110      1120       1130      1140

          870        880         890           900       910       920
  CCTGGACAC-AGAG-GAAGTTG--GCTAGAGGCCGGT----CCCTTCCTTGGGCCCCTCTCATTCCCTCCCC
  ||   || | ||||  ||| ||  |||  | |  | |    |||  ||   || |||       ||  | ||
  CC--CACCCTAGAGCCAAGGTGACGCTGAATGGGGTTCCAGCCCAGCCACTGGGCCC-GAGGGCCCAGCTCC
   1150      1160      1170      1180      1190      1200      1210

     930       940       950       960       970       980       X
  AGAATGGAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
   |  || |||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
  TG-CTGAAGGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGCC
   1220      1230      1240        1250      1260          1270  X   1280

  GG


8. US-08-162-407-5 (1-988)
   Q06583        Sequence encoding bovine metalloproteinase inhibit

 ID    Q06583 standard; cDNA; 1045 BP.
 AC    Q06583;
 DT    21-FEB-1991  (first entry)
 DE    Sequence encoding bovine metalloproteinase inhibitor.
 KW    Tumour; chemotherapy; cancer; Paget's disease; osteoporosis;
 KW    scleroderma; cholesteatoma; ds.
 OS    Bos taurus.
 FH    Key              Location/Qualifiers
 FT    CDS              289..948
 FT    /*tag=  a
 FT    mat_peptide      367..948
 FT    /*tag=  b
 PN    EP-398753-A.
 PD    22-NOV-1990.
 PF    18-MAY-1990; 305433.
 PR    19-MAY-1989; US-355027.
 PR    29-MAR-1990; US-501904.
 PA    (AMGE-) AMGEN INC.
 PA    (CHIL-) CHILDREN'S HOSPITAL OF LA.
 PI    Langley KE, Boone TC, DeClerck YA;
 DR    WPI; 90-350481/47.
 DR    P-PSDB; R07954.
 PT    New metallo-proteinase inhibitor polypeptide(s) - and DNA
```

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PT    encoding them, for treatment of tumour cell dissemination and
PT    rheumatoid arthritis
PS    Claim 12; Fig 1; 63pp; English.
CC    Sequence may be used to transform a procaryotic or eukaryotic
CC    expression system to give a product with all the biological
CC    properties of naturally occuring metalloproteinase inhibitor.
CC    The product has therapuetic use in inhibiting tumour dissemination
CC    during chemotherapy and radiation therapy, impurged bone marrow cell
CC    harvesting etc. The inhibitor may also be useful in encapsulating
CC    tumours aiding clean excision, and in treatment of enphysema, Paget's
CC    disease, osteoporosis, scleroderma and bedsores.
CC    The gene product also has application in autoimmune disorders eg.
CC    rheumatoid arthritis and multiple sclerosis.
CC    See also Q06584.
SQ    Sequence   1045 BP;    219 A;    350 C;    311 G;    165 T;

Initial Score    =    143  Optimized Score   =    326  Significance =  8.05
Residue Identity =    50%  Matches           =    393  Mismatches   =   292
Gaps             =     95  Conservative Substitutions                =     0

  250       260       270       280       290       300       310
  CTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAG-GCT
             | | |||      ||  |||||||  |||  |||     | | ||||  |  ||  |  ||
            ATTCCGGC----TTCT--ATGGAGC-ACTCGGGAC-----CAG-GTCCGCGGCGCGCGCACT
            X          10           20             30         40

 320       330        340           350       360       370       380
  TGCTGGAGCGCGTGAACACGG--AGAT-ACACTT---TGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCT
   ||| |  |||     | | |  || |  | |||    | | |||   | |||   | || || || | |||
  CGCTCGCTCGCCGCCCCCCAGCCAGCTCTCGCTTCCGCGCCGCCAGCCGCGCC---CCGCGCCTCCTC-GCT
 50        60          70        80        90       100          110

      390       400       410       420        430       440       450
  G-TCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGA-GACCTCCGAGCAGCTGGTGGCGCTGAA
  |  |  |||  | |  || ||||| |     |  |   |   || | ||   ||| ||   | | |   | |
  GCACCCCGCGACCTAGAG-CCAAGAAAGTTTGTGTGGCGAGTGAGGGCCGGAGAGGAGAGCGCGCCCGCGGA
  120       130        140       150       160       170       180

     460       470       480         490       500       510       520
  GCCCTGGATCACTCGCCAGAACTTCTCC--CGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTG
  |  | |  || |   ||||  |  | ||  ||| |   ||||| ||   |  ||||| |  |  |    | |
  GTGCCG--TC-CAGACCAGCGCGGCCCCGGCGGAGAGGGGAGC-GCCCCG--AGCCC-AGGCGGC--GGCGG
 190        200       210         220        230          240         250

     530         540       550         560       570       580
  CCACCCCCA--TGGAGTCCCCGGCCCCT--GGAGGCCACAGCCCCGACAGCCCCGCAGCC-CCCTCT-GC-T
  | | ||| |    | | |||| ||||||  |   ||||  | | |  | | |||||||||  || || || |
  CTAGCCCGAGTCCGCGACCCCCGCCCCTCCGCCCGCCATGGGCGCCGCCG-CCCGCAGCCTGCCGCTCGCGT
        260       270       280      290        300        310      320

590        600       610       620       630       640         650
  CCT-CCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGC--CTGCACTG-GCA-GAGG
   || ||| |||||||||   | |   || || |  | |||||  ||||| ||  || | | | |||   |
  TCTGCCTCCTGCTGCTG---GGGACGCTGCTCCCCCGGGCCGACGCCTGCAGCTGCTCCCCGGTGCACCCGC
       330          340       350       360       370       380      390

   660        670       680       690         700       710       720
  ACGCGGCG-GAGGACACCCCGCCCTGGGGAGCAGGTGCC--CCCCGTCCCCAGTCCCCAGGACCTGCTGCTT
  |   ||||    |  |  | | | | | || |||| |||    | ||   || |    ||||  ||  |  |
  AACAGGCGTTTTGCAATGCAGACATAGTGATCAGG-GCCAAAGCAGT---CAATAAGAAGGAGGTG--GACT
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      400       410       420        430          440       450

  730       740          750       760       770       780       790
GTGGAGCACTGACCTGGCCAAGG---CCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACATCTAT
 ||  |||  ||| |  | | ||   || ||||  |||||  |   |  |   ||   ||| | | || | |
CTG--GCAACGACAT--CTACGGCAACCCCATCAAGCGGATTCAGTATGAGATCAAGCAGATAAAGATGT-T
460         470         480       490       500       510       520

   800        810       820       830       840       850        860
CATCCCATTTTA-CAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAG-GATGTATAGCCTG
||    |  | | ||||  |      | |   ||||||      | | |   |  | | |  || | | |||
CAAGGGACCTGATCAGGACATAGAGTTTATCTACACAG-CCCCCGCCGCTGCCGTGTGTGGGGTCTCG-CTG
   530       540       550       560        570       580       590

    870        880            890       900           910        920
GACA-CAGAGG-AAGTTGG-----CTAGAGGCCGGTCCCTTCCTTGG----GCCCCTCT-CATTCCCTCCCC
||||   |||| |||  ||     ||    || ||      |   ||    | |  | | |||  |  || |
GACATTGGAGGAAAGAAGGAGTATCTCATTGCAGGGAAGGCCGAGGGGAATGGCAATATGCATATCACCCTC
   600       610       620       630       640       650       660

   930         940          950       960       970        980       X
AGAATGGAGGCAAC--GCC---AGAATCCAGCACCGGCCCCATTTACCCAACTCTGAA-CAAAGCCCCCG
 |  ||    || |  |||    ||  ||   |  | | ||    |    |  ||||| || ||   ||
TG--TGACTTCATCGTGCCCTGGGACACCCTGAGTGCCACCCAGAAGAAGAGCCTGAACCACAGGTACCAGA
   670       680       690       700       710       720       730   X

TGGGCTGT
 740

9. US-08-162-407-5 (1-988)
   Q55132        Sequence encoding enzyme which desulphurises a fos

 ID   Q55132 standard; DNA; 5535 BP.
 AC   Q55132;
 DT   02-AUG-1994  (first entry)
 DE   Sequence encoding enzyme which desulphurises a fossil fuel.
 KW   Enzyme; biocatalyst; fossil fuel; oxidation; cleavage;
 KW   organosulphur compounds; coal; ds.
 OS   Rhodococcus rhodochrous.
 FH   Key             Location/Qualifiers
 FT   CDS             2148..3245
 FT   /*tag=  a
 FT   /label= ORF 2
 PN   WO9401563-A.
 PD   20-JAN-1994.
 PF   09-JUL-1993; U06497.
 PR   10-JUL-1992; US-911845.
 PA   (ENER-) ENERGY BIOSYSTEMS CORP.
 PI   Denome SA,  Kovacevich BR,  Piddington CS,  Rambosek J;
 PI   Young KD;
 DR   WPI; 94-035068/04.
 DR   P-PSDB; R47874.
 PT   DNA encoding a bio catalyst which desulphurises fossil fuels -
 PT   obtd. from Rhodococcus rhodochrous bacteria, used to produce
 PT   microorganisms which degrade organic sulphur cpds.
 PS   Claim 42; Page 75-79; 104pp; English.
 CC   Microorganisms transformed with the DNA can be used to produce
 CC   the enzyme/biocatalyst for the selective oxidative cleavage of
 CC   carbon-sulphur bonds for desulphurisation of fossil fuels which
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 CC   contain organosulphur compounds.
 SQ   Sequence   5535 BP;    1028 A;    1812 C;    1726 G;    969 T;

Initial Score    =    143  Optimized Score  =     449  Significance =  8.05
Residue Identity =    50%  Matches          =     535  Mismatches   =   399
Gaps             =    120  Conservative Substitutions                =     0

            X       10             20           30            40
            CGGCCGGAATTCCGGGGC-----CCC---CGGCCGAAA----TGACAGTGCTGGCGCCAG-C
             || ||    | ||||||     |||   | | |||||    | || |   ||  ||| |
  ATCAAAGCCGAGGTCGACGCTGCGGGGCGCGATCCCGATCAGACGAAAATCTTCACCGCCGTGATGCCGGTA
      1580  X   1590      1600      1610      1620      1630      1640

 50        60          70        80         90        100       110
  CTGGAGCCCAA--CAACCTATCTCCTCCTGCTGCTGCT-GCTGAGCTCGGGACTCAGTGGGACCCAGGACTG
  || | ||  ||  ||  |  |  |   | |   |  || |   | |||   | || |    | || | | ||
  CTCG-GCGAAAGCCAGGCGGTGGC--ACAGGAACGACTGGAATATCTCAACAGTCTGGTCCATCCGGAAGTG
     1650      1660        1670      1680      1690      1700      1710

 120       130       140       150         160       170       180
  CTCCTTCCAACACAGCCCCATCTCCTCCGACTTC--GCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTT
     ||  | || |   ||  ||  | ||| | ||   ||| |      |||   || || ||| ||     |
  GGACTGTCGACGCTATCCAGTC-ACACCGGCATCAACCTGGC----GGCGTACCCTCTC-GAC-ACTCCGAT
     1720      1730       1740      1750          1760       1770

 190       200       210         220       230        240       250
  CAAGATTACCCAGTCACCGTGGCCTCCA--ACCTGCAGGACGAGGAGC-TCTGCGGGGGCCTCTGGCGGCTG
  ||||   | || |    || |  || ||  | | | | | |  |  ||  ||||    |  ||  || || |
  CAAGGACATCCTG----CGGGATCTGCAGGATCGGAATGTCCCGACGCAACTGCACATG-TTC--GCCGCCG
1780      1790          1800      1810      1820      1830         1840

  260       270        280          290          300       310        320
  GTCCTGGCACAGCGCTG-GATGGAGC-GGCTCAA--GACT-GTCGC--TGGGTCCAAGATGCAAGGC-TTGC
    |   ||||||||  | | |   || |||  ||  |  | | |||  |||  ||||  ||     | || |
  --CAACGCACAGCGAAGAGCTCACGCTGGCGGAAATGGGTCGGCGCTATGGAACCAACGTGGGGTTCGTTCC
       1850      1860      1870      1880      1890      1900      1910

         330       340       350        360            370         380
  T-GGAGCGCGTGAACACGGAGATACACTTTG-TCACCAAATGTGCC----TTTC-AG--CCCCCCCCCAGCT
  |  | | ||  | || ||| ||  ||  | | | || |  ||  ||     ||| ||  |  | || | | |
  TCAGTGGGCCGGTAC-CGGGGA-GCAGATGGCTGACGAGCTGATCCGCCACTTCGAGGGCGGCGCCGCGGAT
     1920       1930       1940      1950      1960      1970      1980

     390        400       410       420        430       440       450
  GTCTTC-GCTTCGTCCAGACCAACATCTCCCGCCTCCTGC-AGGAGACCTCCGAGCAGCTGGTGGCGCTGAA
  |  |||  | ||   | | ||  | |  || | ||||| | | |||  |  ||| ||| ||||  || |
  GGTTTCATCATCTCTCCGGCCTTCCT-GCCGGGCTCCTACGACGAGTTCGTCGACCAGGTGGTTCCGGTTCT
     1990      2000       2010      2020      2030      2040      2050

     460       470       480       490       500       510       520
  GCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCC
  |  | ||||| |  || |   |  | ||  || || || ||  ||   || || ||||  ||     ||||
  G--CAGGATCGC-GGCTACTTCCGCACCGAGTACCAGG-GCAACA--CTCTGCGCGACCACTTGGGTCTGCG
      2060       2070      2080       2090        2100      2110      2120

   530     . 540         550       560       570       580            590
  ACCCCCATGGAGTCCCCGGCC--CCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCC---TCTG--CTC-
      |||   | | |  || |  |||  | | || |||| || |  |||||||  ||||   || |  |||
  CGTACCA-CAACTGCAAGGACAACCTTCATGACA-AGCCGCGTCGACCCCGCAAACCCCGGTTCAGAACTCG
         2130      2140      2150       2160      2170      2180      2190
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           600       610       620       630       640         650
   -CTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGC-CTGCAC-TGGCAGAGGACG
     |||  |  | ||  | |   | ||| | ||  ||| ||| | ||    || |||| |  ||||  |||
   ATTCCGCCATCCGCGACACACTGACCTACAGCAACTGCCCGGTACCCAACGCTCTGCTCACGGCATCGGAAT
         2200      2210      2220      2230      2240      2250      2260

 660       670       680       690       700          710       720
   CGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCA--GTCC-CCAGGACCTGCTGCTTGT-
   ||  ||    | |  ||||   || | |  |  | |  ||||| ||  | ||  |||| |  | | | | |
   CG--GGCTTCCTCGACGCCGCCGGCATC--GAACTCGACGTCCTCAGCGGCCAGCAGGGCACGGTTCATTTC
         2270      2280        2290      2300      2310      2320      2330

     730       740       750       760            770       780       790
   --GGAGCACTGACCTGGCCAAGGCCTCATCCTGCG---GAG--CCTTAAACAACGCAGTGAGACAGACATCT
       | |||   ||| ||| |  || | |  || |   |||  ||    ||  | ||| |||   |    |
   ACCTACCACCAGCCT-GCCTACACC-CGTTTTGGGGGTGAGATCCCGCCACTGCTCAGCGAG--GGGTTGCG
         2340       2350       2360      2370      2380      2390

        800       810       820        830       840       850       860
   ATCATCCCATTTTACAGGGGAGGATACTGAGGCA-CACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCT
     ||  ||      ||   | |  ||||  |||| |||    |    |     ||||| |  | | |  ||
   GGCA--CCTGGGCGCA--CGCGTCTACT-CGGCATCAC-CCCGCTCTTGGGGCGCCAGGGCTTCTTTGTCCG
 2400        2410        2420       2430       2440      2450      2460

       870       880       890       900        910       920       930
   GGACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTG-GGCCCCTCTCATTCCCTCCCCAGAATGGAGG
    |||  | ||   | |  | || |||||   ||  |||||  |  | ||  ||   |  | | |  |   ||
   CGAC-GACAGCCCGATCAC-AGCGGCCG---CCGACCTTGCCGGACGTCGAATCGGCGTCTCGGCCT--CGG
      2470      2480       2490         2500      2510      2520

      940       950       960         970       980       X
   CAACGCCAGAATCCAGCACCGGCCCCATTTAC--CCAACTCTGAACAAAGCCCCCG
   |||  |  | |||| ||  |||||   |   |  | | |||       | ||| ||
   CAATTC--GCATCCTGC-GCGGCCAGCTGGGCGACTACCTCGAGTTGGATCCCTCGCGGCAAACGC
2530        2540       2550      2560      2570      2580 X    2590
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10. US-08-162-407-5 (1-988)
    Q38735        Human OP-2.

 ID   Q38735 standard; cDNA; 1723 BP.
 AC   Q38735;
 DT   15-JUL-1993  (first entry)
 DE   Human OP-2.
 KW   morphogenic; osteogenic protein; developmental cascade; hOP-2;
 KW   inflammation; anti-inflammatory; Transforming Growth Factor;
 KW   TGF-beta super-family; hippocampus; ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             490..1698
 FT   /*tag=  a
 FT   /note= "hOP2"
 FT   mat_peptide     1279..1695
 FT   /*tag=  b
 FT   /note= "contains conserved 7 cysteine skeleton"
 PN   WO9304692-A.
 PD   18-MAR-1993.
 PF   28-AUG-1992; U07358.
 PR   30-AUG-1991; US-752764.
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 PR   30-AUG-1991; US-752861.
 PR   30-AUG-1991; US-753059.
 PA   (CREA-) CREATIVE BIOMOLECULES INC.
 PI   Cohen CM,  Kuberasampath T,  Oppermann H,  Ozkaynak E;
 PI   Pang RHL, Rueger DC,  Smart JE;
 DR   WPI; 93-100652/12.
 DR   P-PSDB; R33410.
 PT   Morphogen-induced modulation of inflammatory response - and
 PT   resulting tissue damage, e.g. in autoimmune diseases, diabetes,
 PT   asthma, ischemia reperfusion injury, etc.
 PS   Claim 26; Page 119-121; 165pp; English.
 CC   Human osteogenic protein (OP)-2 is a preferred morphogen for use in
 CC   treating tissue damage in e.g. inflammatory disease, autoimmune
 CC   disease, arthritis, psoriasis, dermatitis, diabetes and emphysema.
 CC   Proteins having at least 70% homology with OP-2 amino acid
 CC   sequences can also be used. See R33400 for mature hOP-2.
 SQ   Sequence   1723 BP;    266 A;    625 C;    574 G;    258 T;

Initial Score    =    142  Optimized Score  =    393  Significance =  7.98
Residue Identity =    51%  Matches          =    474  Mismatches   =   333
Gaps             =    119  Conservative Substitutions              =     0
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             X       10         20        30           40            50
             CGGCCGGAATTCCG-GGGCCCCCGGCCGAAAT---GACAGTGCTGGCG---CCAGC-CTGGA
              ||  ||| |||||      || | || | ||   | | | |  ||||    ||||   |||
   GGAGCCCCATTGGAAGGAGTTCCGCTTTGACCTGACCCAGATCCCGGCTGGGGAGGCGGTCACAGCTGCGGA
         860 X     870       880       890       900       910       920

             60          70        80        90        100       110
   G--CC-CA---ACAACCTATC--TCCTCCTGCTGCTGCTGCTGAGCTCGGGAC-TCAGTGGGACCCAGGACT
   |  ||  |   ||||  |  |   | |||  ||||| |  | |  | |   || ||||   |  |||||  |
   GTTCCGGATTTACAAGGTGCCCAGCATCCACCTGCT-CAACAGGACCCTCCACGTCAGCATGTTCCAGG--T
       930       940       950        960       970       980       990

   120       130       140       150        160       170       180
   GCTCCTTCCAACACAGCCCCATCTCCTCCGACTT-CGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTT
   | |||    | ||   |  ||     || |||||   || |    || | | ||  | ||  | | |||
   GGTCC-AGGAGCAGTCCAACAGGGAGTCTGACTTGTTCTTTTTGGAT-CTTCAGACG-CT-CCGAGCTG-GA
        1000      1010      1020      1030       1040        1050

  190       200       210       220       230        240       250
   CAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAG-GAGCTCTGCGGGGGCCTCTGGCGGC---T
    | ||   |    |     |||    ||  | ||||  | || ||   |||| ||   ||   ||| |
   GACGAGGGCTGGCTGGTGCTGGATGTCA--CAGCAG--CCAGTGA---CTGCTGGTTGCTGAAGCGTCACAA
1060      1070      1080        1090        1100         1110      1120

    260       270        280       290       300       310       320
   GGTCCTGGCACAGCG-CTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGC
   || ||||| ||  || ||  |||  | | || | ||| | | | | ||    ||| |  | || || ||
   GGACCTGGGACTCCGCCTCTATGTGGAGACTGAGGACGGGCACAGCGT---GGATCCTGGCCTGGCCGGCCT
     1130      1140      1150      1160      1170         1180      1190

   330       340       350       360       370       380       390
   GCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTC--GCTTCGT
   ||  |  ||  | |   |||  |  || ||     |||||||     |       || |||||  |    ||
   GCTGGGTCAACGGGCCCCACGCTCCCAACA-----GCCTTTCGTGGTC------ACTTTCTTCAGGGCCAGT
      1200      1210      1220           1230            1240      1250

    400        410       420        430       440        450          460
   CC-AGACCAACAT-CTCCCGCCTCCTGCAG-GAGACCTCCGAGCAGCTGG-TGGCGCTG--AAGC-CCTGGA
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|| || ||  ||| | | | ||||  |||| ||| || | ||| ||  ||  ||| |   ||||  |  |
CCGAGTCC--CATCCGCACCCCTCGGGCAGTGAGGCCACTGAGGAGGAGGCAGCCGAAGAAAAGCAACGAGC
  1260        1270      1280      1290      1300      1310      1320

       470       480         490       500         510         520
T--CACTCGCCAGAACTTCTCCC--GGTGCCTGGAGCTGCAGT-GTCAGC-CCGAC--TCCTCAACCCTGCC
|  | |  |||| | |  |||||  ||  | | ||  ||  ||   | || || ||   |  ||   |||||
TGCCGCAGGCCA-ACCGACTCCCAGGGATCTTTGA--TGACGTCCACGGCTCCCACGGCCGGCAGGTCTGCC
  1330       1340      1350        1360      1370      1380      1390

 530       540        550        560          570        580       590
ACCCCCATGGAGTCCCCGGC-CCCTGGAGG-CCACAGC---CCCGACAGCCCCGCAGC-CCCCTCTGCTCCT
  |  || |   ||  || |  | | |  ||| || | ||   |  ||| |   |   || ||||    || ||
GTCGGCACGAGCTCTACGTCAGCTTCCAGGACCTCGGCTGGCTGGACTGGGTCATCGCTCCCCAAGCCTACT
   1400      1410      1420      1430      1440      1450      1460

     600       610       620       630        640       650       660
CCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCT-GCCTGGTGCCTGCACTGGCAGAGGACGCGGC
|   ||  | |||   | |||     |||| ||  || || | ||  ||| || | || ||     | || |
CGGCCTATTACTGTGAGGGGG---AGTGCTCCTTCCCACTGGACTCCTGCATG-AATGCCACCAACCACGCC
 1470      1480        1490      1500      1510       1520      1530

    670       680        690       700       710       720       730
GGAGGACACCCCGCCCTGG-GGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCAC
      |  |   |||||| | | | | ||    ||   | ||||||||| | | |||||  ||     |||
---ATCCTGCAGTCCCTGGTGCACCTGATG-AAGCCAAACGCAGTCCCCAAGGCGTGCTG--TG-----CAC
      1540      1550      1560       1570      1580        1590

   740       750       760        770        780        790       800
TGACCTGGCCAAGGCCTCATCCTGCGGAGC-CTTAAACAAC-GCAGTGAGACAGACATCTATCATCCCATTT
  |||  ||  | ||  || ||| | | || ||   |  || ||||  | |  | ||||   |  | ||
CCACCAAGCTGA-GCGCCA-CCT-CTGTGCTCTACTATGACAGCAGCAACAACGTCATC---CTGCGCA---
  1600       1610        1620      1630      1640      1650

   810       820           830       840        850       860       870
TACAGGGGAGGATACTG----AGGCACACAGAGGGGAGTCA-CCAGCCAGAGGATGTATAGCCTGGACACAG
 |||  | |  ||  ||    ||||   | |  |  | | |  ||||| |   |    ||  |||    |||
AACACCGCAACATGGTGGTCAAGGCCTGCGGCTGCCACTGAGTCAGCCCGCCCAGCCCTA--CTG----CAG
1660     1670      1680      1690      1700      1710        1720      X

      880
AGGAAGTTGG
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11. US-08-162-407-5 (1-988)
    Q01758        cDNA sequence of rat C kinase delta

 ID   Q01758 standard; cDNA; 2909 BP.
 AC   Q01758;
 DT   03-AUG-1990  (first entry)
 DE   cDNA sequence of rat C kinase delta
 KW   Rat phosphorylating enzyme C delta; reagent; diagnostic chemical;
 KW   rat C kinase delta.
 OS   Rat.
 FH   Key                 Location/Qualifiers
 FT   CDS                 363..2384
 FT   /tag= a
 PN   J02000433-A.
 PD   05-JAN-1990.
 PF   08-OCT-1987; 252506.
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PR   08-OCT-1987; JP-252506.
PA   (TAKE) Takeda Chemical Ind Kk.
DR   WPI; 90-047984/07.
DR   P-PSDB; R05228.
PT   Rat C kinase delta enzyme -
PT   expressed in animal cells and used as a reagent or diagnostic
PT   chemical
PS   Disclosure;Fig 1; 23pp; Japanese.
CC   It and its encoded rat phosphorylating enzyme C delta are new.  Also new
CC   are a transformant contg. a vector with it and prepn. of its polypeptide
CC   by culturing the transformant.  Its encoded polypeptide can be used as a
CC   reagent and a diagnostic chemical.
SQ   Sequence   2909 BP;   721 A;   773 C;   757 G;   658 T;

Initial Score     =    142  Optimized Score    =    428  Significance =  7.98
Residue Identity  =    48%  Matches            =    514  Mismatches   =   417
Gaps              =    123  Conservative Substitutions                =     0
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          X         10         20        30         40        50
          CGGCCGG--AATTCCGGGGC-CCCCGGCCGAAAT-GACAGTGCTGGCGCCAGCCTGGAGCCC
           |||| |   |||| | ||| | || | | | || | |  ||   |  || | | ||  |
GGGGAGAACCGGGCCAGCACATTCTGCGGCACTCCTGACTACATCGCCCCTG--AGATCCTG-CAGGGCCTG
1860      1870      1880      1890      1900        1910       1920

60        70          80          90       100       110       120
AACAACCTATCTCCTCCTG--CTGCTG--CTGCTGAGCTCGGGACTCAGTGGGACCCAGGACTGCTCCTTCC
||  ||  || | | | ||  ||| ||  ||  || | ||    |||  || ||        ||||| ||
AAGTACTCATTTTC-CGTGGACTGGTGGTCTTTTGGGGTC-CTCCTCTATGAGA--------TGCTCATT-G
 1930       1940      1950      1960       1970              1980

 130       140       150       160       170        180       190
AACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAG-CTGTCTGACTACCTGCTTCAAGATTAC
  ||   |||| ||      ||    |  | | |  ||  |||| |  || |  |     |  | | | |||
GCCAGTCCCCCTTCCATGGTGATGATGAGGACGAGCTCTTTGAGTCCATCCGGGTGGACAC-ACCACACTAC
1990      2000      2010      2020      2030      2040       2050

      200       210         220       230         240       250
CC------AGTCACCGTGGCCTCCAA--CCTGCAGGACGAGGAGCTCT--GCGGGGGCCTCTGGCGGCTGGT
||        |||||  ||  |||||   |  || |  ||| ||||||  | | ||| | ||| |    ||
CCGCGCTGGATCACCAAGGAGTCCAAGGACATCATG--GAGAAGCTCTTCGAGAGGGACCCTGCCAAGAGG-
2060     2070      2080      2090        2100      2110      2120

260     270       280         290        300       310       320
CCTGGCACAGCGCTGGATGGAGC-GGC-TCAAGACTGTCGC-TGGGTCCAAGATGCAAGGCTTGCTGGAG-C
 |||| |     | |||   | | ||| |||   || |  |  |  |   |  || ||  | ||||||||
-CTGGGA-GTAACAGGAAACATCAGGCTTCACCCCTTTTTCAAGACTATCAACTGGAA--CCTGCTGGAGAA
 2130       2140      2150      2160      2170      2180        2190

330       340       350        360          370       380       390
GCGTGAACACGGAGATACACTTTGTCACCAAA-TG---TGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTC
||| |||   ||||   | ||||    ||||| ||   | || |||||  |  |  || || |   |
GCG-GAAGGTGGAGCCGCCCTTTAAGCCCAAAGTGAAATCCCCTTCAG-ACTACAGCAACTTTGACCCAGAG
   2200      2210      2220      2230      2240       2250      2260

  400       410         420       430       440        450       460
GTCCAGACCAACATCTCCCGCC--TCCTGCAGGAGACCTCCGAGCAGCTGGT-GGCGCTGAAGCCCTGGATC
 ||| ||   | |   |||  |  |||| || | ||    | || | ||  | | | || | |  |  ||
TTCCTGAATGAGAAACCCCAACTTTCCTTCA-GTGA----CAAGAACCTCATCGACTCT-ATGGACCAGACA
  2270      2280      2290           2300      2310       2320      2330
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       470       480       490       500             510       520       530
    ACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGC----CC--GACTCCTCAACCCTGCCACCC
     |   | ||  ||||| ||  ||  || | |   | | | |||    ||  || |  | | | |    |||
    GCCTTCAAGGGCTTCT-CCTTTG--TGAACCCCAAATATGAGCAATTCCTGGAATAGTGAGCTCCCAGACCT
          2340       2350        2360      2370      2380      2390

           540       550       560       570       580       590         600
    CCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTGCTCCT--CCTACTGC
     | |  | | ||| | |   | ||||| || |  |  | |    |||  || | |||| | |     |  |
    GCTTTTAATGCCCCGGCAGAGTAGGCC-CATCTGC-CCTGGTTTGCA-TCCTCACTGCCCATGAAGAAGAGT
 2400      2410      2420       2430       2440       2450      2460

           610       620         630        640       650       660
    TGCTGCCCGTGGGCCTCCTGCTGCTG--GCCGCTGCCT-GGTGCCTGCACTGGCAGAGGACGCGGCGGAGGA
     | || | | | |  |||||||||||   || || ||| || |  |   |||||    |  |    ||   |
    GGGTGACTG-GTGATTCCTGCTGCTGCCCCCTCTTCCTCGGAGAGT---CTGGCTCCTGTTGGCTGGGCTCA
  2470       2480      2490      2500      2510         2520      2530

  670       680        690       700       710       720       730       740
    CACCCCGCCCT-GGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCACTGACCT
    ||   |  |||  | || | | |       ||    | |  ||    |||  |||    ||||     | ||
    CAGTACTTCCTCTGTGAACTGTT------TGT--GAATTTGCC--TTCCTTTTGCCATCGGAG--GGAAACT
    2540      2550            2560        2570        2580        2590

           750       760       770       780        790         800
    GGCCAAGGCCTCATCCTGCGGAGCCTTAAACAACGCAGTGAGACAGACA-TCTAT-CAT-CCCAT-TTTACA
    |   ||  |||  |    |    | | ||   |   | ||| | | | | | |||  || | ||| | || |
    G--TAAATCCT-GTGTGTCATTACTTGAATGTAGTTATTGAAATATATATTATATATATGCACATATATATA
      2600       2610      2620      2630      2640      2650      2660

     810       820          830       840       850       860            870
    --GGGGAGGATACTGAGGCAC---ACAGAGGGGAGTCACCAGCCAGAGGATGTATAG-CCT----GGACACA
       ||  | ||| |   || |   | |||  | |   |  || | |  ||||| | | |||      | | |
    ATAGGCTGTATA-TATTGCTCAGTATAGAAAGCATGTAGGAGACTGGTGATGTGTTGACCTTTTTTTAAAAA
     2670       2680      2690      2700      2710      2720      2730

           880       890       900        910         920        930
    GAGGAAGTTGGCTAGAGGCCGGTCCCTTCCT-TGGGCCCCTCT-CAT-TCCCTCCCCA-GAATGGAGGCAAC
     |   |  ||  ||   |    |   | | | |   | | | | ||| |   |    | | ||| | |  |
    AAACCATATGTATACGTGTGTATGTATACATCTACACACGTATACATATATGTATGTATGTATGTATG-TAT
    2740      2750      2760      2770      2780      2790      2800

   940       950       960          970          980       X
    GCCAGAATCCAGCACCGGCCCCATTTA---CCCAA-CT--CTGAACAAAGCCCCCG
    |   | ||  |  |||      |   |   | ||| ||  |||||| |       |
    GTATGTATATATGACCAAAAGAAAAGAGAGCACAAGCTACCTGAACCACAGGATTGTTTATGTGTG
   2810      2820      2830      2840      2850      2860  X   2870


12. US-08-162-407-5 (1-988)
    Q55131        Sequence encoding enzymes which desulphurise a fos

 ID   Q55131 standard; DNA; 5533 BP.
 AC   Q55131;
 DT   02-AUG-1994  (first entry)
 DE   Sequence encoding enzymes which desulphurise a fossil fuel.
 KW   Enzyme; biocatalyst; fossil fuel; oxidation; cleavage;
 KW   organosulphur compounds; coal; ds.
 OS   Rhodococcus rhodochrous.
 FH   Key             Location/Qualifiers
```

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 FT   CDS             790..2151
 FT   /*tag=  a
 FT   /label= ORF 1
 FT   CDS             3256..4506
 FT   /*tag=  b
 FT   /label= ORF 3
 PN   WO9401563-A.
 PD   20-JAN-1994.
 PF   09-JUL-1993; U06497.
 PR   10-JUL-1992; US-911845.
 PA   (ENER-) ENERGY BIOSYSTEMS CORP.
 PI   Denome SA,  Kovacevich BR,  Piddington CS,  Rambosek J;
 PI   Young KD;
 DR   WPI; 94-035068/04.
 DR   P-PSDB; R47872, R47873.
 PT   DNA encoding a bio catalyst which desulphurises fossil fuels -
 PT   obtd. from Rhodococcus rhodochrous bacteria, used to produce
 PT   microorganisms which degrade organic sulphur cpds.
 PS   Claim 39; Page 67-72; 104pp; English.
 CC   Microorganisms transformed with the DNA can be used to produce
 CC   the enzymes/biocatalysts for the selective oxidative cleavage of
 CC   carbon-sulphur bonds for desulphurisation of fossil fuels which
 CC   contain organosulphur compounds.
 SQ   Sequence   5533 BP;    1027 A;    1808 C;    1729 G;    969 T;

Initial Score    =    142  Optimized Score   =    450  Significance =  7.98
Residue Identity =    50%  Matches           =    536  Mismatches   =   399
Gaps             =    118  Conservative Substitutions             =     0

              X       10             20           30            40
              CGGCCGGAATTCCGGGGC-----CCC---CGGCCGAAA----TGACAGTGCTGGCGCCAG-C
               || ||    | ||||||     |||   | | |||||    | || |   ||  ||| |
    ATCAAAGCCGAGGTCGACGCTGCGGGGCGCGATCCCGATCAGACGAAAATCTTCACCGCCGTGATGCCGGTA
        1580  X   1590      1600      1610      1620      1630      1640

   50        60          70        80         90       100       110
    CTGGAGCCCAA--CAACCTATCTCCTCCTGCTGCTGCT-GCTGAGCTCGGGACTCAGTGGGACCCAGGACTG
    || | ||  ||  ||  |  |  |   | |   |  || |   | |||   | || |    | || | | ||
    CTCG-GCGAAAGCCAGGCGGTGGC--ACAGGAACGACTGGAATATCTCAACAGTCTGGTCCATCCGGAAGTG
       1650      1660        1670      1680      1690      1700      1710

   120       130       140       150         160       170       180
    CTCCTTCCAACACAGCCCCATCTCCTCCGACTTC--GCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTT
       ||  | || |   ||  ||  | ||| | ||   ||| |      |||   || || ||| ||     |
    GGACTGTCGACGCTATCCAGTC-ACACCGGCATCAACCTGGC----GGCGTACCCTCTC-GAC-ACTCCGAT
       1720      1730       1740      1750          1760       1770

   190       200       210         220       230        240       250
    CAAGATTACCCAGTCACCGTGGCCTCCA--ACCTGCAGGACGAGGAGC-TCTGCGGGGGCCTCTGGCGGCTG
    ||||   | || |    || |  || ||  | | | | | |  |  ||  ||||    |  ||  || || |
    CAAGGACATCCTG----CGGGATCTGCAGGATCGGAATGTCCCGACGCAACTGCACATG-TTC--GCCGCCG
  1780      1790          1800      1810      1820      1830         1840

    260       270        280          290          300       310        320
    GTCCTGGCACAGCGCTG-GATGGAGC-GGCTCAA--GACT-GTCGC--TGGGTCCAAGATGCAAGGC-TTGC
      |   ||||||||  | | |   || |||  ||  |  | | |||  |||  ||||  ||     | || |
    --CAACGCACAGCGAAGAGCTCACGCTGGCGGAAATGGGTCGGCGCTATGGAACCAACGTGGGGTTCGTTCC
         1850      1860      1870      1880      1890      1900      1910

           330       340         350        360         370         380
   T-GGAGCGCGTGAACACGGAGA-TACA-CTTTGTC-ACCAAATGTGCC-TTTC-AG--CCCCCCCCCAGCTG
   |  | | ||  | || ||| ||  | | |  || | | |  ||  |||  ||| ||  |  | || | | ||
   TCAGTGGGCCGGTAC-CGGGGAGCAGATCGCTGACGAGCTGATCCGCCACTTCGAGGGCGGCGCCGCGGATG
      1920      1930       1940      1950      1960      1970      1980

     390        400       410       420        430       440       450
   TCTTC-GCTTCGTCCAGACCAACATCTCCCGCCTCCTGC-AGGAGACCTCCGAGCAGCTGGTGGCGCTGAAG
     |||  | ||   | | ||  | |  || | ||||| | | |||  |  ||| ||| ||||  || |   |
   GTTTCATCATCTCTCCGGCCTTCCT-GCCGGGCTCCTACGACGAGTTCGTCGACCAGGTGGTTCCGGTTCTG
     1990      2000       2010      2020      2030      2040      2050

     460       470       480       490       500       510       520
   CCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCA
     | ||||| |  || |   |  |  || || || ||  ||   || || ||||  ||   | ||||  
   --CAGGATCGC-GGCTACTTCCGCACCGAGTACCAGG-GCAACA--CTCTGCGCGACCACTTGGCTCTGCGC
        2060      2070      2080      2090        2100      2110      2120

   530       540         550       560       570       580            590
   CCCCCATGGAGTCCCCGGCC--CCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCC---TCTG--CTC--
      |||   |   |  || |  |||    | || |||| || |  |||||||  ||||   || |  |||  
   GTACCA-CAACTGCAAGGACAACCTTCATGACA-AGCCGCGTCGACCCCGCAAACCCCGGTTCAGAACTCGA
         2130      2140      2150       2160      2170      2180      2190

          600       610       620       630       640         650       660
   CTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGC-CTGCAC-TGGCAGAGGACGC
    |||  |  | ||  | |   | ||| | ||   || ||| | ||    || |||| |  ||||   ||  |
   TTCCGCCATCCGCGACACACTGACCTACAGCAACTGCCCGGTACCCAACGCTCTGCTCACGGCATCGGAATC
        2200      2210      2220      2230      2240      2250      2260

          670       680       690       700          710       720
   GGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCA--GTCC-CCAGGACCTGCTGCTTGTGG
   |  ||    | |  ||||   || | |  |  | |  ||||| ||  | ||  |||| |  | | | | |  
   G--GGCTTCCTCGACGCCGCCGGCATC--GAACTCGACGTCCTCAGCGGCCAGCAGGGCACGGTTCAT-TTC
        2270      2280        2290      2300      2310      2320       2330

 730       740          750       760            770       780       790
   AGCACTGACCTG---GCCAAGGCCTCATCCTGCG---GAG--CCTTAAACAACGCAGTGAGACAGACATCTA
   | |   |||| |   ||| |  || | |  || |   |||  ||    ||  | ||| |||   |    |  
   ACCTACGACCAGCCTGCCTACACC-CGTTTTGGGGGTGAGATCCCGCCACTGCTCAGCGAG--GGGTTGCGG
         2340      2350      2360      2370      2380      2390

       800       810       820        830       840       850       860
   TCATCCCATTTTACAGGGGAGGATACTGAGGCA-CACAGAGGGGAGTCACCAGCCAGAGGATGTATAGCCTG
    ||  ||      ||   | |  ||||  |||| |||    |    |     ||||| |  | | |  ||  
   GCA--CCTGGGCGCA--CGCGTCTACT-CGGCATCAC-CCCGCTCTTGGGGCGCCAGGGCTTCTTTGTCCGC
2400          2410      2420      2430      2440      2450      2460

       870       880       890       900        910       920       930
   GACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTG-GGCCCCTCTCATTCCCTCCCCAGAATGGAGGC
   |||  | ||   | |  | || |||||   ||  |||||  |  | ||  ||   |  | | |  |   |||
   GAC-GACAGCCCGATCAC-AGCGGCCG---CCGACCTTGCCGGACGTCGAATCGGCGTCTCGGCCT--CGGC
     2470      2480      2490        2500      2510      2520          2530

     940       950       960         970       980       X
   AACGCCAGAATCCAGCACCGGCCCCATTTAC--CCAACTCTGAACAAAGCCCCCG
   ||  |  | ||||  |  |||||   |   |  | | |||       | |||  |
   AATTC--GCATCCTGC-GCGGCCAGCTGGGCGACTACCTCGAGTTGGATCCCTGGCGGCAAACGC
             2540      2550      2560      2570   .2580 X    2590
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13. US-08-162-407-5 (1-988)
    Q55342          tICAM(452) cysteine mutant.

 ID   Q55342 standard; cDNA; 1359 BP.
 AC   Q55342;
 DT   12-JUN-1994  (first entry)
 DE   tICAM(452) cysteine mutant.
 KW   ICAM-1; intercellular adhesion molecule-1; human rhinovirus; HRV;
 KW   probe; primer; polymerase chain reaction; PCR; hybridizations; ss.
 OS   Homo sapiens.
 PN   WO9400485-A.
 PD   06-JAN-1994.
 PF   22-JUN-1993; U05972.
 PR   22-JUN-1992; US-903069.
 PA   (MILE ) MILES INC.
 PI   Greve JM,  McClelland A;
 DR   WPI; 94-026146/03.
 PT   Multimeric forms of inter-cellular adhesion mol. (ICAM) -
 PT   displaying enhanced binding of human rhinovirus and able to
 PT   reduce its infectivity
 PS   Example; Page 47; 70pp; English
 CC   Oligonucleotides Q55327-35 were used to create forms of
 CC   ICAM-1 (R48038) that facilitate cross-linking and
 CC   multimerization.  The primers given in Q55336-39 were used to clone
 CC   ICAM(185)/IgG immunoadhesin fusion protein.  ICA(453)/IgG fusion
 CC   (R48037) in encoded by sequence Q55340.  Mutein Q55342, a mutated
 CC   form of Q55340, encodes tICAM(452) cysteine mutant terminated at
 CC   residue 452.  Probe Q55341 was used for HRV identification.
 SQ   Sequence   1359 BP;    294 A;    418 C;    411 G;    236 T;

Initial Score     =    141  Optimized Score   =    453  Significance =  7.92
Residue Identity  =    50%  Matches           =    531  Mismatches   =   415
Gaps              =    108  Conservative Substitutions               =     0

          X          10           20        30        40         50
          CGGCCGGAA--TTCCG---GGGCCCCCGGCCGAAATGACAGTG-CTGGCGCCAG-CCTGGAG
          |  | || |   ||||    ||   |  || | |    | ||| |  || | ||   | | |
AGTCATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGG
     30   X    40        50        60        70        80        90

    60        70         80        90           100       110         120
CCCA-ACAACCTATCTCCT--CCTGCTGCTGCTGCTGAGCTCGGGAC--TCAGTGGGACCCAGGACT--GCT
|  | | | ||  |  |||     |  | |||| |||  || || ||   | |  ||     | |||  || 
CATAGAGACCCCGTTGCCTAAAAAGGAGTTGCTCCTG-CCTGGGAACAACCGGAAGGTGTATGAACTGAGCA
   100       110       120       130       140       150       160

       130       140       150        160        170      180       190
CCTTCCAACACAGCCCCATCTCCTCCGACTTCGCT-GTCAAAAT-CCGTGAGCTGTCTGACTACCTGCTTCA
   | ||| | ||    ||  ||  | | |  |||  ||||| | || |||   | | | | | | ||| |
ATGTGCAAGA-AG----ATAGCCAACCAATGTGCTATTCAAACTGCCCTGA-TGGGCAGTC-AACAGCTAAA
   170           180       190       200       210        220        230

       200       210       220       230                  240       250
AGATTACCCA--GTCACCGTGGCCTCCA-ACCTGCAGG-ACGAGGAGCTCTGC------GGGGGCCTCTGGC
|  || | ||  ||   | ||| ||||| | | |  || ||  | | | || |      ||  |||  ||| 
ACCTTCCTCACCGTGTAC-TGGACTCCAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGG-
      240         250       260       270       280       290        300

      260       270       280       290       300       310       320
GGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGG
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  |   |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |   |||||
  GCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGGTGCTGC
        310       320       330       340          350       360       370

     330       340        350       360              370       380
  AGCGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAGCTGTCT
    || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  ||| | ||
  TCCGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-CGGTGC
         380       390         400       410       420       430

 390       400       410       420       430        440         450
  TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCTGAAGCC
  | | |  |   ||| || ||  |   |||   | |  | | | | | || | |  |  | ||| |  |||
  T-GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CCCAAGGG
440        450         460       470       480       490        500

  460       470       480       490        500        510       520
  CTGGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACCCTGCCA
  ||||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  | || |  |||
  CTGGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACTCCCCCA
  510        520        530       540       550       560        570

  530       540       550        560       570        580           590
  CCCCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-CTCCTC
  |  |     || |||||| ||| ||||   |||  |  |  | |   | | |  ||||   | | ||  ||
  CAACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTC
   580       590       600       610       620       630       640

      600       610       620           630       640       650       660
  CTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGG----CCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCG
  | | | . |  | ||  || || ||||   ||||    ||   |  ||   ||  ||| | ||      ||
  CCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCC--CACAGTCACCTATGGCA
 650       660       670       680       690       700         710

        670       680            690        700         710       720
  GCGGAGGACACCCCGCCCTGGG---GAG-CAG-GTGCCCCCCG-TCCCCAG--TCCCCAGGACCTGCTG-CT
   | ||   |  | || ||  ||    || ||| ||| || | |    | ||    |||||   | |||| |
  AC-GACTCCTTCTCGGCCAAGGCCTCAGTCAGTGTGACCGCAGAGGACGAGGGCACCCAG---CGGCTGACG
 720        730       740       750       760       770          780

     730       740       750       760        770       780       790
  TGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCT-TAAACAACGCAGTGAGACAGACATCTATC
  |||| || | | || |||  ||  ||  | || |  ||  ||  | |||  |       ||||   ||   |
  TGTGCAGTAAT-AC-TGGGGAA--CCAGAGCCAGGAGACACTGCAGACAGTGACCATCTACAGCTTTCCGGC
   790         800         810       820       830       840       850

    800       810       820       830       840       850         860
  ATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGA-TGT-ATAGCC---
    || |  | |    |  | |  | ||||  | |||| ||||   |   | ||| | | ||| |  |||
  GCCCAACGTGATTCTGACGAAGCCAGAGG-TCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGTGCCACC
     860       870       880        890       900       910       920

         870       880       890       900       910       920       930
  --TGGACACAGAGGAAGTTGGCTAGAGGCCGGTCCCTTCCTTGGGCCCCTCTCATTCCCTCCCCAGAATGGA
     || |  ||  || | ||  | | |  |   |||  ||   || |||       ||  | || |  || |
  CGCGGGCCAAGGTGACGCTGAATGGGGTTCCAGCCCAGCCACTGGGCCC-GAGGGCCCAGCTCCTG-CTGAA
    930       940       950       960       970        980       990

       940       950       960       970       980       X
  GGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
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  ||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
  GGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGCCGG
   1000    . 1010        1020      1030          1040    X 1050

14. US-08-162-407-5 (1-988)
    Q55340       tICAM(453)IgG immunoadhesin.

 ID   Q55340 standard; cDNA; 2043 BP.
 AC   Q55340;
 DT   12-JUN-1994  (first entry)
 DE   tICAM(453)IgG immunoadhesin.
 KW   ICAM-1; intercellular adhesion molecule-1; human rhinovirus; HRV;
 KW   probe; primer; polymerase chain reaction; PCR; hybridization; IgG;
 KW   immunoadhesin; ss.
 OS   Homo sapiens.
 PN   WO9400485-A.
 PD   06-JAN-1994.
 PF   22-JUN-1993; U05972.
 PR   22-JUN-1992; US-903069.
 PA   (MILE ) MILES INC.
 PI   Greve JM,  McClelland A;
 DR   WPI; 94-026146/03.
 DR   P-PSDB; R48037.
 PT   Multimeric forms of inter-cellular adhesion mol. (ICAM) -
 PT   displaying enhanced binding of human rhinovirus and able to
 PT   reduce its infectivity
 PS   Example; Page 37; 70pp; English
 CC   Oligonucleotides Q55327-35 were used to create forms of
 CC   ICAM-1 (R48038) that facilitate cross-linking and
 CC   multimerization.  The primers given in Q55336-39 were used to clone
 CC   ICAM(185)/IgG immunoadhesin fusion protein.  ICA(453)/IgG fusion
 CC   (R48037) in encoded by sequence Q55340.  Mutein Q55342, a mutated
 CC   form of Q55340, encodes tICAM(452) cysteine mutant terminated at
 CC   residue 452.  Probe Q55341 was used for HRV identification.
 SQ   Sequence   2043 BP;    467 A;    643 C;    591 G;    342 T;

Initial Score     =    141  Optimized Score    =    454  Significance =  7.92
Residue Identity  =    50%  Matches            =    535  Mismatches   =   409
Gaps              =    112  Conservative Substitutions          =     0

            X         10           20        30         40         50
            CGGCCGGAA--TTCCG---GGGCCCCCGGCCGAAATGACAGTG-CTGGCGCCAG-CCTGGAG
            |  | || |   ||||    ||   |  || | |    | ||| |  || | ||   | | |
  AGTCATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGG
       30   X    40        50        60        70        80        90

      60        70          80        90         100       110         120
  CCCA-ACAACCTATCTCCT--CCTGCTGCTGCTGCTGAGCTCGGGAC--TCAGTGGGACCCAGGACT--GCT
  |  | | | ||  |  |||     |  | |||| |||  || || ||   | |  ||     | |||  ||
  CATAGAGACCCCGTTGCCTAAAAAGGAGTTGCTCCTG-CCTGGGAACAACCGGAAGGTGTATGAACTGAGCA
    100       110       120       130        140       150       160

         130       140       150        160       170       180       190
  CCTTCCAACACAGCCCCATCTCCTCCGACTTCGCT-GTCAAAAT-CCGTGAGCTGTCTGACTACCTGCTTCA
     | ||| | ||    ||  ||  | | |  |||  ||||| | || |||   | | | | | | |||  |
  ATGTGCAAGA-AG----ATAGCCAACCAATGTGCTATTCAAACTGCCCTGA-TGGGCAGTC-AACAGCTAAA
   170            180       190       200       210        220        230

         200         210        220        230             240       250
 AGATTACCCA--GTCACCGTGGCCTCCA-ACCTGCAGG-ACGAGGAGCTCTGC------GGGGGCCTCTGGC
 |  || | ||  ||   | ||| ||||| | | |  || ||  | | | || |      ||  |||  |||
 ACCTTCCTCACCGTGTAC-TGGACTCCAGAACGGGTGGAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGG-
      240         250       260       270       280       290       300

      260       270       280       290       300       310       320
 GGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGG
 |   |  |||  | |  |||||   || |  |     | |   | | ||| ||||  |    |   |||||
 GCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGC--ACCCCGGG-CCAACCTCACCGTGGTGCTGC
       310       320       330       340          350       360       370

    330       340       350       360                370      380
 AGCGCGTGAACACGGAGAT-ACACTTTGTCACCAAATGTG-------CCTTTCAGCCCCCCCCCAGCTGTCT
   || | | | | |||| | | ||   |   |||  ||||       ||  | ||  | |  ||| | ||
 TCCGTGGGGAGAAGGAGCTGAAAC--GGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCA-CGGTGC
            380       390      400      410       420       430

390       400       410       420       430       440          450
 TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGAC-CTCCGAGCAG--CTGGTGGCGCTGAAGCC
 | | |  |   ||| || ||  |   |||   | |  | | | | | || | |  |  | ||| |  |||
 T-GGTGAGGAGAGATCACCA--TGGAGCCAATTTCTCGTGCCGCACTGAACTGGACCTGCGGC-CCCAAGGG
440       450          460      470       480       490        500

 460       470       480       490        500        510        520
 CTGGATCACTCGCCAGAACTTCTCCCGGTGCCT-GGAGCTGCAG-TGTCAGCCCGACTCCTCAACCCTGCCA
 ||||| |  |    |||||  || | |   |||   |||| |||   |  | ||  | |  | || |  |||
 CTGGAGCTGT-TTGAGAACACCT-CGGCCCCCTACCAGCTCCAGACCTTTGTCCTGC-CAGCGACTCCCCCA
 510        520        530       540       550       560        570

 530       540       550        560       570       580            590
 CCCCCATGGAGTCCCCGGCCCCTGGAGG-CCACAGCCCCGACAGCCCCG-CAGCCCCCT---CTG-CTCCTC
 |  |     || ||||||  ||| ||||   |||  |  |  | |   | | |  ||||   | | ||  ||
 CAACTTGTCAGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTCTGTTCCCTGGACGGGCTGTTC
  580       590       600       610       620       630       640

     600       610       620           630       640       650       660
 CTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGG----CCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCG
 | | |   |  | ||  || || ||||   ||||    ||   |  ||   ||  ||| | ||      ||
 CCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCC--CACAGTCACCTATGGCA
650       660       670       680       690       700         710

       670       680           690         700         710       720
 GCGGAGGACACCCCGCCCTGGG---GAG-CAG-GTGCCCCCCG-TCCCCAG--TCCCCAGGACCTGCTG-CT
  | ||   |  | || ||  ||    || ||| ||| || | |    | ||    |||||   | |||| |
 AC-GACTCCTTCTCGGCCAAGGCCTCAGTCAGTGTGACCGCAGAGGACGAGGGCACCCAG---CGGCTGACG
720       730        740       750       760       770          780

    730       740      750       760         770       780       790
 TGTGGAGCACTGACCTGGCCAAGGCCTCATCCTGCGGAGCCT-TAAACAACGCAGTGAGACAGACATCTATC
 |||| || | | || |||  ||  ||  | || |  ||  ||  | |||  |       ||||   ||   |
 TGTGCAGTAAT-AC-TGGGGAA--CCAGAGCCAGGAGACACTGCAGACAGTGACCATCTACAGCTTTCCGGC
  790         800         810       820       830       840       850

   800       810       820       830       840       850        860
 ATCCCATTTTACAGGGGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGA-TGTATAGCCTGGA
   || |  | |    |  | |  | |||| | |||| ||||   |   | ||| | | |||   |||   |
 GCCCAACGTGATTCTGACGAAGCCAGAGG-TCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCC--CA
    860       870       880       890       900       910       920

   870       880          890           900       910       920       930
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CAC-AGAG-GAAGTTG--GCTAGAGGCCGGT----CCCTTCCTTGGGCCCCTCTCATTCCCTCCCCAGAATG
| | ||||  ||| ||  |||  | |  | |  . |||  ||   || |||       ||  | || |  ||
CCCTAGAGCCAAGGTGACGCTGAATGGGGTTCCAGCCCAGCCACTGGGCCC-GAGGGCCCAGCTCCTG-CTG
    930       940       950        960       970        980       990

       940       950       960        970       980      X
GAGGCAACGCCAGAATCCAGCACCGGCCCCATTTACCCAACTCTGAACAAAGCCCCCG
 |||| || |||||   ||  || ||| |   ||  ||  |||||  |||  |||  |
AAGGCCACCCCAGAGGACA--ACGGGCGCAGCTTCTCCTGCTCTG--CAA--CCCTGGAGGTGGCCGG
   1000      1010         1020      1030          1040   X 1050


15. US-08-162-407-5 (1-988)
    Q57016        PKC delta.

 ID   Q57016 standard; DNA; 2891 BP.
 AC   Q57016;
 DT   31-AUG-1994  (first entry)
 DE   PKC delta.
 KW   110 kD catalytic subunit; phosphatidyl inositol 3-kinase;
 KW   transformation; Schizosaccharomyces pombe; nmt promoter; thiamine;
 KW   PtdIns 3-kinase; assay; detection; cell growth; regulation; cancer;
 KW   blood vessel plaques; ss.
 OS   Bos taurus.
 PN   WO9403609-A.
 PD   17-FEB-1994.
 PF   05-AUG-1993; G01651.
 PR   05-AUG-1992; GB-016654.
 PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
 PI   Goode NT,  Nurse PM,  Parker PJJ,  Waterfield MD;
 DR   WPI; 94-065697/08.
 PT   Eukaryotic cells transformed with mammalian phospholipid or
 PT   protein kinase DNA - useful in assays for compounds involved in
 PT   cell growth regulation and for treating cancers
 PS   Disclosure; Page 42-44; 71pp; English.
 CC   The sequences given in Q57014-17 encode protein kinase C (PKC)
 CC   epsilon, gamma, delta and nu respectively.  These sequences were
 CC   transformed into Schizosaccharomyces pombe cells under the regulatory
 CC   control of the nmt promoter in an embodiment of the invention.  In the
 CC   presence of thiamine the promoter is inactive and the cells carrying
 CC   the PKC plasmids grow as the parental strain.  In the absence
 CC   of thiamine the nmt promoter functions and the PKC is induced.  PKC
 CC   activity is substantially increased under these conditions.  Cells
 CC   containing constructs such as this, are useful in assays for detecting
 CC   compounds involved in cell growth regulation.  It is also used as the
 CC   basis for detecting compounds for treating cancers and the formation
 CC   of blood vessel plaques.
 SQ   Sequence   2891 BP;    718 A;    770 C;    751 G;    652 T;

Initial Score     =    141  Optimized Score    =    431  Significance =  7.92
Residue Identity  =    48%  Matches            =    514  Mismatches   =   419
Gaps              =    119  Conservative Substitutions              =     0

           X         10         20         30          40         50
           CGGCCGG--AATTCCGGGGC-CCCCGGCCGAAAT-GACAGTGCTGGCGCCAGCCTGGAGCCC
            |||| |   |||| | ||| | || | | | || | |  ||   |  || | | ||  |
 GGGGAGAACCGGGCCAGCACATTCTGCGGCACTCCTGACTACATCGCCCCTG--AGATCCTG-CAGGGCCTG
1850      1860      1870      1880      1890        1900       1910

 60        70        80         90       100       110        120
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   AACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGTGGACCCCAGGA-CTGCTCCTTCCAAC
   ||  ||  || | | | ||   ||| || |    | ||| |    |     | ||||  ||||| ||
   AAGTACTCATTTTC-CGTG-GACTGGTGGTCTTTTGGGGTCCTCCT-----CTAGGAGATGCTCATT---GG
   1920      1930        1940      1950      1960           1970

 130       140       150       160 ·     170       180       190
   ACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGA-TTACC-C
    ||| |||    ||| | |    | ||   |   |   ||||| | ||| | | | |     ||   ||| |
   CCAGTCCC----CCTTCCATGGTGATGATGAGGAC---GAGCTCTTTGAGTCCATCCGGGTGGACACACCAC
 1980          1990      2000         2010      2020      2030      2040

 200          210        220       230        240       250       260
   AGTCACCG---TGG-CCTCCAACCTGCAGGACGAGGAGCTC-TGCGGGGGCCTCTGGCGGCTGGTCCTGGCA
   | |  |||   |||  | ||||   | ||  | ||||  || ||  |  ||   | | |   |  |||| ||
   ACTACCCGCGCTGGATCACCAA---GGAGTCCAAGGACATCATGGAGAAGCTCTTCGAGAGGGACCCTGCCA
      2050      2060         2070      2080      2090      2100      2110

    270       280            290       300         310           320
   CAGCGCTGGATGGAGCGGC-----TCAAGACTGTCGCTGGGTCCAAGA--TGCAA--GG--CTTGCTGGAG-
       |||||  | | | ||     ||| |  |  | |    | |||||    |||  ||  | ||||||||
   AGAGGCTGGGAGTAACAGCAAACATCAGGCTTCACCCCTTTTTCAAGACTATCAACTGGAACCTGCTGGAGA
       2120      2130      2140      2150      2160      2170      2180

    330       340       350        360          370       380       390
   CGCGTGAACACGGAGATACACTTTGTCACCAAA-TG---TGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTT
    ||| |||   ||||   | ||||    ||||| ||   | || |||||  |  |  || || |   |
   AGCG-GAAGGTGGAGCCCCCCTTTAAGCCCAAAGTGAAATCCCCTTCAG-ACTACAGCAACTTTGACCCAGA
      2190      2200      2210      2220      2230       2240      2250

      400       410         420       430       440        450       460
   CGTCCAGACCAACATCTCCCGCC--TCCTGCAGGAGACCTCCGAGCAGCTGGT-GGCGCTGAAGCCCTGGAT
     ||| ||   | |   |||  |  |||| || | ||    | || | ||  | | | || | |  |  ||
   GTTCCTGAATGAGAAACCCCAACTTTCCTTCA-GTGA----CAAGAACCTCATCGACTCT-ATGGACCAGAC
     2260      2270      2280       2290          2300       2310      2320

       470       480       490       500             510       520
   CACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGC----CC--GACTCCTCAACCCTGCCACC
     |   | ||  ||||| ||  ||  || | |   | | | |||    ||  || |  | | | |    |||
   AGCCTTCAAGGGCTTCT-CCTTTG--TGAACCCCAAATATGAGCAATTCCTGGAATAGTGAGCTCCCAGACC
         2330       2340        2350      2360      2370      2380

 530       540       550       560       570       580       590
   CCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTGCTCCT--CCTACTG
     | |  | | ||| | |   | ||||| || |  |  | |    |||  || | |||| | |     |  |
   TGCTTTTAATGCCCCGGCAGAGTAGGCC-CATCTGC-CCTGGTTTGCA-TCCTCACTGCCCATGAAGAAGAG
2390      2400      2410       2420       2430       2440      2450

 600       610       620         630        640       650       660
   CTGCTGCCCGTGGGCCTCCTGCTGCTG--GCCGCTGCCT-GGTGCCTGCACTGGCAGAGGACGCGGCGGAGG
     | || | | | |  |||||||||||   || || ||| || |  |   |||||    |  |    ||
   TGGGTGACTG-GTGATTCCTGCTGCTGCCCCCTCTTCCTCGGAGAGT---CTGGCTCCTGTTGGCTGGGCTC
 2460       2470      2480      2490      2500         2510      2520

  670       680        690       700       710       720       730
   ACACCCCGCCCT-GGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCACTG-AC
   |||   |  |||  | || | | ||    | || ||   |||    | ||  | |     |||  |||| |
   ACAGTACTTCCTCTGTGAACTGTTGTGAACTGTTCC--TTCCTTTTG-CCATCGG---AGGGA-AACTGTAA
   2530      2540      2550      2560        2570          2580       2590

  740       750           760       770       780       790       800
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   CTGGCCAAGGCCTCAT--CCTG--CGGAGCCTTAAACAACGCAGTGAGACAGACATCTATCATCCCATTTTA
    |  ||   |  ||||  | ||   | ||  |||   ||     |   | | | ||  | |||   || | |
   AT--CCTGTGTGTCATTACTTGAATGTAG--TTATTGAAATATATATTATATATATGCA-CAT-ATATATAA
          2600      2610        2620      2630      2640        2650

    810        820       830       840       850       860            870
   CAGG-GGAGGATACTGAGGCACACAGAGGGGAGTCACCAGCCAGAGGATGTATAG-CCT----GGACACAGA
    |||  |   ||| ||      | |||  | |   |  || | |  ||||| | | |||      | | | |
   TAGGCTGTATATATTGCTCAGTATAGAAAGCATGTAGGAGACTGGTGATGTGTTGACCTTTTTTTAAAAAAA
  2660      2670      2680      2690      2700      2710      2720

        880       890       900        910         920        930        940
   GGAAGTTGGCTAGAGGCCGGTCCCTTCCT-TGGGCCCCTCT-CAT-TCCCTCCCCA-GAATGGAGGCAACGC
      |  ||  ||   |    |   | | | |   | | | | ||| |   |    | | ||| | |  | |
   ACCATATGTATACGTGTGTATGTATACATCTACACACGTATACATATATGTATGTATGTATGTATG-TATGT
2730      2740      2750      2760      2770      2780      2790       2800

          950       960          970          980       X
   CAGAATCCAGCACCGGCCCCATTTA---CCCAA-CT--CTGAACAAAGCCCCCG
     | ||  |  |||      |   |   | ||| ||  |||||| |       |
   ATGTATATATGACCAAAAGAAAAGAGAGCACAAGCTACCTGAACCACAGGATTGTTTATGTGTG
         2810      2820      2830      2840      2850   X  2860
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq5nsqinv.res made by  on Wed 5 Apr 95 17:31:09-PDT.


Query sequence being compared:US-08-162-407-5' (1-988)
Number of sequences searched:                 57621
Number of scores above cutoff:                 4562

      Results of the initial comparison of US-08-162-407-5' (1-988) with:
   Data bank : N-GeneSeq 17, all entries

100000-
      -
N     -
U50000-
M     -
B     -
E     -
R     -
      -
O     - *
F10000-   *
      -  *
S     -
E 5000-    *
Q     -
U     -*
E     -      ** *
N     -     *    * *
C     -        *    *
E     -           *
S 1000-              **
```

```
      -                *
      -                  **
   500-                 *
      -
      -                     **
      -                    *    *
      -                       **
      -
      -                          **
   100-
      -                            *
      -                             ***
    50-
      -                                **
      -
      -                                  *  *
      -                                    *
      -                                   *
      -                                      *
    10*                                       *
      -
      -
     5-                                        *****
      -
      -
      -                                             ** * ***
      -
      -
      -                                               * *      **    *
     0---------------------------------------------------------------------
      |   |  |  |   ||     |    | |   |  |  |   ||     |    | |      |
SCORE 0   | 19  |  38|    57    |76   | 95  | 114|   133    152    171
STDEV     0     1    2     3    4     5     6    7     8    9

                             PARAMETERS

Similarity matrix       Unitary    K-tuple                   4
Mismatch penalty              1    Joining penalty          30
Gap penalty                1.00    Window size              32
Gap size penalty           0.33
Cutoff score                  2
Randomization group           0

Initial scores to save       45    Alignments to save       15
Optimized scores to save      0    Display context          10

                             SEARCH STATISTICS

Scores:                 Mean      Median     Standard Deviation
                         18         14          14.81

Times:                 CPU                   Total Elapsed
                   00:04:06.02               00:04:07.00

Number of residues:             24347505
Number of sequences searched:      57621
Number of scores above cutoff:      4562

Cut-off raised to 11.
```

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Cut-off raised to 17.
Cut-off raised to 26.
Cut-off raised to 31.
Cut-off raised to 36.
Cut-off raised to 41.
Cut-off raised to 45.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                      Init. Opt.
Sequence Name    Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
                   **** 10 standard deviations above mean ****
  1. Q23092       Antigen tc-7a gene.              543   171   244  10.33   0
  2. Q51731       Plasmid pCisEBON for subcloni  10596   170   454  10.26   0
                   ****  9 standard deviations above mean ****
  3. Q14184       N.clavipes dragline silk prot   1995   157   449   9.39   0
  4. N92629       DNA fragment containing acyB    2729   153   457   9.12   0
                   ****  8 standard deviations above mean ****
  5. Q29269       Human calcium channel 27980/1   6232   144   442   8.51   0
  6. Q37817       Sequence encoding the alpha 1   7362   143   442   8.44   0
  7. Q54631       Human oncogene bcl-2 coding s   5086   141   321   8.31   0
  8. N81292       Sequence of bcl-2 cDNA corres   5105   140   320   8.24   0
  9. Q05884       Plasmid clone 409.2.             633   137   238   8.03   0
 10. Q05883       Plasmid clone pUC-SK1.          6767   137   381   8.03   0
                   ****  7 standard deviations above mean ****
 11. Q03842       LFA-1 alpha subunit gene        5139   134   378   7.83   0
 12. Q10388       Encodes skin-specific murine    1912   132   431   7.70   0
 13. Q20541       Mouse retinoic acid receptor    2740   132   417   7.70   0
 14. Q14498       Clone 1 for truncated poly Ig   1876   130   263   7.56   0
 15. Q05272       Sequence encoding secreted GP   2183   126   368   7.29   0
 16. Q62199       Human platelet GPIIIa surface   3170   126   429   7.29   0
 17. N80476       Human Vpre-B gene.               503   124   229   7.16   0
 18. N80470       Gastric inhibitory polypeptid    524   124   237   7.16   0
 19. Q05686       Islets of Langerhans cell clo   3243   122   412   7.02   0
 20. Q31188       Alpha 6A integrin subunit cDN   5629   122   184   7.02   0
                   ****  6 standard deviations above mean ****
 21. Q56906       DNA encoding a glycosyltransf   2043   121   436   6.95   0
 22. Q13330       Glycosyltransferase gene in c   2043   121   436   6.95   0
 23. N91779       Sequence encoding mouse lamin   9520   121   278   6.95   0
 24. Q04735       Gene fragment encoding human    1226   120   232   6.89   0
 25. N91772       Human androgen receptor cDNA.   3569   120   446   6.89   0
 26. Q54431       Barley lectin cDNA clone BLc3    972   119   345   6.82   0
 27. Q27764       Adrenodoxin reductase gene (p   5089   118   440   6.75   0
 28. Q67602       Retinoblastoma protein Ap10.    4868   116   407   6.62   0
 29. Q51557       Loricrin gene.                  6530   116   449   6.62   0
 30. Q40969       Rabbit skeletal muscle ADP-ri   1140   115   442   6.55   0
 31. Q25975       MH mutant porcine ryanodine r  15377   115   439   6.55   0
 32. N71006       Sequence encoding the N-termi   1365   113   343   6.41   0
 33. N71008       Sequence encoding fusion prot   1389   113   367   6.41   0
 34. Q13674       E2A.E12 transcript.             3518   113   292   6.41   0
 35. Q04549       Type I interferon receptor co   3888   113   441   6.41   0
 36. Q47380       Sequence which corresp. to L-  12752   113   429   6.41   0
 37. N71005       Sequence encoding the N-termi    959   112   366   6.35   0
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   38. N60426       Sequence encoding bovine inhi   1182   112   318    6.35   0
   39. Q04081       Vector pASPcg-SV(10)            2720   111   440    6.28   0
   40. N90338       Sequence of human muscular dy  12923   111   393    6.28   0
   41. Q54841       Sequence encoding inner nucle   6306   110   450    6.21   0
   42. Q20733       pAD-CMV1 expression vector.     6414   109   441    6.14   0
   43. Q50991       Human prohibitin gene.          1020   108   284    6.08   0
   44. Q25264       C.glutamicum-derived temp-sen   2958   108   428    6.08   0
   45. Q53993       Myotonic dystrophy (DM) gene    3407   108   457    6.08   0


1. US-08-162-407-5' (1-988)
   Q23092       Antigen tc-7a gene.

 ID    Q23092 standard; DNA; 543 BP.
 AC    Q23092;
 DT    17-AUG-1992  (first entry)
 DE    Antigen tc-7a gene.
 KW    Oocysts; MAb 12-07; sporozoite; ss.
 OS    Eimeria tenella.
 PN    WO9204460-A.
 PD    19-MAR-1992.
 PF    05-SEP-1991; U06430.
 PR    12-SEP-1990; US-581693.
 PA    (GENE-) GENEX CORP.
 PI    Jacobson JW, Strausberg RL, Wilson SD, Pope SH, Strausberg SL;
 PI    Ruff MD, Augustine PC, Danforth HD;
 DR    WPI; 92-114365/14.
 DR    P-PSDB; R22392.
 PT    Vaccine against avian coccidiosis - comprising recombinant
 PT    Eimeria antigen ac-1b or ac-6b gene, or microorganisms expressing
 PT    them
 PS    Claim 5; Page 39 + Fig 5; 56pp; English.
 CC    To identify antigens of E. tenella, expression libraries were
 CC    prepd. in lambda vector, lambda gt11, using cDNA prepd. from polyA
 CC    mRNA isolated from E. tenella oocysts.  The cDNA expression
 CC    library was screened with monoclonal antibody (MAb) 12-07 which was
 CC    raised against the sporozoite stage of E. tenella.  The library
 CC    to be screened was plated on a host that allows lysis and plaque
 CC    formation.  During induction of the antigens encoded by the phage,
 CC    the plaques were identified by screening the filters with Mab 12-07.
 CC    The cDNA inserts from the MAb 12-07 positive phage were cloned into
 CC    bacteriophage M13 and subjected to sequence analysis.  Following
 CC    sequence analysis, E. tenella antigen tc-7a was identified.
 SQ    Sequence   543 BP;    229 A;    135 C;    161 G;    18 T;

Initial Score     =    171  Optimized Score  =    244  Significance = 10.33
Residue Identity =    49%  Matches          =    285  Mismatches   =   232
Gaps              =     54  Conservative Substitutions            =     0

      140     X 150       160       170       180       190       200
    TCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATGGGATGATAGATGTCTG-T
               | ||           | |    || |  |      | | ||   || || ||| |   |
              AGAGAAGAAGACAAAAGAGAAGAAGAAGACAAAAGAGAAGAA---GAAGA-AGAAGAAAGAG
              X       10        20        30        40            50

     210       220       230       240        250       260          270
    CTCACTGCGTTGTTTAAGGCTCCGCAGGATGAGGCCTTG-GCCAGGTCAGTGCTCCA-CA--AGCAGCAGGT
       |  | |  |   |||       || |  ||     | | |||  |  |||  || ||  ||||||||
    AAGAGAGAGGAGAAGAAGAAGAAAAAGAAGAAGAAAGAGCGGCAGCAC-CTGCAGCAGCAACAGCAGCAGCA
    60        70        80        90       100        110       120
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     280       290         300         310       320       330       340
  CCTGGGGACTGGGGACGG--GGGGCACCTGCTCC--CCAGGGCGGGGTGTCCTCCGCCGCGTCCTCTGCCAG
  ||||  | | |   || |  |  ||| | ||  |  | |  ||   |   |  | ||  |  |  ||||
  CCTGCAG-CAG-CAACAGCAGCAGCAACAGCAGCTGCAACAGC--AGCAGCTACAGCAACACCAGCTGCAGC
130         140       150       160       170         180       190

       350         360         370       380       390       400       410
  TGCAGGCACCAG--GCAGCGG--CCAGCAGCAGGAGGCCCACGGGCAGCAGCAGTAGGAGGAGCAGAGGGGG
  |||| |||||||  ||||| |  ||||| |||| ||   ||   |||||| ||| ||  | |||||     |
  TGCA-GCACCAGCTGCAGCAGCACCAGCTGCAGCAG---CAGCAGCAGCAACAGGAGCTGCAGCAGCACCAG
  200        210       220       230          240       250       260

          420       430       440       450       460       470        480
  CTGC-GGGGCTGTCGGGGCTGTGGCCTCCAGGGGCCGGGGACTCCATGGGGGTGGCAGGGTTGA-GGAGTCG
  |||| | | | | ||  || | |  |  |||| || |      | | ||  | || ||     |  ||  |
  CTGCAGCGACAGCCGCAGCAG-GAGCAGCAGGAGCAG------CAAAGGCAGCGGAAGCACGAACAGAAACC
    270       280        290       300             310       320       330

         490       500       510       520       530        540
  GGCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATCCAG-GGCTTCAGC-GC--CACCAG
  |   ||  | ||||   || ||| | | || ||     ||||     | ||  ||  |||| ||  || |||
  GAAGGA-GCAGCAGGAGCA-GCAGCAGAAGCAGAGAAAGCGAAAACACAAGCAGCAACAGCAGCAACAACAG
          340        350       360       370       380       390       400

 550          560       570        580       590       600        610
  CTGCT-CGG--AGGTCTCCTGCAGGAGGCGGGAG-ATGTTGGTCTGGACGAAGCGAAGACAGC-TGGGGGGG
  | ||| | |  ||  |  | |||| |  | | || | ||  | ||||  ||   | || |||| |     |
  CAGCTGCAGCAAGAGCAGCAGCAGCA-TCAGCAGCAGGTAAGCCTGGGGGACATGCAG-CAGCATCAACAGC
         410       420        430       440       450        460       470

    620       630       640       650       660        670       680
  GGCTGAAAGGCACATTTGGTGACAAAGTGTATCTCCGTGTTCACGC-GCTCCAGCAAGCCTTGCATC-TTGG
   ||  ||| |||     |  || |||| |         |   |||| ||  |||||      |||||  ||
  AGC--AAAAGCAGCGCAG--GAAAAAGCGGCGAAAGCAGCAAACGCAGCAACAGCAGCAACAGCATCAAAGG
           480         490       500       510       520       530

    690       700
  ACCCAGCGACAGTCT
  |   |
  AATAA
 540  X


2. US-08-162-407-5' (1-988)
   Q51731       Plasmid pCisEBON for subcloning huHGF variants.

 ID    Q51731 standard; DNA; 10596 BP.
 AC    Q51731;
 DT    31-MAY-1994  (first entry)
 DE    Plasmid pCisEBON for subcloning huHGF variants.
 KW    Hepatocyte Growth Factor; HGF; variant; mutein; in vitro mutagenesis;
 KW    proteolysis resistant; liver; malignancy; CMV-driven;
 KW    Cytomegalovirus; episomal expression plasmid; ss.
 OS    Synthetic.
 FH    Key             Location/Qualifiers
 FT    enhancer        1..611
 FT    /*tag=  a
 FT    /note= "CMV enhancer/promoter"
 FT    promoter        758..775
FT   /*tag=  b
FT   /label= SP6_promoter
FT   misc_feature    845..849
FT   /*tag=  c
FT   /note= "SP6 RNA start"
FT   misc_feature    902..966
FT   /*tag=  d
FT   /function= cloning_linker
FT   polyA_signal    967..1107
FT   /*tag=  e
FT   /note= "SV40 poly A"
FT   misc_feature    1108..1531
FT   /*tag=  f
FT   /function= SV40_origin
FT   misc_feature    1580..4189
FT   /*tag=  g
FT   /label= EBNA-1
FT   misc_feature    4190..6374
FT   /*tag=  h
FT   /function= oriP
FT   repeat_region   4295..4887
FT   /*tag=  i
FT   /note= "family of repeats"
FT   misc_structure  5866..5978
FT   /*tag=  j
FT   /note= "dyad region"
FT   terminator      6375..6457
FT   /*tag=  k
FT   /label= HSV_TK_terminator_3'-end
FT   CDS             6975..7975
FT   /*tag=  l
FT   /phenotype= neomycin_resistance
FT   /note= "Tn5 neomycin phosphotransferase gene"
FT   promoter        7975..8112
FT   /*tag=  m
FT   /label= TK_promoter
FT   misc_feature    8114..8594
FT   /*tag=  n
FT   /function= M13_ori
FT   misc_RNA        8595..10414
FT   /*tag=  o
FT   /label= delta_2a
PN   WO9323541-A.
PD   25-NOV-1993.
PF   17-MAY-1993; U04648.
PR   18-MAY-1992; US-884811.
PR   18-MAY-1992; US-885971.
PA   (GETH ) GENENTECH INC.
PI   Godowski PJ,  Lokker NA,  Mark MR;
DR   WPI; 93-386573/48.
PT   Hepatocyte growth factor variants - are resistant to proteolytic
PT   cleavage into its two-chain form, used to treat malignancies
PT   associated with HGF receptor
PS   Example 1; Fig 6; 87pp; English.
CC   Plasmid pCisEBON (a pRK5 derivative) is an episomal CMV driven
CC   expression plasmid. HuHGF variants with enhanced receptor binding
CC   activity were produced by site-directed mutagenesis. Stable
CC   populations of preferred HGF variants were obtained by transfecting
CC   human embryonic kidney 293 cells and then these were subcloned in
CC   pCisEBON. See R52940-R52949 for examples of pref. HGF variants.
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 SQ   Sequence   10596 BP;    2625 A;    2571 C;    3024 G;    2376 T;

Initial Score     =    170  Optimized Score    =    454  Significance = 10.26
Residue Identity  =    50%  Matches            =    529  Mismatches   =   418
Gaps              =    105  Conservative Substitutions                 =     0

              X       10           20        30        40        50
              CGGGGGCTTTG---TTCAGAGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTG-CCTC
              ||| |||  ||    ||| ||  | |    ||    |  ||   ||    || |  |    |
    CAGAAGGCTCCGGCGGCAGTGGACCTCAAAGAAGAGGGGGTGATAACCATGGACGAGGACGGGGAAGAGGAC
          2040      2050      2060      2070      2080      2090      2100

    60        70          80        90           100       110       120
    CATTCTGGGGAGG-GAATGA-GAGGGGCCCAAGGAAG----GGACCGGCCTCTAGCCAACTTCCTCTGTGTC
     |    | ||||| | | ||  ||| ||||  ||  |     ||| | |    | || ||      |  |||||
    GAGGACGAGGAGGCGGAAGACCAGGAGCCCCGGGCGGCTCAGGATCAGGGCCAAGACATAGAGAT-GGTGTC
        2110      2120      2130      2140      2150      2160       2170

       130       140       150       160       170       180        190
    CAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATG-GGATGA
    | |   | ||  ||     |     | |  | | ||  || |  ||   ||  |  || || | | | | ||
    CGG---AGAC-CCCAAAAACGTCCAAGTTGCAT-TGGCTG-CAAAGGGACCCACGGTGGAACAGGAGCAGGA
          2180       2190      2200        2210      2220      2230

       200       210       220          230         240       250         260
    -TAGATGTCTGTCTCACTGCGTTGTTTAAGGCTC---CGCAGGATGA-GGCCTTGGCCAGG-TCAG-TGCTC
      ||  |   |     |   |  |    |||  |    ||||||| || || |  |  ||||   ||  ||
    GCAGGAGCGGGAGGGGC--AGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGAGGGGCAG
 2240      2250        2260      2270      2280      2290      2300

           270         280           290       300       310       320
    CACAAGCAGCAGGTCCTG--GGGACTGG----GGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCG
     |   |||| |||  | | ||| | ||    ||| | ||||||   |     ||| | || | | |    |
    GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAG-----CAG-GAGGAGGGGCAGGAG
 2310      2320      2330      2340      2350           2360       2370

     330       340       350       360       370          380       390
    CCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGCCC---ACGGGCAGCAGCAGTAG
      ||        ||  | ||||| |  |||  || |  ||||| |||||| |   | |||||| ||||| ||
    GGGCAGGAGGGGCAGGAGCAGG-AGGAGG-GGCAG-GAGCAGGAGGAGGGGCAGGAGGGGCAGGAGCAGGAG
     2380      2390       2400        2410      2420      2430      2440

      400        410       420        430       440        450         460
    GAGGAGCA-GAGGGGGCTGCGGGGCTGTCG-GGGCTGTGGCCTCCAGGGGCCGG-GGA-CTCCATG-GGGGT
    |||| ||| ||||||   | ||||| |  |  ||  | ||    |||| || || |||    || | ||||
    GAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGG--GGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      2450      2460      2470      2480        2490      2500      2510

           470          480        490       500       510       520
    GGCAG--GGTTGAGG---AGTCGGG-CTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATC
     | ||  ||  ||||   ||  ||| | |     ||||   ||||    |||  | |  | || | |  |
    AGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
      2520      2530      2540      2550      2560      2570      2580

   530       540       550       560       570       580       590       600
    CAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGA
      ||||   || | ||  || |   |  || |    |||||||| |||   | |  || | ||| |    |
    AGGGGCAGGAGGGGCAGGAGCAG---GAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGG
    2590      2600         2610      2620      2630      2640      2650
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           610         620           630       640       650       660
    AGACAGCTGGGG-GGGGGC-TGAAAGGCA----CATTTGGTGACAAAGTGTATCTCCGTGTTCACGCGCTCC
    || |||  ||||  || ||  ||  ||||    ||   || | ||  | | |     |     | | ||
    AG-CAGGAGGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGG-GGCA-GGAGCAGGAGGGGCAGGAGGGGCAGG
      2660      2670      2680      2690        2700      2710      2720

     670       680        690         700       710       720       730
    AGCAAGCCTTGCATCTTGGAC-CCAGC--GACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGA---CC
    |||| |    |||    || |   |||  ||  | |  |||  ||   | |  | |  | | |||||    |
    AGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGC
      2730      2740      2750      2760      2770      2780      2790

         740       750        760       770       780           790
    AGCCGCCAGAGGCCCCCGCA-GAGCTCCTCGTCCTGCAGGTTGGAGGCCACGGTGA----CTGGGTAATCTT
    ||  ||  ||||     ||| |||   |  |  | | |||  | |||  | ||  |    | ||     |
    AGGAGCAGGAGG-AGGGGCAGGAGGGGCAGGAGCAGGAGG-GGCAGG--AGGGGCAGGAGCAGGAGGGGCAG
    2800       2810      2820      2830       2840        2850      2860

  800       810         820       830        840       850       860
    GAAGCAGGTAG--TCAGACAGCTCACGGATTTTGACA-GCGAAGTCGGAGGAGATGGGGCTGTGTTGGAAGG
    || |  || ||   |||   |  || |||    | || | | ||  ||||| |  || || |    || |||
    GAGG--GGCAGGAGCAGGAGGGGCA-GGA--GGGGCAGGAGCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGG
        2870      2880       2890        2900      2910      2920      2930

   870       880       890       900       910       920        930
    AGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGA-TAGGTTGTTGGGCTCCAG
    |||||     ||   | | | ||  ||||    ||||  |  || || |  ||  |||| | |||   || |
    AGCAGGAGGTGGAGGC-CGGGGT--CGAG-GAGGCAGTGGAGGCCGGGGTCGAGGAGGTAG-TGGAGGCCGG
         2940       2950         2960      2970      2980       2990

  940       950       960           970        980       X
    GCTGGCGCCAGCACTGTCATTTCGGCCGGG----GGCCCCGGAA-TTCCGGCCG
    | | | |   | | ||  |   || | |||    || |  | ||   || |  |
    GGTCGAGGAGGTAGTG-GAGGCCGCCGGGGTAGAGGACGTGAAAGAGCCAGGGGGGGAAGTCGT
  3000      3010       3020      3030      3040      3050      3060
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3. US-08-162-407-5' (1-988)
   Q14184       N.clavipes dragline silk protein-2 coding sequence

 ID   Q14184 standard; DNA; 1995 BP.
 AC   Q14184;
 DT   15-JAN-1992  (first entry)
 DE   N.clavipes dragline silk protein-2 coding sequence.
 KW   protein superfibre; major ampullate silk; orb web spider; ss.
 OS   Nephilia clavipes.
 FH   Key             Location/Qualifiers
 FT   CDS             1..1788
 FT   /*tag=  a
 FT   /product= silk protein-2
 PN   EP-452925-A.
 PD   23-OCT-1991.
 PF   18-APR-1991; 106217.
 PR   20-APR-1990; US-511792.
 PA   (UYWY-) UNIV OF WYOMING.
 PI   Lewis RV, Xu M, Hinman M;
 DR   WPI; 91-312199/43.
 DR   P-PSDB; R14309.
 PT   DNA encoding spider silk protein-1 and 2 and variants - isolated
 PT   from Nephila clavipes, for prodn. of spider silk protein and
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 PT   fibres having desired characteristics
 PS   Claim 5; Page 30; 48pp; English.
 CC   A N.clavipes major ampullate gland cDNA library was screened with
 CC   a degenerate probe based on the pentapeptide GYGPG. The largest
 CC   positive clone (p6B) was subcloned and sequenced. Plasmid pMB2 is
 CC   a pBluescriptSK+ plasmid with a spider silk 2 insert 173 bp
 CC   shorter than in p6B. E.coli SURE cells containing plasmid pMB2 were
 CC   deposited as ATCC 68568.
 CC   See also Q14183 and Q14185.
 SQ   Sequence   1995 BP;    563 A;    518 C;    586 G;    328 T;

Initial Score     =    157  Optimized Score   =    449  Significance =  9.39
Residue Identity  =    51%  Matches           =    544  Mismatches   =   387
Gaps              =    133  Conservative Substitutions            =     0

              X         10           20        30        40        50
              CGGGGGC--TTTG-TTCAG--AGTTGGGTAAATGGGGCCGGTGCTGGATTCTGGCGTTGCCT
              |  || |  | ||   |||  |||   | |   |  ||||  || |||  ||||     |
    ACCAGGACAACAAGGACCATCTGGAGCAGGCAGTGCAGCAGCAGCAGCCGCAGCAGGA-CCTGG----ACAA
     900       910       920       930       940       950            960

     60        70        80        90         100       110       120
    CCATTCTGGGGAGGGAATGAGAGGGGCCCAAGGAAGGGACCG--GCCTCTAGCCAACTTCCTCTGTGTCCAG
    | |   |  |||||  ||| ||   |  |||  ||||  | |  |  | | | | |   |  |   ||||||
    CAAGGATTAGGAGGTTATG-GACCAGGACAA-CAAGGTCCAGGAGGATATGGACCAGGACAACAAGGTCCAG
        970       980        990       1000      1010      1020      1030

    130       140       150       160       170       180        190
    GCTATACATCCTCTGGCTGGTGACTCCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTA-AAATGGATGATAG
    |    | ||   |  | | |||  ||  |       ||| |||   |    |||| | ||   |||  |  |
    G-AGGATATGGACCAGGTAGTGCATCTGCAGCAGCAGCCGCAG---CAGGACCTGGACAACAAGGACCA-GG
        1040      1050      1060      1070         1080      1090       1100

   200       210       220       230       240        250         260
    ATGTCTGTCTCACTGCGTTGTTTAAGGCTCCGCAGGATGAGGCCTTG-GCCAG-GTCAG-TGCTCCACAAGC
    | |  | |    ||  |      ||||  |  | |||  ||||  ||   | |   |||  ||  ||   ||
    A-GGATATGGACCT--GGACAACAAGGACCATCTGGACCAGGCAGTGCATCTGCAGCAGCAGCCGCAGCCGC
           1110        1120      1130      1140      1150      1160

    270       280       290       300       310       320          330
    AGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCC--GCC-GC---GTC
    |||||| || || |  |  ||||  ||   ||  | |  |||||   || | | | ||  | |  |   | |
    AGCAGGACCAGGAGGATATGGACCAGGACAACAAGGT--CCAGG--AGGATATGCACCAGGACAACAAGGAC
 1170      1180      1190      1200        1210        1220      1230

           340        350         360         370       380          390
    C-TCTG--CCAGTGCAG-GCACCAG--GCAGCGGC--CAGCAGCAGGAGGCCCACGGGCA---GCAGCAG--
    | ||||  |||| |||| ||| | |  ||||| ||  |||| |||| ||| ||| | | |   | | |||
    CATCTGGACCAG-GCAGTGCATCTGCAGCAGCAGCCGCAGCCGCAGCAGGACCAGGAGGATATGGACCAGGA
   1240       1250      1260      1270      1280      1290      1300

          400          410       420         430       440         450
    -TAGGAGGAGCA-GAGG--GGGCTGCGGGGCTGTCGGGGC--TGTGGCCTCCAGG--GGCCGGGGACTCCAT
      |  |||  || ||||    ||  | || |     || |  | |||   |||||  |  | |   |  ||
    CAACAAGGTCCAGGAGGATATGCACCAGGACAACAAGGACCATCTGG--ACCAGGCAGTGCAGCAGCAGCA-
  1310      1320      1330      1340      1350        1360      1370

     460       470       480       490       500        510        520
    GGGGGTGGCAGGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAG-GCACCGGGAGAAGTTCTGG-CGAGTGA
    |  | || ||  ||  ||||  | ||  || | || |   |||| ||| | || ||   ||||| |  |  |
   GCAGCTGCCA--GTGCAGGA-CCTGGTGGATA-TGGA---CCAGCGCAACAGG-GACCATCTGGTCCTGGAA
  1380        1390       1400       1410         1420       1430      1440

     530       540       550         560           570       580       590
   TC-CAGGGCTTCAGCGCCACCAGCTG--CTCGGAGGT----CTCCTGCAGGAGGCGGGAGATGTTGGTCTGG
   || ||  ||||||||  |  |||| |  |  ||||||      || |||  |   ||   |  | | | |||
   TCGCA--GCTTCAGCTGCTTCAGCAGGACCTGGAGGTTATGGACCAGCACAACAAGGACCAGCTGGATATGG
          1450      1460      1470      1480      1490      1500      1510

            600          610        620       630       640       650
   AC---GAAGCGAAG--ACAG-CTGGGGGGGGGC-TGAAAGGCACATTTGGTGACAAAGTGTATCTCCGTGTT
    |   |||||| ||   ||| ||  |  || ||  ||   |||  ||  | | | | ||   ||||    ||
   GCCTGGAAGCGCAGTAGCAGCCTCTGCCGGTGCAGGATCTGCAGGTTATG-GGCCAGGT---TCTCAAGCTT
        1520      1530      1540      1550      1560          1570

     660         670       680       690       700       710       720
   CACGC-GCTCCAGCAAGCCTTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCA
   | ||| ||  |  |  | || || |||     ||||   ||| |   ||  | | ||| |||  ||||  |
   C-CGCTGCAGCTTCTCGTCTGGCTTCT-----CCAGATTCAGGCGCTAG-AGTTGCAT-CAG--CTGTTTCT
1580       1590      1600          1610      1620      1630           1640

   730       740       750       760        770        780       790
   GGACCAGCCGCCAGAGGCCCCCGCAGAGCTCCT-CGTCCTGCAG-GTTGGAGGCCACGGTGACTGGGTAATC
         |   |||| |||||    ||  || || | |  |  || |||    |  ||| ||  ||  | |
   AACTTGGTATCCAGTGGCCCAACTAGCTCTGCTGCCTTATCAAGTGTTATCAGTAACGCTG--TGTCTCAAA
        1650      1660      1670       1680     1690      1700        1710

   800       810       820            830       840       850          860
   TTGAAGCAGGTAGT-CAGACAGCTCACG----GATTTTGACAGCGAAG-TCGGAGGAGAT-GGGGCTG-TGT
   |||  ||| ||| | | |    |||  |    ||| |   ||   ||| ||   ||| || |   ||| |
   TTGGCGCAAGTAATCCTGGTCTCTCTGGTTGCGATGTCCTCATTCAAGCTCTCTGGAAATCGTTTCTGCTTG
        1720      1730      1740      1750      1760      1770      1780

         870       880       890            900        910       920
   TGGAAGGAGCAGTCCTGGGTCC--CACTGAGTCCCG--AGCTCAGCAGCAGC--AGCAGGAGGAGATAGGTT
   || ||  | |  | ||   |||  || || |||  |  |  |  | ||| ||    |||   |    | |||
   TGTAACCATCCTTTCTTCATCCAGCATTG-GTCAAGTTAATTATGGAGCGGCTTCTCAGTTCG-CCCAAGTT
      1790      1800      1810       1820      1830      1840       1850

   930       940       950        960       970       980            X
   GTTGGGCTCCAGGCTG--GCGCCAGCACTGTCATTTCGGCCGGGGGCCCCGGAAT-TCC--GGCCG
   || ||   |||  |||    |   ||| | | |||   |             ||| | |  ||
   GTCGG---CCAATCTGTTTTGAGTGCATTTTAATT---GAAAAATTTATTAAAATATGCATGGATTTTCTAG
         1860      1870      1880         1890      1900      1910  X

   CCTG
1920
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4. US-08-162-407-5'  (1-988)
   N92629       DNA fragment containing acyB gene.

 ID    N92629 standard; DNA; 2729 BP.
 AC    N92629;
 DT    15-MAY-1990  (first entry)
 DE    DNA fragment containing acyB gene.
 KW    Macrolide; antibiotics; Streptomyces; acylation; ds.
 OS    Streptomyces sp.
 PN    EP-345546-A.
 PD    13-DEC-1989.
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  PF    24-MAY-1989; 109425.
  PR    24-MAY-1988; JP-125091.
  PR    03-MAR-1989; JP-050120.
  PA    (SAOC) Sanraku Inc.
  PI    Arisawa A, Kawamura N, Kojima I, Okumura Y, Okamura K, Tone H,
  PI    Okamoto R;
  DR    WPI; 89-365353/50
  PT    DNA coding for enzyme acylating 4"-position of macrolide antibiotics -
  PT    contg. acyB gene and derived from Streptomyces microorganism.
  PS    Claim 7; Page 28-33; 54pp; English.
  CC    DNA fragment contains two open reading frames, one upstream, one down-
  CC    stream, coding for acyB1 and acyB2 genes respectively.
  SQ    Sequence   2729 BP;   475 A;   891 C;   962 G;   401 T;

Initial Score    =    153  Optimized Score    =    457  Significance =  9.12
Residue Identity =    51%  Matches            =    551  Mismatches   =   373
Gaps             =    137  Conservative Substitutions                =     0
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          X       10         20        30         40            50
          CGGGGGCTTTGTTCA-GAGTTGGGTAAATGGGGCCGGTGCTG----GATTCTGGCGTTGCCT
          | |  ||   | |||   |   ||| ||  | ||||| |  |    | ||| |||   ||
CCGAGGCGAGCAGCAGC-GCGATCACCGGGACGGTCAA-CGCGCCGGGGTCGTAGTGGTTC-GGCACCGCGA
    400   X   410        420       430         440       450       460

 60        70         80        90        100       110       120
CCAT-TCTGGGGAGGGAA-TGAGAGGGGCCCAAGGAAGG-GACCGGCCTCTAGCCAACTTCCTCTGTGTCCA
 | |  | | | |      |||||   || | | | |||  |  || | |  |||  | |||   ||  ||
ACGTCACCGCGAACACCGCTGAGAACAGCGCGACGCAGGCCAGGGGACGCGGGCC--CCTCCAGCGT-CCCC
     470       480       490       500       510         520        530

 130       140         150       160       170          180        190
GGCTATACATCCTCTGG--CTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCC---CTGTAAAATG-GGA
|| |   ||   |||||  |  | |  ||||      |  |  ||| | || | |   | | || |||  ||
GGAT---CACGATCTGGGCCATGAGCATCCCGAGCACGAACTCCAGCAGCCGCACCGGCGGGAACATGTAGA
         540       550       560       570       580       590       600

     200       210        220       230       240       250       260
TGATAGATGTCTGTCTCA-CTGCGTTGTTTAAGGCTCCGCAGGATGAGGCCTTGGCCAGGTCAGTGCTCCAC
|||   |   |   | || |||||   | |  || |||   ||  | |||   || | || | |     ||
TGA---ACCACCACCGCAGCTGCGGCATGTCCGGGTCCCACGGCAGGGGC---GGGCTGGCCGG-----CAG
          610       620       630       640          650            660

    270       280       290       300       310       320       330
AAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCGCCGCGTCCT
 |||||   | || ||||  ||| ||||| || |||  |  | ||  ||||    | || |||||    |
CAGCAGTGCGACCAGGGGGATGGAGACGGCGGCCAC--GGACACCGCGGCG----GCCCACCGCCAGAGC--
      670       680       690         700       710           720

  340       350         360       370       380          390        400
CTGCCAGTGCAGGCACCAG-GCAG-CGGCCAGCAGCAGGAGGCCCACGG-GCAGCAG--CAG-TAGGAGGAG
| | | || | | |    | | ||  ||| |  || |   ||  || || | || ||  ||| | | |||||
CGGTCCGTACGGACCTTGGTGAAGAAGGCGAAGAGGAACGGGAACATGGCGTAGAAGAACAGCTCGCAGGAG
  730       740       750       760       770       780       790

       410       420       430       440        450         460
-CAGAGGGGGCTGCGGGGCTGTCGGGGCTGTGGCCTCCAGG-GGCCGGGGACTCCATG--GGGGT-GGCAG-
   ||    ||  | ||| |   |  || ||   |||  || || ||||||  |||||   || |  ||||
AGCGACCACGCCACCGGGTTCATGCTGCCGT--ACTCGTGGTGGTCGGGGA-ACCATGCCTGGATCAGCAGC
800       810       820         830       840        850       860
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     470          480       490       500       510       520       530
    -GGT---TGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATCCAGGGCT
     |||   |||| |||| | |  |||| | | |    ||| |  |  |   |  | | | |  | |  |  |
    AGGTTCGTGAGCAGTCCGTCCCACACCG-ATC----GGCCCATGTTGGGCTCGTTGAGGGCCAGCACGATCA
     870       880       890            900       910       920       930

      540       550         560        570       580       590       600
    TCAGCGCCACCAGCTGCTCGG--AGGTCTCCTGC-AGGAGGCGGGAGATGTTGGTCTGGACGAAGCGAAG-A
     ||||| ||||||| || |||  |||  | | || || | ||| | ||   ||  |  | ||    ||||
    GCAGCGTCACCAGCAGCACGGGCAGG--TGCAGCGAGTACGCGCG-GACCGTGCGC-CGCCG-CCAGAAGTT
        940       950         960       970        980        990       1000

        610           620       630       640       650       660
    CAGCTGGG----GGGGGGCTGAAAGGCACATTTGGTGACAAAGTGTATCTCCGTGTTCACG--CG----CTC
    || || ||    |  |||| ||   || ||  ||  ||| ||     |   | ||   | |  ||    |
    CACCTTGGACTTGTCGGGCAGACCCGCCCAGGTGAGGACGAAACCGCTGAGCATGAAGAAGAACGAGACCGT
          1010      1020      1030      1040      1050      1060      1070

      670       680       690       700       710         720         730
    CAGCAAGCCTTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCA--GCGCTGTGCCAG--GACCA
    ||||  |||  ||   ||     |||||  |  ||  || |||   ||  |          |  |  || |
    CAGCGGGCCCAGCCGGTT-----CAGCGGGA-ACTGCAG-CGCGGAATTGATCTCGGTGTTCTTGAAGAACG
        1080      1090            1100       1110      1120      1130

           740       750       760       770           780        790
    GCCG---CCAGAGGCCCCCGCAGAGCTCCTCGTCCTGCAG-GTTG-GAGGC--CACGGTGA-CTGGGTA--A
    || |   | | |       |  ||  | |  ||   || | | ||  | ||  | ||  || |  || |  |
    GCTGTGTCGATATATGGGAGGTGA-ATACCAGTAGAGCGGAGATGAAACGCATCCCGCCGAGCGCGGGAAGA
   1140      1150      1160       1170      1180      1190      1200

      800       810          820       830       840       850       860
    TCTTGAAGCAGGTAGTCA---GACAGCTCACGGATTTTGACAGCGAAGTCGGAGGAGATGGGGCTGTGTTGG
    | ||   |||||  | ||   |  | ||| |||     ||| |    || |||| ||||  | ||  |  |
    TGTTTCGGCAGG--GGCATGGGTGACCTCGCGG---CGGACGGGTGGGTGGGAGCAGAT--GTCTAAG--GC
  1210      1220        1230         1240      1250      1260          1270

       870        880       890       900       910        920       930
    AAGGAGCAGTC-CTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAG-GAGATAGGTTGTTGGGC
    |  | || | | | |||   ||  | ||  |   |  || ||    ||| |  | | || ||  || || |
    ACCGCGCGGCCGCCGGG---CAAGGCGTATCTGACAAAG-AGTGTGAGCCGCCGCGCGACAG--TGGTGTGT
         1280         1290      1300       1310      1320        1330

         940         950        960         970       980         X
    TCC--AGGCTG-GCG-CCAGC-ACTGTCATTTCG--GCCGGGGGCCCCGGAATT--CCGGCCG
    |||    ||||  || || || || ||  |||||   ||||| | | |||| ||   |  |||
    TCCCACCGCTGCACGGCCGGCGACGGTGGTTTCGTCACCGGGCGACGCGGATTTAATCATCCGGAAACACGG
   1340      1350      1360      1370      1380      1390      1400

    A
 1410

5. US-08-162-407-5' (1-988)
   Q29269       Human calcium channel 27980/11.

 ID   Q29269 standard; DNA; 6232 BP.
 AC   Q29269;
 DT   03-MAR-1993  (first entry)
 DE   Human calcium channel 27980/11.
 KW   Plasmid pR14-5.3.3.1; Ca-flux assay; ss.
```

```
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   polyA_signal    6215..6220
FT   /*tag=  a
FT   repeat_unit     1..252
FT   /*tag=  b
FT   /standard_name= Alu_repeat
FT   /note= "possible cloning artefact"
FT   CDS                 253..6048
FT   /*tag=  c
FT   /note= "amino acids 358 to C-terminus
FT   i.e. Domains II to IV"
FT   misc_difference 3746
FT   /*tag=  d
FT   /note= "undefined"
PN   EP-507170-A.
PD   07-OCT-1992.
PF   23-MAR-1992; 104970.
PR   04-APR-1991; DE-110785.
PA   (FARB ) BAYER AG.
PI   Franz J, Rae P, Unterbeck A, Weingaertner B;
DR   WPI; 92-333446/41.
DR   P-PSDB; R27649.
PT   Cloned human neuronal calcium channel sub-types - useful in
PT   calcium flux assays to screen for neurone-specific calcium
PT   channel ligands
PS   Claim 2; Page 63-77; 101pp; German.
CC   Human neuroblastoma cell line, hippocampus, frontal and temporal
CC   cortex and visual cortex cDNA banks were screened with a probe
CC   containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
CC   pR14-5.3.3.1 overlaps with clone p1247-14.1.1.1 (see Q29263). The
CC   following differences are observed between the two sequences
CC   (nucleotide and position in pR14-5.3.3.1 given in brackets):
CC   1.Cytosine at position 520 (T: 3507); no change in deduced amino
CC   acid sequence. 2.Cytosine at position 775 (G; 3768); no change in
CC   deduced AA sequence. 3.Cytosine at position 1617 (T;4611).
CC   4.Adenosine at position 2360 (G; 5353). 5.deletion of 6 nucleotides
CC   at position 708 (CGGAAA; 3695-3700). 6. deletion of an Adenosine
CC   residue at position 1013 which leads to a stop codon at position
CC   1028-1030. 7. at position 3240 there are a further 2199 nucleotides
CC   of the 3'UTR which are absent from pR14-5.3.3.1. (The deletion of
CC   Adenosine at position 1013 is thought to be a cloning artefact).
CC   The sequence can be inserted into a eukaryotic expression vector for
CC   use in transforming suitable host cells. Cell lines producing human
CC   neuronal calcium channel proteins can be used for screening for Ca
CC   channel ligands (agonists or antagonists). See also Q29259-Q29275.
SQ   Sequence   6232 BP;    1250 A;    1914 C;    1827 G;    1240 T;
SQ   1 Others;

Initial Score     =    144  Optimized Score   =    442  Significance =  8.51
Residue Identity  =    49%  Matches           =    518  Mismatches   =   423
Gaps              =    104  Conservative Substitutions              =     0

              X       10        20          30        40          50
              CGGGGGCTTTGTTCAGAGTTGG--GTAAATGGGGCCGGTGCTG-GATTCTGGCGTTGCCTCC
                |||||  |    ||   |||  ||  |  |  | | ||| | |  |    ||  |   ||
    AGAGATCCCTGTGGGGCGGTCAGGAGCACTGGCTGTGGA-CGTTCAGATGCAGAGCATAACCCGGAGGGGCC
          4920      4930      4940       4950      4960      4970      4980

   60        70        80         90          100        110       120
   ATTCTGGGGAGGGAATGAGAGGGGCCCA-AGGAAGG---GACCGGCCTCTA-GCCAACTTCCTCTGTGTCC-
    |  |||||||     |   |||    | ||  |||   || ||||||| | |||  |  ||| || | ||
   CTGATGGGGAGCCCCAGCCTGGGCTGGAGAGCCAGGGTCGAGCGGCCTCCATGCC--CCGCCT-TGCGGCCG
        4990      5000      5010      5020      5030        5040       5050

     130       140       150       160       170       180       190
   AGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATGGGATGATA
   || ||   || ||  |  | | || |  |||  ||     |||  | ||| | |  |   |  ||
   AGACT---CAGCCCGTCACAGATGCCAGCCCCATGAAGCGCTCCATCTCCACGCTGGCCCAGCGG------C
               5060      5070      5080      5090      5100      5110

   200       210        220       230        240       250         260
   GATGTCTGTCTCACTGCGTTG-TTTAAGGCTCCGCA-GGATGAGGCCTTGGCCAG--GTCAGTGCTCCACAA
      ||  | ||||   | |||    |   | ||| |  |   |  || | |||||  |||   || |||| |
   CCCGTGGGACTCA--TCTTTGCAGCACCACCCCGGACCGCCCACCCCCTAGCCAGGCGTCGTCGCACCACCA
         5120        5130      5140      5150      5160      5170      5180

     270          280       290       300       310       320       330
   GCAGCA--GGT-CCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCGCCGCGTCC
    || ||  | | ||   |     ||||| ||  |||   | ||||  | |  ||| | |  | |||  |||
   CCACCACCGCTGCCACCGCCGCAGGGACAGGAAGCA-GAGGTCCCTGGAGAAGGG-GCC--CAGCC-TGTCT
         5190      5200      5210       5220      5230       5240         5250

         340         350       360       370         380        390       400
   TCTGCCAGTGCAG--GCACCAGGCAGCGGCCAGCAGCAGGAG--GCCCACGGG-CAGCAGCAGTAGGAGGAG
    | |  |  |  |  |||||| |||| |    |  || || |  |||| ||||  ||  ||  ||   |  |
   GCCGATATGGATGGCGCACCAAGCAGTGCTGTGGGGCCGGGGCTGCCCCCGGGAGAGGGGC-CTACAGGCTG
            5260      5270      5280      5290      5300      5310       5320

            410        420       430          440       450       460
   CAGAGGGGGCTGCG-GGGCTGTCGGGGCTGTGGCC--TC-CAGGGGCCGGGGACTCCATGGGGGTGGCAGGG
   | |  |||   | | | || | | ||   | ||||  || |||| || | ||   || |     |  |
   CCGGCGGGAACGAGAGCGCCGGCAGGAGCGGGGCCGGTCCCAGGAGCGGAGGCAGCCCTCATCCT-CCTCCT
           5330      5340      5350      5360      5370      5380       5390

 470       480       490       500       510         520       530
   TTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGT--TCTGGCGAGTGATCCAGGGCT---T
     ||| ||  | |||   ||| | ||  |  ||   ||| |  ||   |   |||  |  | ||  ||   |
   CGGAGAAGCAGCGCTTCTACTCCTGCGAC-CGCTTTGGGGGCCGTGAGCCCCCGA-AGCCCAAGCCCTCCCT
          5400      5410      5420       5430      5440       5450      5460

    540         550       560         570       580       590       600
   CAGC-GCCA-CCAGCTGCTCGGAGGTCTCCTG--CAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGAAGAC
   |||| |||| ||| |  | |  |   |  |||  |||||| |||||         | ||  | || |    |
   CAGCAGCCACCCAACGTCGCCAA---CAGCTGGCCAGGAGCCGGGACCCCACCCACAGG--GCAGTGGTTCC
          5470      5480         5490      5500      5510        5520

       610       620        630          640       650         660
   -AGCTGGGGGGGGGCTGAAAGGC-ACATTTGGTG---ACAAAGTGTATCTCCGTGTTC--ACGC-GCTCCAG
     |   ||| |   ||    | | |||| |||||    ||        | | |||  |  | || |||||
   GTGAATGGGAGCCCCTTGCTGTCAACATCTGGTGCTAGCACCCCCGGCCGCGGTGGGCGGAGGCAGCTCCCC
5530      5540      5550      5560      5570      5580      5590      5600

    670        680       690       700       710       720       730
   C--AAGCC-TTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGAC-CAGCC
   |  | |||  ||  ||   | ||||||  ||      || ||  | |  |  | |    |||   | | |
   CAGACGCCCCTGACTCCCCGCCCCAGCATCACCTACAAGACGGCCAACTCCTCACCCATCCACTTCGCCGGG
           5610      5620      5630      5640      5650      5660      5670

     740         750       760       770       780        790        800
```

```
GC-CAGA--GGCCCCCGCAGAGCTCCTCGTCCTGCAGGTTGGAGGCCACGG-TGACTGGGTA-ATCTTGAAG
|| ||||   ||| || | |  || |||  |  || || |  || |   || |  | |   | | |     |
GCTCAGACCAGCCTCC-CTG-CCTTCTCCCCAGGCCGGCT-CAGCCGTGGGCTTTCCGAACACAACGCCCTG
   5680       5690       5700      5710       5720      5730      5740

    810        820         830       840       850         860       870
CAGGTAGTCAGA-CAGCTCA--CGGATTTTGACAGCGAAGTCGGAGGAGATGGGGCTG--TGTTGGAAGGAG
|  | ||  ||| |  ||||  | |    || |  |   | |    ||  |||  |||    ||    || |
C-TGCAGAGAGACCCCCTCAGCCAGCCCCTGGC--CCCTGGCTCTCGAATTGGCTCTGACCCTTACCTGGGG
     5750      5760      5770        5780      5790      5800      5810

        880       890       900       910       920       930       940
CAG-TCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGATAGGTTGTTGGGCTCCAGGC
|||   ||||    || |||| ||   |  ||    | ||   ||||   | |   || | | |    ||||
CAGCGTCTGG---ACAGTGAGGCCTCTGTCCACGCCCTGCCTGAGGACACGCTCACTT-TCGAG---GAGGC
     5820         5830      5840      5850      5860       5870

      950       960       970       980       X
TGGCGCCAGCACTGTCATTTCGGCCGGGGGCCCCGGAATTCCGGCCG
||  |||| ||     | |  |||||     || ||| ||||  |
TGTGGCCACCA-----ACTCGGGCCGCTCCTCCAGGACTTCCTACGTGTCCTCCCTG
5880           5890      5900      5910      5920
```

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6. US-08-162-407-5' (1-988)
   Q37817          Sequence encoding the alpha 1B-1 human calcium cha

 ID   Q37817 standard; cDNA; 7362 BP.
 AC   Q37817;
 DT   30-JUN-1993  (first entry)
 DE   Sequence encoding the alpha 1B-1 human calcium channel subunit.
 KW   Human calcium channel subunit; diagnosis; agonist; antagonist;
 KW   Lambert Eaton syndrome; ss.
 OS   Homo sapiens.
 FH   Key                Location/Qualifiers
 FT   CDS                144..7163
 FT   /*tag=  a
 PN   WO9304083-A.
 PD   04-MAR-1993.
 PF   14-AUG-1992; U06903.
 PR   15-AUG-1991; US-745206.
 PR   10-APR-1992; US-868354.
 PA   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
 PI   Brenner R,  Ellis SB,  Feldman DH,  Harpold MM,  Mccue AF,
 PI   Williams ME;
 DR   WPI; 93-093936/11.
 DR   P-PSDB; R33549.
 PT   DNA encoding specific human calcium channel sub-units - used for
 PT   identifying calcium channel agonists and antagonists and
 PT   diagnosing Lambert Eaton syndrome
 PS   Disclosure; Page 111-120; 150pp; English.
 CC   DNA encoding the alpha 1B subunit was isolated by screening a
 CC   human basal ganglia cDNA library with  fragments of the rabbit
 CC   skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
 CC   A portion of one of the positive clones was used to screen an IMR32
 CC   cell cDNA library. Clones that hybridized to the basal ganglia
 CC   DNA prove were used to further screen an IMR32 cell cDNA library
 CC   to identify overlapping clones that in turn were used to screen a
 CC   human hippocampus cDNA library. In this way, a sufficient series of
 CC   clones to span nearly the entire length of the nucleotide sequence
CC   encoding the human alpha 1B subunit was obtained. PCR amplification
CC   of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC   additonal segments of the alpha 1B coding sequence. A full-length
CC   alpha 1B DNA clone was constructed by ligating portions of the
CC   partial cDNA clones (see Q37817, Q37818). Alpha 1B-1 and alpha
CC   1B-2 are derived by alternative splicing of the alpha 1B subunit
CC   transcript.
SQ   Sequence   7362 BP;    1446 A;    2276 C;    2214 G;    1426 T;

Initial Score     =    143  Optimized Score  =    442  Significance =  8.44
Residue Identity =    49%  Matches          =    518  Mismatches   =   423
Gaps              =    104  Conservative Substitutions              =     0

            X       10        20          30        40         50
            CGGGGGCTTTGTTCAGAGTTGG--GTAAATGGGGCCGGTGCTG-GATTCTGGCGTTGCCTCC
              |||||  |    ||   |||  ||  |  |  | | ||| | |  |    ||  |   ||
  AGAGATCCCTGTGGGGCGGTCAGGAGCACTGGCTGTGGA-CGTTCAGATGCAGAGCATAACCCGGAGGGGCC
   6030      6040      6050      6060       6070      6080      6090

 60        70        80         90          100        110       120
  ATTCTGGGAGGGGAATGAGAGGGGCCCA-AGGAAGG---GACCGGCCTCTA-GCCAACTTCCTCTGTGTCC-
   |  |||||||     |   |||    | ||  |||   || ||||||| | |||  |  ||| || | ||
  CTGATGGGGAGCCCCAGCCTGGGCTGGAGAGCCAGGGTCGAGCGGCCTCCATGCC--CCGCCT-TGCGGCCG
  6100      6110      6120      6130      6140      6150         6160

    130       140       150       160       170       180       190
  AGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGTATCCTCCCCTGTAAAATGGGATGATA
  || ||   || ||  |  | | || |  |||  ||     |||  | ||| | |  |   |  ||
  AGACT---CAGCCCGTCACAGATGCCAGCCCCATGAAGCGCTCCATCTCCACGCTGGCCCAGCGG------C
   6170         6180      6190      6200      6210      6220

  200       210        220       230        240       250         260
  GATGTCTGTCTCACTGCGTTG-TTTAAGGCTCCGCA-GGATGAGGCCTTGGCCAG--GTCAGTGCTCCACAA
     ||  | ||||   | |||    |   | ||| |  |   |  || | |||||  |||   || |||| |
  CCCGTGGGACTCA--TCTTTGCAGCACCACCCCGGACCGCCCACCCCCTAGCCAGGCGTCGTCGCACCACCA
6230      6240        6250      6260      6270      6280      6290

    270          280       290       300       310       320       330
  GCAGCA--GGT-CCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTCCGCCGCGTCC
   || ||  | | ||   |     ||||| ||  |||   | ||||  | |  ||| | |  | |||  |||
  CCACCACCGCTGCCACCGCCGCAGGGACAGGAAGCA-GAGGTCCCTGGAGAAGGG-GCC--CAGCC-TGTCT
6300      6310      6320      6330       6340      6350         6360

     340         350       360       370         380        390       400
  TCTGCCAGTGCAG--GCACCAGGCAGCGGCCAGCAGCAGGAG--GCCCACGGG-CAGCAGCAGTAGGAGGAG
   | |  |  |  |  |||||| |||| |    |  || || |  |||| ||||  ||  ||  ||   |  |
  GCCGATATGGATGGCGCACCAAGCAGTGCTGTGGGGCCGGGGCTGCCCCCGGGAGAGGGGC-CTACAGGCTG
   6370      6380      6390      6400      6410      6420       6430

        410        420       430          440       450       460
  CAGAGGGGGCTGCG-GGGCTGTCGGGGCTGTGGCC--TC-CAGGGGCCGGGGACTCCATGGGGGTGGCAGGG
  | |  |||   | | | || | | ||   | ||||  || |||| || | ||   || |     |  |
  CCGGCGGGAACGAGAGCGCCGGCAGGAGCGGGGCCGGTCCCAGGAGCGGAGGCAGCCCTCATCCT-CCTCCT
  6440      6450      6460      6470      6480      6490      6500

470       480       490       500       510         520       530
  TTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGT--TCTGGCGAGTGATCCAGGGCT---T
    ||| ||  | |||   ||| | ||  |  ||   ||| |  ||   |   |||  |  | ||  ||   |
  CGGAGAAGCAGCGCTTCTACTCCTGCGAC-CGCTTTGGGGGCCGTGAGCCCCCGA-AGCCCAAGCCCTCCCT
 6510      6520      6530       6540      6550      6560       6570
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   540           550       560         570       580       590       600
  CAGC-GCCA-CCAGCTGCTCGGAGGTCTCCTG--CAGGAGGCGGGAGATGTTGGTCTGGACGAAGCGAAGAC
  |||| |||| ||| |  | |  |   |  |||  |||||| |||||         | ||  | || |    |
  CAGCAGCCACCCAACGTCGCCAA---CAGCTGGCCAGGAGCCGGGACCCCACCCACAGG--GCAGTGGTTCC
 6580      6590      6600         6610      6620      6630        6640

      610       620        630          640       650         660
  -AGCTGGGGGGGGGCTGAAAGGC-ACATTTGGTG---ACAAAGTGTATCTCCGTGTTC--ACGC-GCTCCAG
    |   ||| |   ||    | | |||| |||||    ||        | | |||  |  | || |||||
  GTGAATGGGAGCCCCTTGCTGTCAACATCTGGTGCTAGCACCCCCGGCCGCGGTGGGCGGAGGCAGCTCCCC
    6650      6660      6670      6680      6690      6700      6710

   670        680       690       700       710       720       730
  C--AAGCC-TTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGAC-CAGCC
  |  | |||  ||  ||   | ||||||  ||      || ||  | |  |  | |    |||   | | |
  CAGACGCCCCTGACTCCCCGCCCCAGCATCACCTACAAGACGGCCAACTCCTCACCCATCCACTTCGCCGGG
  6720      6730      6740      6750      6760      6770      6780

    740         750       760       770       780        790        800
  GC-CAGA--GGCCCCCGCAGAGCTCCTCGTCCTGCAGGTTGGAGGCCACGG-TGACTGGGTA-ATCTTGAAG
  || ||||   ||| || | |  || |||  |  || || |  || |   || |  | |   | | |     |
  GCTCAGACCAGCCTCC-CTG-CCTTCTCCCCAGGCCGGCT-CAGCCGTGGGCTTTCCGAACACAACGCCCTG
6790      6800        6810      6820       6830      6840      6850

      810        820         830       840       850         860       870
  CAGGTAGTCAGA-CAGCTCA--CGGATTTTGACAGCGAAGTCGGAGGAGATGGGGCTG--TGTTGGAAGGAG
  |  | ||  ||| |  ||||  | |    || |  |   | |    ||  |||  |||    ||    || |
  C-TGCAGAGAGACCCCCTCAGCCAGCCCCTGGC--CCCTGGCTCTCGAATTGGCTCTGACCCTTACCTGGGG
  6860      6870      6880        6890      6900      6910      6920

          880       890       900       910       920       930       940
  CAG-TCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGATAGGTTGTTGGGCTCCAGGC
  |||   ||||    || |||| ||   |  ||    | ||   ||||   | |   || | | |    ||||
  CAGCGTCTGG---ACAGTGAGGCCTCTGTCCACGCCCTGCCTGAGGACACGCTCACTT-TCGAG---GAGGC
  6930         6940      6950      6960      6970      6980          6990

        950       960       970       980       X
  TGGCGCCAGCACTGTCATTTCGGCCGGGGGCCCCGGAATTCCGGCCG
  ||  |||| ||     | |  |||||     || ||| ||||  |
  TGTGGCCACCA-----ACTCGGGCCGCTCCTCCAGGACTTCCTACGTGTCCTCCCTG
       7000           7010      7020      7030  X   7040


7. US-08-162-407-5' (1-988)
   Q54631        Human oncogene bcl-2 coding sequence.

ID   Q54631 standard; cDNA to mRNA; 5086 BP.
AC   Q54631;
DT   23-JUN-1994  (first entry)
DE   Human oncogene bcl-2 coding sequence.
KW   Cell death; senescence; programmed cell death; ced-9; myocardial
KW   infarction; stroke; brain injury; neurodegenerative disease;
KW   muscular degenerative disease; ageing; hypoxia; ischaemia; toxaemia;
KW   infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
KW   oncogene; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1459..2178
FT   /*tag=  a
FT   /product= Bcl-2.
PN   WO9325683-A.
PD   23-DEC-1993.
PF   14-JUN-1993; U05651.
PR   12-JUN-1992; US-898933.
PR   10-AUG-1992; US-927681.
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PI   Hengartner M,  Horvitz HR;
DR   WPI; 94-007540/01.
DR   P-PSDB; R47344.
PT   Caenorhaboitis elegans cell death-protective gene - used to
PT   develop agents for preventing cell death or for reducing
PT   population of cells
PS   Disclosure; Page 61-64; 112pp; English.
CC   The protein product of the human oncogene bcl-2 was found to have a
CC   similar sequence to the ced-9 protein.  ced-9 is essential for
CC   C. elegans development and apparently functions by protecting cells
CC   during development from programmed cell death.  ced-9 was shown to
CC   function by antagonising the activities of cell death genes ced-3
CC   and ced-4.  The ced-9 gene can be used for developing agents for
CC   treating a condtion characterised by increased cell death such as
CC   myocardial infarction, stroke, traumatic brain injury,
CC   neurodegenerative disease, muscular degenerative disease, ageing,
CC   hypoxia, ischaemia, toxaemia, infection or hair loss.  It can also
CC   be used for reducing a population of cells in the treatment of
CC   neoplastic growth cancerous tissue, infected cells or autoreactive
CC   immune cells.
SQ   Sequence   5086 BP;    1262 A;    1222 C;    1288 G;    1314 T;

Initial Score    =    141  Optimized Score  =    321  Significance =  8.31
Residue Identity =    47%  Matches          =    381  Mismatches   =   327
Gaps             =     88  Conservative Substitutions            =     0

230       240       250       260       270       280        290       300
  GCAGGATGAGGCCTTGGCCAGGTCAGTGCTCCACAAGCAGCAGGTCCTGGGGACTG-GGGACGGGGGGCACC
            ||    ||| |  |    |||| |  || ||  | ||    | | |  |  |    | |  |
            GC----GCCCGCCC----CTCCGC--GCCGCCTGCCCGCCCGCCCGCCGCGCTCCCGCCCGC
            X           10              20        30        40        50

         310       320         330       340       350       360       370
  TGCTCCCCAGGGCGGGGTGTC-CT-CCGCCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCA
   |||| ||  |||   |  || || |||||||  || ||||||| | |||  || ||  ||  || |   |
  CGCTCTCCGTGGCCCCGCCTCGCTGCCGCCGCCGCCGCTGCCAGCGAAGGTGCCGGG--GC-TCCGGGCCCT
        60        70        80        90       100         110        120

         380       390       400       410       420       430       440
  GGAGGCCCACGGGCAGCAGCAGTAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGGGGCTGTGGCCTCCAGGG
      |||  ||| |  ||||  |    |||||  |  | || |  |||  ||| ||   | |||  ||   |
  CCCTGCCGGCGGCCGTCAGCGCT---CGGAGCGAACTGCGC-GACGGGAGGTCCGG---GAGGCGACCGTAG
        130       140          150        160       170          180

       450       460       470       480       490       500       510
  GCCGGGGACTCCATGGGGGTGGCAGGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGT
   |  | | | ||  |  ||   || ||  ||||||   || || | | ||  |   ||||   | | |  |
  TC--GCGCCGCCGCGCAGG-ACCA-GGAGGAGGAGAAAGGGTG-CGCAGC--CCGGAGGCGGGGTGCGCCGG
     190       200         210       220        230         240       250

     520         530       540       550         560          570
  TCTGGCG-AG-TGATCCAGGGCTTCAGCGCCACCAGCTGCTCGGAG--GTC-TCC--TGCAGG--AGGCGGG
  |  || | ||  ||    ||| | ||| |     | ||  ||| ||  ||| |||  |  |||  | | |||
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  TGGGGTGCAGCGGAAGAGGGGGTCCAGGGGGGAGAACT--TCGTAGCAGTCATCCTTTTTAGGAAAAGAGGG
        260       270       280         290       300       310       320

     580       590         600       610       620       630       640
  ---AGATGTTGGTCTGGACGA--AGCGAAGACAGCTGGGGGGGGGCTGAAAGGCACATTTGGTGACAAAGTG
     | ||      ||   | |  | |     |  |         || | |   ||||    | |      |
  AAAAAATAAAACCCTCCCCCACCACCTCCTTCTCCCCACCCCTCGCCGCA--CCACACACAGCGCGGGCTTC
        330       340       350       360       370         380       390

     650       660        670        680       690       700
  TATCTCCGTGTTCACGCGCTCCA-GCAAG-CCTTGCATCTTGGACCCAGCGACAGTCTTGA----GCCGCT-
  || | |   |  |  |||  ||| ||  | |||  | || |  | |||||  |  |   ||    ||   |
  TAGCGCTCGGCACCGGCGGGCCAGGCGCGTCCTGCCTTCATTTATCCAGCAGCTTTTCGGAAAATGCATTTG
        400       410       420       430       440       450       460

710       720         730         740       750       760       770
  CCATCCAGCGCTGTGCCAG--GACCA--GCCGCCAGAGGCCCCCGCAGAGCTCCTCGTCCTGCAGGTTGGAG
  |  | | | |    |||  ||| |   | |||   | |||| ||     || ||||||  ||  |
  CTGTTCGGAGTTTAATCAGAAGACGATTCCTGCCTCCGTCCCCGGC-TCCTTCATCGTCC--CATCTCCCCT
      470       480       490       500        510       520         530

  780       790       800           810       820       830        840
  GCCACGGTGACTGGGTAATCTTGAAGCAG----GTAGTCAGACAGCTCACGGATTTTGACAGCG-AAGT---
  | | |  |  ||||| |  | |||||| |    || |  ||| |  |||  |  | || | |||   ||
  GTCTCTCT-CCTGGGGAGGCGTGAAGCGGTCCCGTGGATAGAGA-TTCA-TGCCTGTGTCCGCGCGTGTGTG
         540        550       560       570         580       590       600

         850       860       870       880       890       900       910
  CG-GAGGAGATGGGGCTGTGTTGGAAGGAGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGCAGCAGCA-G
  || | | |    || | |  ||    | ||   | ||    |   || | |||  || |  |     |
  CGCGCGTATAAATTGCCGAGAAGGGGAAAACATCACAGGACTTCTGCGAATACCGGACTGAAAATTGTAATT
        610       620       630       640       650       660       670

        920       930       940       950         960       970
  CAGGAGGAGATAGGTTGTTGGGCTCCAGGCTGGCGCCAGCAC-TGTCAT-TTCGGCCGGGGGCCC--CGGA-
  ||   |  |    |  | |  ||   |      | | ||| | ||  || | |||  |||   ||  ||||
  CATCTGCCG--CCGCCGCT--GCCAAAAAAAAACTCGAGCTCTTGAGATCTCCGGTTGGGATTCCTGCGGAT
      680         690         700       710       720       730       740

     980       X
  ----ATTCCGGCCG
      ||| | |
  TGACATTTCTGTGAAGCAGAAGTC
        750    X  760


8. US-08-162-407-5'  (1-988)
   N81292         Sequence of bcl-2 cDNA corresp. to the 5.5 kb tran

ID   N81292 standard; cDNA; 5105 BP.
AC   N81292;
DT   17-DEC-1990  (first entry)
DE   Sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript encoding
DE   bcl-2-alpha
KW   B-cell neoplasm; diagnosis; follicular lymphomas; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1459..2178
FT   /*tag=  a
PN   EP-252685-A.
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PD   13-JAN-1988.
PF   02-JUL-1987; 305863.
PR   09-JUL-1986; US-883687.
PA   (WIST-) Wistar Corp.
PI   Tsujimoto Y, Croce CM;
DR   WPI; 88-008633/02.
DR   P-PSDB; P80987.
PT   Detection of B-cell neoplasms -
PT   by extn. of proteins or RNA from B-cells and quantitation using
PT   specific antibody or DNA probe
PS   Claim 8; Fig 2A-2D; 23pp; English.
CC   A human bcl-2 gene substantially free of introns is claimed. Also claimed
CC   is a substantially pure preparation of a protein having an N-terminal end
CC   encoded by the first exon of the human bcl-2 gene wherein said protein is
CC   bcl-2-alpha having about 239 (P80987) or 205 (P80988) AA residues. B-cell
CC   neoplasms which are associated with t(14;18) chromosome translocations
CC   cause an increase in the expression of both mRNA and the protein prods.
CC   of the bcl-2 gene. This is used to detect B-cell neoplasms including
CC   follicular lymphomas as well as other lymphomas. Bacterial isolates
CC   available as ATCC 67147 and 67148 can be used to express gene prods.
CC   alpha (n81292) and beta (n91293) resp. in bacteria.
SQ   Sequence   5105 BP;   1281 A;   1225 C;   1286 G;   1313 T;

Initial Score     =    140  Optimized Score    =    320  Significance =  8.24
Residue Identity  =    48%  Matches            =    386  Mismatches   =   312
Gaps              =     95  Conservative Substitutions              =     0

   230       240       250       260       270       280        290
  TCCGCAGGATGAGGCCTTGGCCAGGTCAGTGCTCCACAAGCAGCAGGTCCTGGGACT-GGGACGGGGGGC
            | | ||   |||   || | || |  |   | ||  | ||   |  ||   |  ||  |  |
            GCGCCC---GCC-CCTCCGCGC-CGCCTGCCCGCCCGCCCGCCGCGCTCCCGCCCGCCGCTC
            X           10         20         30         40         50

  300       310       320       330       340       350       360
  ACCTGCTCCCCAGGGCGGGGTGTCCTCCGCCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGC
   ||    ||||  | || | || || ||||||   || ||||||| | |||  || ||  ||  || |   |
  TCCGTGGCCCC--GCCGCGCTG-CCGCCGCCG---CCGCTGCCAGCGAAGGTGCCGGG--GC-TCCGGGCCC
   60          70         80           90       100         110        120

370       380       390       400       410       420       430       440
  AGGAGGCCCACGGGCAGCAGCAGTAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGGGGCTGTGGCCTCCAGG
       |||  ||| |  ||||  |    |||||  |  | || |  |||  ||| ||   | |||  ||
  TCCCTGCCGGCGGCCGTCAGCGCT---CGGAGCGAACTGCGC-GACGGGAGGTCCGG---GAGGCGACCGTA
         130       140          150        160       170          180

        450       460       470       480       490       500       510
  GGCCGGGGACTCCATGGGGGTGGCAGGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAG
  | |  | | | ||  |  ||   || ||  ||||||   || || | | ||  |   ||||   | | |  |
  GTC--GCGCCGCCGCGCAGG-ACCA-GGAGGAGGAGAAAGGGTG-CGCAGC--CCGGAGGCGGGGTGCGCCG
      190       200         210       220        230         240       250

      520         530       540       550         560          570
  TTCTGGCG-AG-TGATCCAGGGCTTCAGCGCCACCAGCTGCTCGGAG--GTC-TCC--TGCAGG--AGGCGG
   |  || | ||  ||    ||| | ||| |     | ||  ||| ||  ||| |||  |  |||  | | ||
  GTGGGGTGCAGCGGAAGAGGGGGTCCAGGGGGGAGAACT--TCGTAGCAGTCATCCTTTTTAGGAAAAGAGG
         260       270       280         290       300       310       320

      580       590         600       610       620       630       640
  G---AGATGTTGGTCTGGACGA--AGCGAAGACAGCTGGGGGGGGCTGAAAGGCACATTTGGTGACAAAGT
  |   | ||      ||   | | | |     |  |         || | |   ||||    | |      |
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  GAAAAAATAAAACCCTCCCCCACCACCTCCTTCTCCCCACCCCTCGCCGCA--CCACACACAGCGCGGGCTT
         330       340       350       360       370         380       390

      650       660        670        680       690       700
  GTATCTCCGTGTTCACGCGCTCCA-GCAAG-CCTTGCATCTTGGACCCAGCGACAGTCTTGA----GCCGCT
   || | |   |  |  |||  ||| ||  | |||  | || |  | |||||  |  |   ||    ||   |
  CTAGCGCTCGGCACCGGCGGGCCAGGCGCGTCCTGCCTTCATTTATCCAGCAGCTTTTCGGAAAATGCATTT
         400       410       420       430       440       450       460

 710       720         730         740       750       760       770
  -CCATCCAGCGCTGTGCCAG--GACCA--GCCGCCAGAGGCCCCCGCAGAGCTCCTCGTCCTGCAGGTTGGA
   |  | | | |    |||  ||| |   | |||   | |||| ||     || ||||||  ||  |
  GCTGTTCGGAGTTTAATCAGAAGACGATTCCTGCCTCCGTCCCCGGC-TCCTTCATCGTCC--CATCTCCCC
       470       480       490       500        510       520         530

   780       790       800           810       820       830       840
  GGCCACGGTGACTGGGTAATCTTGAAGCAG----GTAGTCAGACAGCTCACGGATTTTGACAGCGAAGTCGG
   | | |  |  ||||| |  | |||||| |    || |  ||| |  |||  |  | || | |||    ||
  TGTCTCTCT-CCTGGGGAGGCGTGAAGCGGTCCCGTGGATAGAGA-TTCA-TGCCTGTGTCCGCG----CG-
        540        550       560       570         580       590

      850       860       870        880        890       900       910
  AGGAGATGGGGCTGTGTTGGAAGGAGCAGTCCTGGGTCCCAC-TGAGTCCCGAGCTCAGCAGCAGCAGCAGG
    | |   | || || |   ||   || |    |||    || | |  |  ||  || || | |  | | |
  -TGTGTGCGCGC-GTAT---AAATTGCCGAGAAGGGGAAAACATCA--CAGGACTTCTGC-GAA-TACCGGA
      600        610           620       630         640        650

     920       930         940       950       960         970
  AGGAGATAGGTTGTTGGGCTCCAG--GCTGGCGCCAGCACTGTCATTTCG-GC-CGGGGG----CCC--CGG
    || |   ||  ||   || | |  || |  ||||  |     |  ||| || |  | |    |||   ||
  CTGAAAATTGTAATTCATCTGCCGCCGCCGCTGCCA--AAAAAAAACTCGAGCTCTTGAGATCTCCCGTTGG
 660       670       680       690         700       710       720

  980       X
  AATTCCGGCCG
   ||||| || |
  GATTCCTGCGGATTGACATTT
 730       740


9. US-08-162-407-5' (1-988)
   Q05884       Plasmid clone 409.2.

   ID   Q05884 standard; DNA; 633 BP.
   AC   Q05884;
   DT   11-JAN-1991  (first entry)
   DE   Plasmid clone 409.2.
   KW   Basic fibroblast growth factor; tissue regeneration; infarction; ss.
   FH   Key             Location/Qualifiers
   FT   CDS             1..633
   FT   /*tag=  a
   FT   /label=basic fibroblast growth factor
   PN   FR2642086-A.
   PD   27-JUL-1990.
   PF   26-JAN-1989; 000973.
   PR   26-JAN-1989; FR-000973.
   PA   (SNFI ) SANOFI SA.
   PI   Caput D, Ferrara P, Kaghad M;
   DR   WPI; 90-277408/37.
   DR   P-PSDB; R07076.
 PT   New recombinant gene encoding basic fibroblast growth factor - in
 PT   new high mol. wt. form, useful e.g. for stimulating tissue
 PT   regenerating or treating infarction
 PS   Disclosure; fig 8; 43pp; French.
 CC   This recombinant gene encodes an extended basic fibroblast growth
 CC   factor (bFGF) of 210 amino acids.  It stimulates growth of meso-
 CC   dermal and neuroectodermal cells.  It is thus potentially useful
 CC   e.g. for regenerating damaged tissues, and for treating myocardial
 CC   infarctions, Parkinsons disease and Alzheimers disease.  It can be
 CC   produced on a large scale using recombinant DNA methods without
 CC   risk of contamination.  See also Q05883.
 SQ   Sequence   633 BP;    134 A;    172 C;    211 G;    116 T;

Initial Score    =    137  Optimized Score  =    238  Significance =  8.03
Residue Identity =    50%  Matches          =    286  Mismatches   =   206
Gaps             =     69  Conservative Substitutions          =     0

      460     X 470         480       490       500       510       520
    TGGGGGTGGCAGGGTTGA--GGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTG
              | || |||  |  |||| | |  | | || |  || ||   ||||||  | |  || |   |
              ATGGGTGACCGTGGTCGTGGTCGCGC-GCTG--CCGGG---CGGGAG--GCTGGGGGGCCGG
              X       10        20         30             40          50

      530       540        550       560       570       580        590
    ATCCAGGGCTTCAGCGCCAC-CAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGTTGG-TCTGGACGA
      || |||   | | ||| |  ||| | ||||||| |    || || | |||| || |  || ||    ||
    GGCCGGGG---CCGTGCCCCGGAGCGGGTCGGAGG-CCGGGGCCGGGGCCGGGGGACGGCGGCTCCCCGCGC
        60           70        80         90       100       110       120

      600       610       620       630       640       650         660
    AGCGAAGACAGCTGGGGGGGGGCTGAAAGGCACATTTGGTGACAAAGTGTATCTCCGTG-TTCA-CGCGCTC
     ||     | ||| ||||    | |   ||| |    || ||| | | | | |   | |  ||| | ||||
    GGCTCCAGCGGCTCGGGGATCCCGGCCGGGCCCCGCAGG-GACCATG-GCAGCCGGGAGCATCACCACGCT-
         130       140       150       160         170       180       190

      670       680       690       700       710       720       730
    CAGCAAGCCTTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCCAGGACC---AG
      ||  |||||||  |  |||    ||| |||    | |||  |||  || |  |  | | ||||||   ||
    --GCCCGCCTTGC-CCGAGGA--TGGCGGCAG--CGGCGCC-TTCCCGCCCGGCCACTTCAAGGACCCCAAG
            200          210         220        230       240       250

       740       750       760       770             780       790       800
    CCGCCAGAGGCCCCCGCAGAGCTCCTCGTCCTGCAGGT-----TGGA-GGCCACGGTGACTGGGTAATCTTG
    | ||   |   |      | |  | || ||||||   |       || ||||  | |||| ||||      |
    CGGCTGTACTGCAAAAACGGGGGCTTCTTCCTGCGCATCCACCCCGACGGCCGAGTTGACGGGGTCCGGGAG
      260       270       280       290       300       310       320

             810         820       830        840       850        860
    AAGCAGGTA--GTCAGA-C-AGCTCACGGATTTTGACAGC-GAAGTCGGAGGAGATGGGGCTGT-GTTGGAA
    ||| ||  |   ||| | | |||| ||  |  || | ||| ||||   |||||| || | || |    |||
    AAG-AGCGACCCTCACATCAAGCT-AC--AACTTCA-AGCAGAAGAGAGAGGAGTTGTGTCTATCAAAGGAG
    330        340       350           360       370       380       390

     870               880        890       900       910       920
    GGAG------CAGT--CCTGGGTCCCACTG-AGTCCCGAGCTCAGCAGCAGCAGCAGGAGGAGATA-GGTTG
     | |      | ||  ||||| |   |  | ||     || | | | |  ||  |   | | | || || ||
    TGTGTGCTAACCGTTACCTGGCTATGAAGGAAGATGGAAGATTA-CTG--GCTTCTAAATGTGTTACGGATG
       400       410       420       430        440         450       460

   930       940        950       960             970       980       X
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    TTGGGCTCCAGGCTG-GCGCCAGCACTGTCATTTCGGC------CGGGGGCCCCGGAATTCCGGCCG
       |  ||     ||  ||   | | | | ||  |  |          || |  |||| | |  | |
    AGTGTTTCTTTTTTGAACGATTGGAATCTAATAACTACAATACTTACCGGTCAAGGAAATACACCAGTTGGT
        470       480       490       500       510       520       530

    ATGTG
      540

10. US-08-162-407-5’  (1-988)
    Q05883        Plasmid clone pUC-SK1.

 ID   Q05883 standard; DNA; 6767 BP.
 AC   Q05883;
 DT   11-JAN-1991  (first entry)
 DE   Plasmid clone pUC-SK1.
 KW   Basic fibroblast growth factor; tissue regeneration; infarction; ss.
 FH   Key             Location/Qualifiers
 FT   CDS             302..934
 FT   /*tag=  a
 FT   /label=basic fibroblast growth factor
 PN   FR2642086-A.
 PD   27-JUL-1990.
 PF   26-JAN-1989; 000973.
 PR   26-JAN-1989; FR-000973.
 PA   (SNFI ) SANOFI SA.
 PI   Caput D, Ferrara P, Kaghad M;
 DR   WPI; 90-277408/37.
 DR   P-PSDB; R06685.
 PT   New recombinant gene encoding basic fibroblast growth factor - in
 PT   new high mol. wt. form, useful e.g. for stimulating tissue
 PT   regenerating or treating infarction
 PS   Disclosure; fig 3; 43pp; French.
 CC   This recombinant gene encodes a basic fibroblast growth factor (bFGF)
 CC   which stimulates growth of mesodermal and neuroectodermal cells.
 CC   It is thus potentially useful e.g. for regenerating damaged tissues,
 CC   and for treating myocardial infarctions, Parkinsons disease and
 CC   Alzheimers disease.  It can be produced on a large scale using rec-
 CC   ombinant DNA methods without risk of contamination.  There are a
 CC   further 3 potential initiation codons allowing expression of larger
 CC   forms of the protein.  See also Q05884.
 SQ   Sequence   6767 BP;    2047 A;    1201 C;    1334 G;    2185 T;

Initial Score    =    137  Optimized Score  =    381  Significance =  8.03
Residue Identity =    51%  Matches          =    442  Mismatches   =   338
Gaps             =     86  Conservative Substitutions          =     0

        170   X   180       190        200        210       220         230
    GCCTCAGTATCCTCCCCTGTAAAATGGGATGA-TAGATGTCTG-TCTCACTGCGTTGTTTAA--GGCTCCGC
              |  |||| | |||   |   || |||  | | |  | ||    |  |   ||  ||   |||
              CGGCCCCAGAAAACCCGAGCGAGTAGGGGGCGGCGCGCAGGAGGGAGGAGAACTGGGGGCGC
              X       10        20        30        40        50        60

          240       250        260       270       280       290       300
    AGGATGAGGCCTTGGCCAG-GTCAGTGCTCCACAAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTG
     |   |||||  |||   | ||| | | |  | | | || || |  ||  | |  ||  ||| |||  || |
    GG---GAGGC--TGGTGGGTGTCGGGGGTGGAGATGTAGAAGAT-GTGACGCCGCGGCCCGGCGGGTGCCAG
               70        80        90       100        110       120

         310       320       330       340        350         360       370
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  CTCCCAGGGCGGGGTGTCCTCCGCCGCGTCCTCTGCCAGTGC-AGGCA-CCAGGCA-GCGGCCAGCAGCAG
   |   | || | || || || | |  ||  |     || | ||   ||| |  || | |||||   |  |||
  ATTAGC-GGAC-GGCTGCCCGCGGTTGCAACGGGATCCCGGGCGCTGCAGCTTGGGAGGCGGCTCTCCCCAG
 130         140       150       160       170       180       190

        380        390       400       410       420       430       440
  GAGGCCCACGGGCAG-CAGCAGTAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGGGGCTGTGGCCTCCAGGG
  | |||   || | || || |  |  | | | |  |||     | | |||| | |||  |   |  | ||||||
  GCGGCGTCCGCGGAGACACCCATCCGTGAACCCCAGG----TCCCGGGCCGCCGGCTCGCCGCGCACCAGGG
 200       210       220       230           240       250       260

        450        460       470       480           490       500
  GCCGG-GGACTCCA-TGGGGGTGGCAGGGTTGAGGAGTCGG----GCTGACACTGCAGCTCCAGGCACCGGG
  ||||| ||||   |  | ||  |   || | ||||    ||    || | | | || || |   ||   | |
  GCCGGCGGACAGAAGAGCGGCCGAGCGGCTCGAGGCTGGGGACCGCGGGCGCGGCCGCGCTGCCGGGCG
   270       280       290       300       310       320       330

 510       520       530       540        550       560       570
  AGAAGTTCTGGCGAGTGATCCAGGGCTTCAGCGCCAC-CAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAG
   || | |  || |   |  || |||   | | ||| |  |  |||| | |||||| |    || || | |||| |
  GGAGGCTGGGGGCCGGGGCCGGGG---CCGTGCCCCGGAGCGGGTCGGAGG-CCGGGGCCGGGGCCGGGGG
 340       350       360          370       380        390       400

580        590       600       610       620       630       640       650
  ATGTTGG-TCTGGACGAAGCGAAGACAGCTGGGGGGGGCTGAAAGGCACATTTGGTGACAAAGTGTATCTC
  | |  || ||    ||  ||     | |||  ||||    |   ||| |    || |||| | | | | |
  ACGGCGGCTCCCCGCGCGGCTCCAGCGGCTCGGGGATCCCGGCCGGGCCCCGCAGG-GACCATG-GCAGCCG
   410       420       430       440       450       460         470

           660       670       680       690       700       710       720
  CGTG-TTCA-CGCGCTCCAGCAAGCCTTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGC
   | |  ||| | ||||   ||  |  |||||||  |  |||    ||| |||    | |||  |||  || |  |
  GGAGCATCACCACGCT---GCCCGCCTTGC-CCGAGGA--TGGCGGCAG--CGGCGCC-TTCCCGCCCGGCC
   480       490          500        510           520        530

         730          740       750       760       770            780
  TGTGCCAGGACC---AGCCGCCAGAGGCCCCCGCAGAGCTCCTCGTCCTGCAGGT-----TGGA-GGCCACG
    | | ||||||   ||| ||   |   |      | |  | || ||||||   |       || ||||  |
  ACTTCAAGGACCCCAAGCGGCTGTACTGCAAAAACGGGGGCTTCTTCCTGCGCATCCACCCCGACGGCCGAG
540       550       560       570       580       590       600       610

      790       800         810         820       830        840       850
  GTGACTGGGTAATCTTGAAGCAGGTA--GTCAGA-C-AGCTCACGGATTTTGACAGC-GAAGTCGGAGGAGA
   |||| ||||      |||| ||  |   ||| | | |||| ||  |  || | ||| |||| ||   ||||||
  TTGACGGGGTCCGGGAGAAG-AGCGACCCTCACATCAAGCT-AC--AACTTCA-AGCAGAAGAGAGAGGAGT
        620       630        640       650          660        670

          860       870              880        890       900       910
  TGGGGCTGT-GTTGGAAGGAG------CAGT--CCTGGGTCCCACTG-AGTCCCGAGCTCAGCAGCAGCAGC
  || | || |    |||  | |      | ||  ||||| |   |  | ||     || | | |  ||  |
  TGTGTCTATCAAAGGAGTGTGTGCTAACCGTTACCTGGCTATGAAGGAAGATGGAAGATTA-CTG--GCTTC
 680       690       700       710       720       730        740

       920        930       940        950       960             970
  AGGAGGAGATA-GGTTGTTGGGCTCCAGGCTG-GCGCCAGCACTGTCATTTCGGC------CGGGGGCCCCG
     | | | || || ||   |  ||     ||  ||   | | | | || |  |          || |  |
  TAAATGTGTTACGGATGAGTGTTTCTTTTTGAACGATTGGAATCTAATAACTACAATACTTACCGGTCAAG
  750       760       770       780       790       800       810

   980       X
       |
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  GAATTCCGGCCG
  ||| | |  | |
  GAAATACACCAGTTGGTATGTG
820       830       840

 11. US-08-162-407-5' (1-988)
     Q03842        LFA-1 alpha subunit gene

ID   Q03842 standard; DNA; 5139 BP.
AC   Q03842;
DT   23-AUG-1990  (first entry)
DE   LFA-1 alpha subunit gene
KW   Lymphocyte function associated antigen; inflammation; metastasis; ss.
FH   Key             Location/Qualifiers
FT   CDS             95..1095
FT   /*tag=  a
FT   /label=LFA-1 alpha subunit
FT   sig_peptide     95..67
FT   /*tag=  b
FT   misc_RNA        446..490
FT   /*tag=  c
FT   /label=tryptic peptide
FT   misc_RNA        770..803
FT   /*tag=  d
FT   /label=tryptic peptide
FT   misc_RNA        938..961
FT   /*tag=  e
FT   /label=tryptic peptide
FT   misc_RNA        1391..1417
FT   /*tag=  f
FT   /label=tryptic peptide
FT   misc_RNA        1655..1687
FT   /*tag=  g
FT   /label=tryptic peptide
FT   misc_RNA        1799..1840
FT   /*tag=  h
FT   /label=tryptic peptide
FT   misc_RNA        1862..1906
FT   /*tag=  i
FT   /label=tryptic peptide
FT   misc_RNA        2585..2626
FT   /*tag=  j
FT   /label=tryptic peptide
FT   misc_RNA        2963..3016
FT   /*tag=  k
FT   /label=tryptic peptide
FT   misc_feature    3512..3514
FT   /*tag=  l
FT   /label=serine phosphorylation site
FT   misc_feature    3527..3529
FT   /*tag=  m
FT   /label=serine phosphorylation site
FT   misc_feature    3581..3583
FT   /*tag=  n
FT   /label=serine phosphorylation site
FT   misc_feature    3587..3589
FT   /*tag=  o
FT   /label=serine phosphorylation site
FT   misc_RNA        3359..3445
FT   /*tag=  p
FT   /label=transmembrane domain
FT   polyA_signal    5107..5112
FT   /*tag=  q
FT   repeat_region   4623..4912
FT   /*tag=  r
FT   /label=Alu 1
FT   /note="tandem repeat"
FT   misc_feature    287..295
FT   /*tag=  s
FT   /label=N-glycosylation site
FT   misc_feature    359..367
FT   /*tag=  t
FT   /label=N-glycosylation site
FT   misc_feature    656..664
FT   /*tag=  u
FT   /label=N-glycosylation site
FT   misc_feature    2039..2047
FT   /*tag=  v
FT   /label=N-glycosylation site
FT   misc_feature    2102..2110
FT   /*tag=  w
FT   /label=N-glycosylation site
FT   misc_feature    2270..2278
FT   /*tag=  x
FT   /label=N-glycosylation site
FT   misc_feature    2282..2290
FT   /*tag=  y
FT   /label=N-glycosylation site
FT   misc_feature    2678..2686
FT   /*tag=  z
FT   /label=N-glycosylation site
FT   misc_feature    2747..2755
FT   /*tag=  aa
FT   /label=N-glycosylation site
FT   misc_feature    2783..2791
FT   /*tag=  bb
FT   /label=N-glycosylation site
FT   misc_feature    3272..3280
FT   /*tag=  cc
FT   /label=N-glycosylation site
FT   misc_feature    3305..3313
FT   /*tag=  dd
FT   /label=N-glycosylation site
FT   misc_RNA        170..3358
FT   /*tag=  ee
FT   /label=extracellular domain
PN   EP-362526-A.
PD   11-APR-1990.
PF   17-AUG-1989; 115160.
PR   09-MAR-1989; US-321017, US-235227.
PA   (DANA-) Dana Farber Cancer.
PI   Springer TA, Larson R;
DR   WPI; 90-108985/15.
DR   P-PSDB; R05782.
PT   Pure alpha subunit of lymphocyte function associated antigen -
PT   and encoding DNA sequences, useful eg for suppressing
PT   inflammation or metastasis
PS   Disclosure; fig 3; 27pp; English.
CC   This sequence encodes lymphocyte function associated antigen (LFA-1)
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CC   which suppresses inflammation, metastasis and growth of alpha subunit-
CC   expressing tumour cells and is used in the treatment of viral infections.
CC   The pref. dose is 1 pg - 10 mg/kg.
SQ   Sequence   5139 BP;   1165 A;   1439 C;   1399 G;   1135 T;   1 Others;

Initial Score     =    134  Optimized Score  =     378  Significance =  7.83
Residue Identity  =    48%  Matches          =     452  Mismatches   =   366
Gaps              =    106  Conservative Substitutions               =     0

 100       110       120       130       140       150       160       170
   GCCTCTAGCCAACTTCCTCTGTGTCCAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTCAGT
              | |||| || | | ||  || |  |     | ||  |  | | ||| | |   |||||
             GAATTCC-CTCT-TTCACCCTGTCTA---GGTTGCCAGCAAAT-CCCACGG---GCCTCCTG
             X        10         20           30         40           50

         180       190       200       210       220       230        240
   ATCCTCCCCTGTAAAATGGGATGATAGATGTCTGTCTCACTGCGTTGTTTAAGGCTCCGCAGGATGA-GGCC
   |  || |||       ||||   | || |  ||      ||||   | | |||| | | | | || |  |
   ACGCTGCCC------CTGGGGCCACAGGTCCCTCGAGTGCTGCAAGGATGAAGGATTC-CTGCATCACTGTG
        60              70        80        90       100        110

        250       260       270       280       290        300        310
   TTGGCCAGGTCAGTGCTCCACAAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGC-ACCTGCTC-CCCAGGG
    |||||| | |  ||||   |  |   |   | ||  |  | ||   || |   | |||||  |   | |||
   ATGGCCATGGCGCTGCT-GTCTGGGTTCTTTTTCTTCGCGCCGGCCTCGAGCTACAACCTGGACGTGCGGGG
  120       130        140       150       160       170       180

        320       330       340       350        360       370       380
   CGGGGTGTCCTCCGCCGCGTCCTCTGCCAGTGCAGGCAC-CAGGCAGCGGCCAGCAGCAGGAGGCCCACGGG
   || |  |  || | || |  || | ||    | ||||||   ||   | ||   | |||||  |   ||| |
   CGCGCGGAGCTTCTCC-CCACCGC-GCGCCGGGAGGCACTTTGGATACCGCGTCCTGCAGGTCGGAAACGCG
 190       200        210        220       230       240       250

       390       400        410        420       430       440         450
   CAGCAGCAGTAGGAGGAGCAGAGG-GGGCTGCGGGGC-TGTCGGGGCTGTGGCCTCCAG--GGGCCGGGGAC
      ||   || ||||   ||| || |||   | |  |  |  |   || |     ||||  ||||   ||||
   -GTCA-TTGTGGGAGCTCCAGGGGAGGGGAACAGCACAGGAAGCCTCTATCAGTGCCAGTCGGGCACAGGAC
  260        270       280       290       300       310       320

         460       470       480       490       500       510        520
   TCCATGGGGGTGGCAGGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTC-TGGCGA
    |  ||    || |||       |||   || |   |||  | ||||| | ||  ||  | |  | |||| |
   AC--TG--CCTGCCAGTCACCCTGAG--AGGTTCCAACTATACCTCCAAGTACTTGGGAATGACCTTGGCAA
 330           340       350         360       370       380       390

           530         540       550          560       570          580
   GTGATC---CAG--GGCTTCAGCGCCACCAGCTG---CTCGGAGGTCTCCTGCAGGAGGCGGG---AGATGT
     || |   |||  ||   ||      || | ||   || ||  |||||   |  | | |  |   |  | |
   CAGACCCCACAGATGGAAGCATTTTGGCCTG-TGACCCTGGGCTGTCTCGAACGTGTGACCAGAACACCTAT
     400       410       420        430       440       450       460

       590       600       610       620        630       640       650
   TGGTCTGGACGAAGCGAAGACAGCTGGGGGGGGGCTGAAAGG-CACATTTGGTGACAAAGTGTATCTCCGTG
     |  ||| |   |  |   |  |  |   |   ||| | || | ||  || || ||  | |   |   ||
   CTGAGTGGCCTGTGTTACCTCTTC-CGCCAGAATCTGCAGGGTCCCA--TGCTG-CA-GGGGCGCCCTGGTT
    470       480       490        500       510           520       530

      660       670       680       690       700       710       720
   TTCACGCGCTCCAGCAAGCCTTGCATCTTGGACCCAGCGACAGTCTTGAGCCGCTCCATCCAGCGCTGTGCC
   |||| |   |  | ||||    ||| | | ||||        || ||   | | |  ||    || || ||
 470       480       490       500        510       520          530
GGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCG-GGAGAAGTTCTGGCGAG-TG--ATCCAGGGC
      |||||   ||||  | ||   | |  || ||| | | |  || || |  ||| ||  | ||||  |
TCCCCAAGGAG-ATGGCT-TCTCTCTCGGTGGAGACACAGAGCACCAGCTCGGAGGAGATGGTACCCAGCTC
  480        490        500       510       520       530       540

      540       550       560       570       580        590       600
T---TCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATG-TTGGTCTGGACGAAGCGAAG
|   ||| | |||||| || ||||  |||||     |  || |     ||| || || ||  | | |  |||
TCCCTCACCCCCACCACCTCCTCG--GGTCT-----ATAAGCC-----ATGCTTTGTATG--CAATGACAAG
  550       560         570            580            590         600

     610       620       630       640        650       660       670
ACAGCTGGGGGGGGGCTGAAAGGCACATTTGGTGACAAAG-TGTATCTCCGTGTTCACGCGCTCCAGCAAGC
 |  || ||      || |  ||  ||  |  ||  || | || |    | | ||||  |||  ||   ||
TCTTCT-GGCTACCACT-ATGGGGTCAGCTCCTGTGAAGGCTGCAAGGGCTTCTTCAGACGCAGCATTCAGA
     610        620       630       640       650       660       670

    680       690          700       710       720        730       740
CTTGCATCTTGGACCCA-GCGACAGT--CTTGAGCCGCTCCATCCAGCGCTGT-GCCAGGACCAGCCGCCAG
    |||  || |  || |  || ||  |   | | |   ||| || |   ||  |||| |   |  |||||
AAAACATGGTGTATACATGTCACCGTGACAAAAACTGTATCAT-CAACAAGGTCACCAGAAATCGATGCCAG
    680       690       700       710        720       730       740

      750         760        770         780       790          800
AGGCCCCCGCAGAGCTCC--TCGTCCTGC-AGGTTGG-AGG-CCACGGTGACTG---GGTAATCTTGAAGCA
      | |||| ||| |    ||  | | | || || | | ||| ||   |||   || |   | ||| ||
----TACTGCAG-GCTACAAAAGTGTTTCGAAGTGGGCATGTCCAAGGAAGCTGTAAGGAACGATCGAAACA
       750        760       770       780       790       800       810

  810        820       830       840         850        860        870
GGTAGTCAGA-CAGCTCACGGATTTTGACAGCGAAGTCGG--AGGAGATG-GGGCTGTGTTGGAAGGA-GCA
 | ||  | |  || | |  ||    | |      | | |  | ||  || |  |   ||| || | |  ||
AGAAGAAAAAGGAGGTAAAAGAGGAGGGCTCGCCCGACAGCTATGAACTGAGTCCACAGTTAGAGGAACTCA
      820       830       840       850       860       870       880

      880        890              900         910       920       930
-GTCCTGGGTC-CCACTGAGTCCC--GAG-CT----CAGCA-GCAG-CAGCAGGAGGAGATAGGTTGTTGGG
   ||  ||||  ||  |    ||  ||| ||    |  ||  | | |||| || | |  ||       |
TCACCAAGGTCAGCAAAGCCCACCAGGAGACTTTTCCCTCACTCTGCCAGCTGG-GCAAGTA-CACCACGAA
    890       900       910       920       930        940        950

     940        950       960       970           980          X
CTCCAG-GCTG-GCGCCAGCACTGTCATTTCGGCCGGGGGCCCCGG----AATTCCG---GCCG
|||||| || |  | || |   || ||  | | || |||||   ||    | ||| |   || |
CTCCAGTGCAGATCACCGG--GTG-CAGCTGGACCTGGGGCTGTGGGACAAGTTCAGCGAGCTGGCCACCAA
    960       970          980       990      1000      1010   X  1020

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13. US-08-162-407-5' (1-988)
    Q20541        Mouse retinoic acid receptor isoform clone lambda-

 ID   Q20541 standard; DNA; 2740 BP.
 AC   Q20541;
 DT   10-MAR-1993  (revised)
 DT   22-APR-1992  (first entry)
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DE   Mouse retinoic acid receptor isoform clone lambda-mE13.20.
KW   RAR-gamma-A; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             253..1629
FT   /*tag=  a
FT   polyA_signal    2697..2702
FT   /*tag=  b
FT   polyA_site      2716..2740
FT   /*tag=  c
FT   misc_feature    1..435
FT   /*tag=  d
FT   /note= "point of divergence from RAR-gamma-B"
PN   CA2015766-A.
PD   31-OCT-1991.
PF   30-APR-1990; 015766.
PR   30-APR-1990; CA-015766.
PA   (MOUN ) MOUNT SINAI HOSPITAL.
PA   (HSCR-) HSC RES DEV CORP.
PI   Giguere V, Varmuza SL, Rossant J;
DR   WPI; 92-024769/04.
DR   P-PSDB; R20465.
PT   DNA segments to produce iso-forms and chimeric forms of RAR -
PT   have sequence encoding protein which display ligand binding and
PT   transcription activating properties of a gamma iso-form of RAR
PS   Claim 5; Fig 1; 52pp; English.
CC   The sequence is that of a clone lambda-mE13.20 which encodes mouse
CC   retinoic acid receptor (RAR) isoform RAR-gamma-A, it was isolated
CC   from a 7.5 day mouse embryo lambda-gt10 cDNA library. It diverges
CC   from the clone lambda-mE7.1 as indicated at nucleotides 1 to 435,
CC   this corresponds to with a splice junction between exon 1 and exon
CC   2 of the human RAR-alpha gene. It can be used for screening of
CC   agonists and antagonists of the gamma receptor effector system and
CC   for identifying ligands capable of binding to a gamma isoform of RAR.
CC   See also Q20542.
SQ   Sequence   2740 BP;    602 A;    840 C;    741 G;    557 T;
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Initial Score    =     132  Optimized Score    =    417  Significance =  7.70
Residue Identity =     50%  Matches            =    508  Mismatches   =   380
Gaps             =     125  Conservative Substitutions                =     0

  30        40          50        60        70        80        90
  GGGGCCGGTGCTGGATTCT--GGCGTTGCCTCCATTCTGGGGAGGGAATGAGAGGGGCCCAAGGAAGGGACC
            | ||  |||  ||| || | |||   | |           ||  |   |||    |||  ||
            CGGGGCTCTGCGGCCTTCCTTCC--CCCGCCCTCCCCTCCAGCAGTTTCCA--CCAGGTCCC
            X       10        20          30        40          50

  100       110       120        130       140       150       160
  -GGCCTCTAGCCAACTTCCTCTGTGT-CCAGGCTATACATCCTCTGGCTGGTGACTCCCCTCTGTGTGCCTC
     |||| ||||     ||  | |||   |||  ||   | |   |||  | |     |||  |    || |
  TCACCTC-AGCC-TGGCCCAGTATGTAGGAGGGAATCTCTGCAGAGGCCAGAG-GGATCCTTGGAAACCCAC
  60          70        80        90       100        110       120

 170       180       190        200       210       220       230
  AGTATCCTCCCCTGTAAAATGGG-ATGATAGATGTCTGTCTCACTGCGTTGTTTAAGGCTCCGCAGGATGAG
   | | |   ||  | |   |||| | |     |  | | | ||  ||  ||   | ||   ||  || ||
  TGGA-CAGACCAGGCAGGGTGGGCACGGAGCCTCCCAGGC-CAGGGCAGTGGGCATGG--GCGGGGGCTGTA
  130        140       150       160        170       180         190

240       250       260       270        280       290         300
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  GCCTTGGCCAGGTCAGTGCTCCACAAGCAGCAG-GTCCTGGGGACTGGGGACG-GGGGGC-ACC-TGCTCCC
  ||  ||   ||  ||   | || |  || |||| ||||  |||| |    |||  |  || ||| ||  | |
  GC--TG--AAGACCA--CCCCCGCCTGCTGCAGAGTCCAAGGGA-TTCCCACGCCGCAGCTACCATGGCCAC
        200         210       220       230        240       250       260

  310       320       330         340       350       360       370
  CAGGGCGGGGTGTC-CT--CCGCCGCGTCCTCTGCCAGTGCAGGCACCAGGCAGCGGCCAGCAGCAGGAGGC
  ||    || | | | ||   ||||  || | |||   | ||  | | | ||   |  |||| ||||||   |
  CAATAAGGAGAGACTCTTTGCGCCCGGTGCCCTG---GGGCCTGGATCTGGTTAC--CCAGGAGCAGGCTTC
         270       280       290          300       310         320

   380        390       400       410           420       430       440
  CCACGGGCAGCAGCAGTAGGAGGAGCAGAGGG-GGCTGC----GGGGCTGTCGGGGCTGTGGCCTCCAGGGG
  |||   ||     |||  | |    |||||||  ||  |     | | || | | || | || ||| ||||
  CCATTCGCCTTCCCAGGTGCA--CTCAGAGGGTCGCCACCATTTGAGATG-CTGAGCCCTAGCTTCC-GGGG
  330       340         350       360       370       380        390

      450       460       470       480       490       500        510
  CCGGGGACTCCATGGGGGTGGCAGGGTTGAGGAGTCGGGCTGACACTGCAGCTCCAGGCACCG-GGAGAAGT
  || |||   |||   |  || |       |||||   ||||  | ||   | |  || ||| | | |  ||
  CCTGGG---CCA---GCCTGACCTCCCCAAGGAG-ATGGCT-TCTCTCTCGGTGGAGACACAGAGCACCAGC
    400             410       420          430      440       450

     520          530          540       550       560       570       580
  TCTGGCGAG-TG--ATCCAGGGCT---TCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGA
  || |  ||| ||  | ||||  ||   ||| | |||||| || ||||  |||||     |  || |     |
  TCGGAGGAGATGGTACCCAGCTCTCCCTCACCCCCACCACCTCCTCG--GGTCT-----ATAAGCC-----A
460       470       480       490       500         510

          590       600       610       620       630       640        650
  TG-TTGGTCTGGACGAAGCGAAGACAGCTGGGGGGGGGCTGAAAGGCACATTTGGTGACAAAG-TGTATCTC
  || || || ||  | | |  ||| |  || ||      || |  ||  ||  |  ||  || | || |
  TGCTTTGTATG--CAATGACAAGTCTTCT-GGCTACCACT-ATGGGGTCAGCTCCTGTGAAGGCTGCAAGGG
520       530         540       550         560       570       580

         660       670       680       690          700       710
  CGTGTTCACGCGCTCCAGCAAGCCTTGCATCTTGGACCCA-GCGACAGT--CTTGAGCCGCTCCATCCAGCG
  | | ||||  |||  ||   ||     |||  || |  || |  || ||  |   | | |   ||| || |
  CTTCTTCAGACGCAGCATTCAGAAAAACATGGTGTATACATGTCACCGTGACAAAAACTGTATCAT-CAACA
  590       600       610       620       630       640       650

720        730       740       750         760        770         780
  CTGT-GCCAGGACCAGCCGCCAGAGGCCCCCGCAGAGCTCC--TCGTCCTGC-AGGTTGG-AGG-CCACGGT
    ||  |||| |   |  ||||      | |||| ||| |    ||  | | | || || | | ||| ||
  AGGTCACCAGAAATCGATGCCAG----TACTGCAG-GCTACAAAAGTGTTTCGAAGTGGGCATGTCCAAGGA
 660       670       680          690       700       710         720

    790          800       810       820       830       840         850
  GACTG---GGTAATCTTGAAGCAGGTAGTCAGA-CAGCTCACGGATTTTGACAGCGAAGTCGG--AGGAGAT
    |||   || |   | ||| || | ||  | |  || | |  ||    | |      | | |  | ||  |
  AGCTGTAAGGAACGATCGAAACAAGAAGAAAAAGGAGGTAAAAGAGGAGGGCTCGCCCGACAGCTATGAACT
    730       740       750       760       770       780       790

          860       870       880       890                900         910
  G-GGGCTGTGTTGGAAGGA-GCA-GTCCTGGGTC-CCACTGAGTCCC--GAG-CT----CAGCA-GCAG-CA
  | |  |   ||| || | |  ||   ||||  ||  |    ||  ||| ||    |  ||  | | ||
  GAGTCCACAGTTAGAGGAACTCATCACCAAGGTCAGCAAAGCCCACCAGGAGACTTTTCCCTCACTCTGCCA
  800       810       820       830       840       850       860

         920       930        940        950       960       970
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    GCAGGAGGAGATAGGTTGTTGGGCTCCAG-GCTG-GCGCCAGCACTGTCATTTCGGCCGGGGGCCCCGG---
    || || | |  ||       |  ||||||  || |  | || |   || ||  | | || |||||   ||
    GCTGG-GCAAGTA-CACCACGAACTCCAGTGCAGATCACCGG--GTG-CAGCTGGACCTGGGGCTGTGGAC
  870        880        890       900         910        920       930

     980          X
    -AATTCCG---GCCG
     | ||| |   || |
    AAGTTCAGCGAGCTGGCCACCAAAT
     940       950       960


14. US-08-162-407-5' (1-988)
    Q14498       Clone 1 for truncated poly Ig-receptor.

 ID   Q14498 standard; DNA; 1876 BP.
 AC   Q14498;
 DT   10-MAR-1993  (revised)
 DT   30-JAN-1992  (first entry)
 DE   Clone 1 for truncated poly Ig-receptor.
 KW   Rabbit; insemination; pregnancy; ss.
 OS   Oryctolagus cuniculus.
 FH   Key            Location/Qualifiers
 FT   CDS            124..1876
 PN   WO9116061-A.
 PD   31-OCT-1991.
 PF   16-APR-1991; U02604.
 PR   16-APR-1990; US-510161.
 PA   (HARD ) HARVARD COLLEGE.
 PA   (SURE-) INST SUISSE RECH EXPER C.
 PI   Kraehenbuhl JP, Weltzin RA, Neutra MR;
 DR   WPI; 91-339549/46.
 DR   P-PSDB; R14670.
 PT   Stabilised poly-Ig complex contg. portion of poly-Ig receptor -
 PT   useful in protection against pathogens or against pregnancy
 PS   Disclosure; Fig 8; 51 pp; English.
 CC   The sequence was obtd. from a cDNA clone of allele no. 1 and
 CC   encodes a truncated poly-Ig receptor.  The native gene (Mostov et
 CC   al) is mutated to delete the portion encoding the transmembrane and
 CC   intra-cellular domains.  The recombinant protein produced by
 CC   expression of the sequence is used as a stabiliser protein with a
 CC   poly-Ig specific for a selected antigen or family of antigens. The
 CC   compsn. can be administered directly to the mucosal surfaces of a
 CC   mammal to protect against a pathogen or against insemination. It
 CC   protects against allergens that contact the respiratory or digestive
 CC   mucosal surfaces and protects against pregnancy by cross-linking
 CC   sperm in the vagina.
 CC   See also Q14499.
 SQ   Sequence   1876 BP;    441 A;    525 C;    549 G;    361 T;

Initial Score    =    130  Optimized Score    =    263  Significance =  7.56
Residue Identity =    51%  Matches            =    325  Mismatches   =   226
Gaps             =     85  Conservative Substitutions          =     0

         400  X    410       420         430       440       450        460
    TAGGAGGAGCAGAGGGGGCTGCGGGGCTGTCGG--GGCTGTGGCCTCCAGGGGCCGGGGACTCCATG-GGGG
               |  |||| | ||||   | |  |||||||  | || | | ||  || |  || | ||||
              GGCCGGGGTTACGGGCTGGCCAGCAGGCTGTG--CCCCCGAGTCC--GGTCAGCAGGAGGGG
              X       10        20        30          40        50
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          470       480        490       500       510       520       530
    TGGCAGGGTTGAGGAGTCGGGCTGACA-CTGCAGCTCCAGGCACCGGGAGAAGTTCTGGCGAGTGATCCAGG
      | || |      | ||   |   || | ||||| |||||  ||  | |   | |  || |   | ||| |
    AAGAAGTGGCCTAAAATCTCTCCCGCATCGGCAGC-CCAGG--CCTAGTGCCCTACCAGCCA-CCAGCCATG
    60        70        80        90          100       110        120

          540           550       560         570           580       590
    GCT-TCAGC--GC-CACCAG-CTGCTCGGAGGTCTCCTGCA--GGAGGCGG----GAGATGTTGGTCTGGAC
    ||| ||  |  || |||| | ||||| ||  ||||  | ||  ||   |||     || |  |  |  || |
    GCTCTCTTCTTGCTCACCTGCCTGCT-GGCTGTCT-TTTCAGCGGCCACGGCACAAAGCTCCTTATTGGGTC
     130       140       150        160        170       180       190

        600       610          620       630       640       650        660
    GAAGCGAAGACAGCTGG---GGGGGGGCTGAAAGGCACATTTGGTGACAAAGTGTATCTC-CGTGTTCACGC
      |||    | |  |||    |||| | |||| |        || |||   ||||   || | || | ||
    CCAGC-TCCATATTTGGTCCCGGGGAGGTGAATGTTTTGGAAGGCGACTCGGTGTCCATCACATGCT-AC-T
     200        210       220       230       240       250       260

          670       680       690       700          710       720       730
    GCTCCAGCAAGCCTTGCATCTTGGACCCAGCGACAGTCTTGAG--CCGCT-CCATCCAGCGCTGTGCCAGGA
     | ||| ||| |||  | ||    |||| || |||| |   ||  | | | ||    || |  | ||  ||
    AC-CCAACAA-CCT-CCGTC----ACCCGGC-ACAGCCGGAAGTTCTGGTGCCGGGAAGAGGAGAGC--GG-
       270         280            290       300       310       320

           740          750       760       770               780       790
    CCAGCCGCCAGAGGC---CCCCGCAGAGCTCCTCGTCCTGCAGG-------TTGGAG-GCCACGGTGACTGG
     | || ||  || ||   || ||    ||| | |||||  ||||         |||| | || | | || |
    -CCGCTGCGTGACGCTTGCCTCGACCGGCTACACGTCC--CAGGAATACTCCGGGAGAGGCAAGCTCACCGA
      330       340       350       360         370       380       390

            800         810        820       830         840       850
    GTAATCT--TGAA--GCAGGTAGT-CAGACAGCTCACGGATTTTGACAG--CGAAGTCGGAGGAGATGGGGC
     |   ||  | ||  | || | ||   ||| | | ||  | |    |||  || | || | |||| |
    CTTCCCTGATAAAGGGGAGTTTGTGGTGACTGTTGACCAACTCACCCAGAACG-ACTCAG-GGAGCTACAAG
      400       410       420       430       440        450        460

     860          870       880       890       900          910       920
    TGTG--TTGGAAG-GAGCAGTCCTGGGTCCCACTGAGTCCCGAGCTCAGC-AGCAG--CAGCAGGAGGAGAT
    ||||   ||| ||  | | | | |||  ||    || | | | | ||| |  || |  ||||  || |  |
    TGTGGCGTGGGAGTCAACGGCCGTGG--CC--TGGACTTCGGTG-TCAACGTGCTGGTCAGCCAGAAGCCAG
      470       480       490           500        510       520       530

         930         940       950       960       970         980        X
    AGGTTGTTG-GGCTCCAGGCTGGCGCCAGCACTGTCATTTCGGCCGGGGGCCCCGG--AATTC-CGGCCG
    ||  || ||  | |     |   |   |  |  || | | | |       | || |    ||| |    |
    AGCCTGATGACGTTGTTTACAAACAATATGAGAGTTA-TACAGTAACCATCACCTGCCCTTTCACATATGCG
         540       550       560        570       580       590       600

    ACTAGGCA
        610


15. US-08-162-407-5' (1-988)
    Q05272       Sequence encoding secreted GPIIIa subunit of multi

 ID  Q05272 standard; DNA; 2183 BP.
 AC  Q05272;
 DT  22-NOV-1990  (first entry)
 DE  Sequence encoding secreted GPIIIa subunit of multiple subunit
 DE  polypeptide (MSP) GPIIb-IIIa.
```

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 KW   GPIIb; GPIIIa; MSP GPIIb-IIIa; anti-coagulant; anti-inflamatory;
 KW   immunosuppressant; ds.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             13..2166
 FT   /*tag=  a
 FT   misc_signal     89
 FT   /*tag=  b
 FT   /label=Signal processing site.
 PN   WO9006953-A.
 PD   28-JUN-1990.
 PF   20-DEC-1989; U05743.
 PR   22-DEC-1988; US-290224.
 PR   01-DEC-1989; US-444490.
 PA   (GETH ) GENENTECH INC.
 PI   BODARY SC, GORMAN CM, NAPIER MA, MCLEAN JW;
 DR   WPI; 90-224496/29.
 DR   P-PSDB; R05936.
 PT   Soluble analogues of multi-sub-unit polypeptide prodn. - by
 PT   transforming host cells with nucleic acid modified to prevent
 PT   membrane attachment, useful in diagnosis and ligand purificn.
 PS   Disclosure; 47pp; English.
 CC   Peptide product is analogous to MSP with better stability, it is
 CC   not membrane bound and so may be collected as a cell secretion from
 CC   a transformed host. The product is useful as a diagnostic reagent
 CC   eg. immunoassay of MSP; in purification of ligands and matrix
 CC   proteins; and therapeutically as agonists or antagonists of the
 CC   corresponding membrane bound receptor.
 SQ   Sequence   2183 BP;    506 A;    563 C;    621 G;    493 T;

Initial Score    =    126  Optimized Score     =    368  Significance =  7.29
Residue Identity =    50%  Matches             =    455  Mismatches   =   323
Gaps             =    127  Conservative Substitutions                 =     0

              X       10        20        30          40         50
              CGGGGGCTTTGTTCAGAGTTGGGTAAATGGGGCCGGT--GCT-GGATTCTGGCGTTGCCT-C
              || ||||    ||||  |   |    || |  | |||   ||  |||| || |  ||||| |
    CCATAAAGCCCGTGGGC----TTCAAGGACAGCCTGATCGTCCAGGTCACCTTTGATTGTGACTGTGCCTGC
       1340   X  1350          1360      1370      1380      1390      1400

    60        70         80         90         100       110       120
    CATTCTGGGGAGGGA-ATGAGAGGGGCCCAAGGAAGGGAC-CGGCCTCTAGCCAACTTCCTCTGTGTCCAGG
    ||  |    |  | |  | | ||    |||  |  |  ||   | |  | |  | |||  |  ||||   ||
    CAGGCCCAAGCTGAACCTAATAG----CCATCGCTGCAACAATGGCAAT-GGGACCTT--TGAGTGT--GGG
         1410     1420          1430      1440       1450        1460

   130            140        150       160             170        180
    CTAT-ACATCCT----CTGGCTGG-TGACTCCCCTCTGTGTG-CCTC-----AGTATCCTC-CCCTGTAAAA
     |||  | |  |    |||||||| ||    |||  |||| |  |||     || |   || ||||    |
    GTATGCCGTTGTGGGCCTGGCTGGCTGGGATCCCAGTGTGAGTGCTCAGAGGAGGACTATCGCCCTTCCCAG
      1470      1480      1490      1500      1510      1520      1530

    190       200       210            220       230        240       250
    TGGGATGATAGATGTCTGTCTCACTGCGT-----TGTTTAAGGCTCCGCAGGATGAG-GCCTTGGCCAGGTC
      ||| ||  |  | |   |  |  | ||      || |   || | || ||  ||| ||||  |   ||||
    CAGGACGAGTGCAGCC--CCCGAGAGGGTCAGCCCGTCTGCAGC-CAGCGGGGCGAGTGCCTCTG--TGGTC
    1540      1550        1560      1570       1580      1590        1600

         260       270       280       290       300       310       320
    AGTG-CTCCACAAGCAGCAGGTCCTGGGGACTGGGGACGGGGGGCACCTGCTCCCCAGGGCGGGGTGTCCTC
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  | ||  ||  | | ||||||   ||  ||   |   ||   |||||  | ||  | || | |  |  | |||
  AATGTGTCTGCCA-CAGCAGTGACTTTGGCAAGATCAC---GGGCAAGTACT-GCGAGTGTGACGACTTCTC
     1610       1620      1630      1640         1650       1660      1670

     330       340          350        360         370       380       390
  CGCCGCGTCCTCTGCCA-GTGCAG--GCAC-CAGGCAGCGGCCA--GCAGCAGGAGGCCCACGGGCAGCAGC
    | | |||| || | | | | ||  |  | |||||   |||||  ||||| |  ||   || | | |
  --CTGTGTCCGCTACAAGGGGGAGATGTGCTCAGGCCATGGCCAGTGCAGCTGTGGG--GACTGCCTGTGTG
          1680      1690      1700      1710      1720        1730

           400       410       420            430       440          450
  AGTAGGA--GGAGCAGAGGGGGCTGCGGGGCTGT----CG-GGGCTGTGGCCTCCAGG---GGCCGGGGACT
  | |  ||  ||| | |      ||||    ||||    || |  |||   ||| || |    ||   || ||
  ACTCCGACTGGACCGGCTACTACTGC--AACTGTACCACGCGTACTGACACCTGCATGTCCAGCAATGGGCT
1740      1750      1760        1770      1780      1790      1800

           460         470       480        490       500       510
  -CCATG--G-GG--GTGGCAGGGTTGAGGAGTCG-GGCTGACACTGCAGCTCCAGGCACCGGGAGAAGTTCT
   |  ||  | ||  | |||| |  |||   || |  ||||   ||| |  |||||   ||||  |    | |
  GCTGTGCAGCGGCCGCGGCAAGTGTGA-ATGTGGCAGCTGTGTCTGTA--TCCAG---CCGG--GCTCCTAT
1810      1820      1830       1840      1850        1860           1870

  520       530       540       550       560       570       580
  GGCGAGTGATCCAGGGCTTCAGCGCCACCAGCTGCTCGGAGGTCTCCTGCAGGAGGCGGGAGATGT-TGGTC
  || ||     || | |    || ||| ||| |||| | || | || |  |   | |   || |||| |||
  GGGGA---CACCTGTG-AGAAGTGCC-CCACCTGCCCAGATGCCTGCACCTTTAAGAAAGA-ATGTGTGGAG
         1880       1890       1900      1910      1920       1930

 590       600       610       620         630       640       650
  TGGACGAAGCGAAGACAGCTGGGGGGGGGCTGAAAGGC--ACATTTGGTGACAAAGTGTATCTCCGTGTTCA
  || | ||||    |||      ||| |  ||  | | |  | | |   || |||    ||   |||||   |
  TGTAAGAAG-TTTGAC-----CGGGAGCCCTACATGACCGAAAATACCTG-CAACCGTTACTGCCGTG---A
1940       1950           1960      1970      1980       1990         2000

 660       670       680         690       700           710       720
  CGCGCTCCAGCAAGCCTTGCATCTT--GGACCCAGCGACAGTCT----TGAGCCGCTCCATCCAGCGCTGTG
  || | |  ||  ||      | |||  |||| | | |  ||  |    |||   | | | |  |    || |
  CGAGATTGAGTCAGTGAAAGAGCTTAAGGACACTG-GCAAGGATGCAGTGAATTG-TACCTATAAGAATGAG
        2010      2020      2030       2040      2050       2060      2070

     730        740       750       760       770        780       790
  CCAGGAC-CAGCCGCCAGAGGCCCCCGCAGAGCTCCTCGTCCTGCAGGTTG-GAGGCCACGGTGACTG-GGT
    | |||   | || ||||  |     |||  ||  |     | |  || |  || |||   ||  || |||
  -GATGACTGTGTCGTCAGATTC-----CAGTACT-ATGAAGATTCTAGTGGAAAGTCCATCCTGTATGTGGT
         2080      2090            2100      2110      2120      2130

      800       810       820        830       840  X    850
  AATCTTGAAGCAGGTAGTCAGACAGCTCACGGA-TTTTGACAGCGAAGTCGGAGGAGATGG
  |     ||  |||   |||  | ||  | | || |  ||| | | |||
  A--GAAGAGCCAGAGTGTCCCA-AGGGCCCTGACTGATGAGATCTAAGCTT
     2140      2150       2160      2170      2180  X
```

maryh@stic **stdin**

NeWSprinter20

Thu Apr 06 10:17:12 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq6_28na.res made by  on Wed 5 Apr 95 17:26:04-PDT.


Query sequence being compared:US-08-162-407-6 (1-235)
Number of sequences searched:                 313646
Number of scores above cutoff:                  3849

      Results of the initial comparison of US-08-162-407-6 (1-235) with:
   Data bank : EMBL-NEW 1, all entries
   Data bank : GenBank 86, all entries
   Data bank : GenBank-NEW 1, all entries
   Data bank : UEMBL 41_86, all entries

1000000-
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U00000-
M      -
B      -
E      -
R      -
       -
O      - *
F00000-   *
       -  *
S      -
E50000-
Q      -
U      -
E      -*
N      -
C      -    *
E      -
S10000-
       -     *
       -
  5000-       *
       -
       -
       -
       -
       *
       -
  1000-
       -
       -        *
   500-         *
       -
       -
       -
       -
       -
       -
```

Spector 243545

```
   100-
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      -         *
    50-
      -
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      -          **
      -
      -
      -
    10-
      -
      -
     5-
      -
      -            *
      -
      -
      -
      -             *                                                *
     0---------------------------------------------------------------------------
      ||   |||  |||  |      |      |      |      |      |      |      |      |
SCORE 0|   |10  |||  20     30     40     50     60     70     80     90
STDEV -1    3    7  9

                             PARAMETERS

Similarity matrix       Unitary     K-tuple                  2
Translation Frame             1
Mismatch penalty              1     Joining penalty         20
Gap penalty                1.00     Window size             32
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

Initial scores to save       45     Alignments to save      15
Optimized scores to save      0     Display context         10

                             SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                             4           6             1.79

Times:                      CPU                    Total Elapsed
                        00:14:41.08                00:15:02.00

Number of residues:              96133774
Number of sequences searched:      313646
Number of scores above cutoff:       3849

Cut-off raised to 4.
Cut-off raised to 5.
Cut-off raised to 6.
Cut-off raised to 7.
Cut-off raised to 8.
Cut-off raised to 9.
Cut-off raised to 10.
Cut-off raised to 11.
Cut-off raised to 12.
```

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The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                   Init. Opt.
Sequence Name  Description                  Length Score Score  Sig. Frame
---------------------------------------------------------------------------
                   **** 48 standard deviations above mean ****
  1. MMU04807    Mus musculus FLT3/FLK2 ligand   384   90   111  48.15   1
                   ****  9 standard deviations above mean ****
  2. SSVHNF1     S.scrofa mRNA for vHNF-1.       940   21    25   9.52   1
                   ****  8 standard deviations above mean ****
  3. AIBDVVP2    Avian infectious bursal disea   490   19    26   8.40   1
  4. IBDLGVP2    Infectious bursal disease vir   502   19    26   8.40   1
  5. SCINVE      Yeast gene SUC2 encoding inve   957   19    32   8.40   1
                   ****  7 standard deviations above mean ****
  6. ATT13408    1474 Arabidopsis thaliana cDN   124   18    26   7.84   1
  7. T04557      604 Arabidopsis thaliana cDNA   124   18    26   7.84   1
  8. SFIURA5A    Sordaria macrospora orotate p   415   18    31   7.84   1
  9. RATNOSI     Rat nitric oxide synthase mRN  1198   18    35   7.84   1
 10. RATNWUT     Rat mRNA.                      1204   18    35   7.84   1
 11. MUSINOSL    Mus musculus nitric oxide syn  1230   18    34   7.84   1
 12. RNU03699    Rattus norvegicus Sprague Daw  1314   18    35   7.84   1
 13. MUSRGEETS   Mouse 18S ribosomal RNA gene   1398   18    30   7.84   1
 14. T35584      EST87799 Homo sapiens cDNA 5'   106   17    22   7.28   1
 15. CHKRERYF1   Chicken erythroid-specific tr   356   17    31   7.28   1
 16. CHKHOX7     Chicken mRNA for Chox-7 prote   442   17    29   7.28   1
 17. SYORPOD1    Synechococcus sp. rpoD1 gene    453   17    32   7.28   1
 18. AFPECB      Aspergillus flavus 70 polygal   467   17    36   7.28   1
 19. YSKHAP3A    Kluyveromyces lactis (HAP3) g   833   17    26   7.28   1
 20. MUSTWISTG   Mouse M-twist gene, complete    920   17    31   7.28   1
 21. SMIGCU      Suncus murinus mu-immunoglobu   947   17    28   7.28   1
 22. RMU10426    Rhodothermus marinus R-21 pla   978   17    28   7.28   1
 23. SCSUC1G     Yeast SUC1 gene (EC 3.2.1.26)  1000   17    30   7.28   1
 24. BOVNE3B     Bos taurus neurexin III-beta   1135   17    32   7.28   1
 25. HUMCACH1A   Human neuroendocrine/beta-cel  2397   17    30   7.28   1
                   ****  6 standard deviations above mean ****
 26. MUS68E11    Mouse embryonal carcinoma F9     86   16    20   6.72   1
 27. MM68E11     Mouse embryonal carcinoma F9     86   16    20   6.72   1
 28. T38268      EST103700 Saccharomyces cerev   128   16    23   6.72   1
 29. MMLRP       M.musculus Lrp, alpha-2-Mr ge   233   16    30   6.72   1
 30. S66868S1    platelet-derived growth facto   466   16    32   6.72   1
 31. DROTFIIB    Drosophila melanogaster RNA p   488   16    33   6.72   1
 32. LESALMSGB   L.esculentum S-adenosyl-L-met   555   16    29   6.72   1
 33. TMALPTUB    T.marmorata mRNA for alpha-tu   566   16    33   6.72   1
 34. MUSAPRF     Mus musculus acute phase resp   884   16    31   6.72   1
 35. MMAPRF      Mus musculus acute phase resp   884   16    31   6.72   1
 36. CHKHSF3C    Chicken mRNA sequence.          891   16    31   6.72   1
 37. CEPMTTGRG   Cephalophus maxwelli mitochon   893   16    31   6.72   1
 38. OCPHOR      Rabbit mRNA for muscle glycog   943   16    29   6.72   1
 39. RABPYGM     Rabbit muscle glycogen phosph   945   16    29   6.72   1
 40. CHKMYOSIND  Chicken fast myosin heavy cha   981   16    29   6.72   1
 41. OPOHBBE     Opossum beta-hemoglobin epsil  1194   16    28   6.72   1
 42. DVHB        Drosophila virilis hunchback   2935   16    30   6.72   1
 43. RATCYP45I   Rat cytochrome P450IIE1 gene,  4242   16    31   6.72   1
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 44. HSAPOBA2    Human apolipoprotein B-100 mR  4624   16    32   6.72   1
 45. CHKMYHE     Chicken embryonic myosin heav 10370   16    29   6.72   1


1. US-08-162-407-6 (1-235)
   MMU04807     Mus musculus FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS       MMU04807     1152 bp    mRNA             ROD       11-MAY-1994
 DEFINITION  Mus musculus FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION   U04807
 KEYWORDS    .
 SOURCE      mouse.
   ORGANISM  Mus musculus
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Rodentia; Myomorpha; Muridae; Mus.
 REFERENCE   1  (bases 1 to 921)
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1152)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483846
 FEATURES             Location/Qualifiers
      source          1..1152
                      /clone="mouse Flt3/Flk2 ligand T110"
                      /clone_lib="TA4 cDNA"
                      /organism="Mus musculus"
                      /cell_line="TA4 stroma"
      CDS             256..954
                      /note="NCBI gi: 483847"
                      /codon_start=1
                      /product="FLT3/FLK2 ligand"
                      /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                      KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                      NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQ
                      CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARR
                      RGELHPGVPLPSHP"
 BASE COUNT      238 a    346 c    324 g    244 t
 ORIGIN

Initial Score    =     90  Optimized Score  =     111  Significance = 48.15
Residue Identity =    71%  Matches          =     112  Mismatches   =    43
Gaps             =      2  Conservative Substitutions              =     0
Translation Frame=      1

                 X       10        20        30        40        50        60
                 QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTV
                  || | |||||| | || ||| | || ||||||| |||||  |  || | ||||| | ||||
       LLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTV
           110   X   120       130       140       150       160       170
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          70        80        90       100       110         120       130
    AGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWI--TRQNFSRCLELQCQ
    |||||| ||| ||||||||| | ||| | |||||||||| ||  |  ||  ||| |    |||||||| |||
    AGSKMQTLLEDVNTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQCQ
      180       190       200       210       220       230       240

         140       150    X
    PDSSTLPPPWSPRPLEATAPTAP
    |||||| || ||  ||||    |
    PDSSTLLPPRSPIALEATELPEPRPRQLLLLLL
    250       260       270       280


2. US-08-162-407-6 (1-235)
   SSVHNF1      S.scrofa mRNA for vHNF-1.

 LOCUS       SSVHNF1      2821 bp    RNA             MAM       17-APR-1993
 DEFINITION  S.scrofa mRNA for vHNF-1.
 ACCESSION   X69675
 KEYWORDS    DNA binding protein; homeoprotein; nucleus; transcription factor;
             vHNF-1.
 SOURCE      pig.
   ORGANISM  Sus scrofa
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Artiodactyla; Suiformes; Suidae.
 REFERENCE   1  (bases 1 to 2821)
   AUTHORS   Menoud,P.A., Matthies,R., Hofsteenge,J. and Nagamine,Y.
   TITLE     Purification and cDNA cloning of a transcription factor which
             functionally cooperates within a cAMP regulatory unit in the
             porcine uPA gene
   JOURNAL   Nucleic Acids Res. 21, 1845-1852 (1993)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 2821)
   AUTHORS   Nagamine,Y.
   TITLE     Direct Submission
   JOURNAL   Submitted (08-DEC-1992) to the EMBL/GenBank/DDBJ databases. Y.
             Nagamine, Friedrich Miescher Institute, PO Box 2543, CH-4002 Basel,
             SWITZERLAND
   STANDARD  full automatic
 COMMENT     NCBI gi: 2156
 FEATURES             Location/Qualifiers
      source          1..2821
                      /organism="Sus scrofa"
                      /haplotype="2n"
                      /tissue_type="kidney"
                      /cell_type="epithelia"
                      /cell_line="LLC-PK-1"
                      /clone_lib="lambda-gt11 cDNA"
                      /clone="BluescriptKS"
      CDS             150..1829
                      /note="NCBI gi: 2157"
                      /codon_start=1
                      /product="porcine vHNF-1"
                      /translation="MVSKLTSLQQELLSALLSSGVTKEVLVQALEELLPSPSFGVKLE
                      TLPLSPGSGTEPDTKPVFHTLTNGHAKGRLSGDEGSEDGDDYDTPPILKELQALNTEE
                      AADDGAEVDRMLSEDPWRAAKMIKGYMQQHNIPQREVVDVTGLNQSHLSQHLNKGTPM
                      KTQKRAALYTWYVRKQREILRQFNQTVQSSGNLTDKSSQDQLLFLFPEFSQQSQGPGQ
                      SDDACSEPTNKKMRRNRFKWGPASQQILYQAYDRQKNPSKEEREALVEECNRAECLQR
                      GVSPSKAHGLGSNLVTEVRVYNWFANRRKEEEAFRQKLAMDAYSSNQTHSLNTLLSHS
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                        SPHHQPSTSPPNKLPGVRYNQQGNNEVTSSSTISHHGNSAMVTSQSVLQQVSPASLDP
                        GHNLLSPDGKMQISVSGGGLPPVSTLTNIHSLSHHNPQQSQNLIMTPLSGVMAIAQSL
                        NSSQAQSVPVINSVAGSLAALQPVQFSQQLHSPHQQPLMQQSPGSHMAQQPFMAAVTQ
                        LQNSHMYTHKQEPPQYSHTSRFPPAMVVTDTSSISTLTNMSSSKQCPLQAW"
      misc_feature      150..245
                        /note="dimerization domain"
      misc_feature      718..890
                        /note="POU motif"
      misc_feature      891..1196
                        /note="homeodomain"
 BASE COUNT      686 a    919 c    686 g    530 t
 ORIGIN

Initial Score     =     21  Optimized Score   =    25  Significance =  9.52
Residue Identity =     25%  Matches           =    32  Mismatches   =    72
Gaps              =     22  Conservative Substitutions             =     0
Translation Frame=       1

        40    X   50        60            70        80        90       100
    SNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQG----LLERVNTEIHFVTKCAFQPPPSCLRFVQTNISR
                 | |       |||   ||   |    |     |  |  |     |  | |       ||
              PGPRGV---TGVWRLKGGGGSWTWGSPVKLPSTLLTGTHPPT--PSPPSFSVL-GKWCPSSR
              X          10        20        30          40         50

         110       120       130       140                  150    X
    LLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEA-----------TAPTAP
         |       |   |   ||     | |  |       | || |             |||
    RSNKNS-XAPCXAPGSPRRCWSRPWRSCCHPRVSGXSWRRCPCPLGAGLSRTPSRSSTLSPTATPRAACPGT
      60         70        80        90       100       110       120

    RA


3. US-08-162-407-6 (1-235)
   AIBDVVP2      Avian infectious bursal disease virus RNA for VP2

 LOCUS       AIBDVVP2      1471 bp    RNA             VRL       11-MAY-1994
 DEFINITION  Avian infectious bursal disease virus RNA for VP2 and (partial)VP4
             proteins.
 ACCESSION   X54858
 KEYWORDS    capsid protein.
 SOURCE      infectious bursal disease virus.
   ORGANISM  infectious bursal disease virus
             Viridae; ds-RNA nonenveloped viruses; Birnaviridae.
 REFERENCE   1  (bases 1 to 1471)
   AUTHORS   Vakharia,V.N.
   TITLE     Direct Submission
   JOURNAL   Submitted (11-OCT-1990) to the EMBL/GenBank/DDBJ databases.
             Vakharia V.N., Univ. of Maryland, Ctr. for Agricultural
             Biotechnology and VA-MD Regional College of Veterinary Medicine,
             Veterinary Science Drive, College Park, MD 20742, USA
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1471)
   AUTHORS   Vakharia,V.N., Ahamed,B. and He,J.
   TITLE     Use of polymerase chain reaction for efficient cloning of dsRNA
             segments of infectious bursal disease virus
   JOURNAL   Avian Dis. 36, 736-742 (1992)
   STANDARD  full automatic
 COMMENT     Isolated from Chicken, subspecies Leghorn.
```

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             NCBI gi: 486622
 FEATURES             Location/Qualifiers
      source          1..1471
                      /organism="Avian infectious bursal disease virus"
                      /strain="E/DEL"
                      /tissue_type="bursa"
                      /clone="pE.Del-2"
                      /map="large segment A"
      mRNA            1..1471
      CDS             52..>1471
                      /note="NCBI gi: 486623"
                      /codon_start=1
                      /product="VP2 structural protein and partial for VP4"
                      /translation="MTNLQDQTQQIVPFIRSLLMPTTGPASIPDDTLEKHTLRSETST
                      YNLTVGDTGSGLIVFFPGFPGSIVGAHYTLQSNGNYKFDQMLLTAQNLPASYNYCRLV
                      SRSLTVRSSTLPGGVYALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLV
                      GEGVTVLSLPTSYDLGYVRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADNYQFSS
                      QYQTGGVTITLFSANIDAITSLSVGGELVFKTSVQSLVLGATIYLIGFDGTAVITRAV
                      AANNGLTAGIDNLMPFNLVIPTNEITQPITSIKLEIVTSKSDGQAGEQMSWSASGSLA
                      VTIHGGNYPGALRPVTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDP
                      GAMNYTKLILSERDRLGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRA
                      IRRIAVPVVSTLFPPAAPVAHAI"
      mat_peptide     52..1407
                      /product="VP2 structural protein"
      mat_peptide     1408..>1471
                      /product="VP4 structural protein"
 BASE COUNT      403 a    390 c    365 g    313 t
 ORIGIN

Initial Score    =     19  Optimized Score  =     26  Significance =  8.40
Residue Identity =    18%  Matches          =     31  Mismatches   =  118
Gaps             =     18  Conservative Substitutions            =    0
Translation Frame=      1

              X       10        20        30        40               50
              QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGG-------LWRLVLAQR-
                      || |         ||          ||        ||          ||   |
    IDNLMPFNLVIPTNEITQPITSIKLEIVTSKSDGQAGEQMSWSASGSLAVTIHGGNYPGALRPVTLVAYERV
          310 X      320       330       340       350       360       370

        60        70        80        90       100       110       120
    WMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITR-QNFSR
          ||||     |          ||      |         |   |       |     | ||     |
    ATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDP------GAMNYTKLILSERDRLGIKTVWPTREYTDFR
       380       390       400            410       420       430       440

     130           140       150    X
    CLELQCQPDSSTL---PPPWSPRPLEATAPTAP
              | |             |    |
    EYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPA
           450       460       470  X     480

4. US-08-162-407-6 (1-235)
   IBDLGVP2     Infectious bursal disease virus genomic RNA for VP

 LOCUS       IBDLGVP2     1506 bp ss-RNA             VRL       24-JUL-1992
 DEFINITION  Infectious bursal disease virus genomic RNA for VP2, partial
             sequence.
```

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 ACCESSION   D10065 D01240
 KEYWORDS    host-protective immunogen; structural protein.
 SOURCE      Infectious bursal disease virus (strain Delaware variant E) cDNA to
             genomic RNA.
   ORGANISM  Infectious bursal disease virus
             Viridae; ds-RNA nonenveloped viruses; Birnaviridae.
 REFERENCE   1  (bases 1 to 1506)
   AUTHORS   Heine,H.-G., Haritou,M., Failla,P., Fahey,K. and Azad,A.
   TITLE     Sequence analysis and expression of the host-protective immunogene
             VP2 of a variant strain of infectious bursal disease virus which
             can circumvent vaccination with standard type 1 strains
   JOURNAL   J. Gen. Virol. 72, 1835-1843 (1991)
   STANDARD  full automatic
 COMMENT     Submitted (07-Nov-1991) to DDBJ by: Hans-Georg Heine
             CSIRO, Australian Animal Health Laboratory
             P.O.Bag 24
             Geelong VIC 3220
             Australia
             Phone:  052-26-5222
             Fax:    052-23-1424
             E mail: hans@aahl.dah.csiro.au.

             NCBI gi: 221889
 FEATURES             Location/Qualifiers
      source          1..1506
                      /organism="Infectious bursal disease virus"
      misc_feature    1..48
                      /note="5'PCR primer N527"
      CDS             19..>1506
                      /gene="vp2"
                      /note="NCBI gi: 221890"
                      /codon_start=1
                      /product="VP2"
                      /translation="MTNLSDQTQQIVPFIRSLLMPTTGPASIPDDTLEKHTLRSETST
                      YNLTVGDTGSGLIVFFPGFPGSIVGAHYTLQSNGNYKFDQMLLTAQNLPASYNYCRLV
                      SRSLTVRSSTLPGGVYALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLV
                      GEGVTVLSLPTSYDLGYVRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADNYQFSS
                      QYQTGGVTITLFSANIDAITSLSVGGELVFKTSVQSLVLGATIYLIGFDGTAVITRAV
                      AANNGLTAGIDNLMPFNLVIPTNEITQPITSIKLEIVTSKSDGQAGEQMSWSASGSLA
                      VTIHGGNYPGALRPVTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDP
                      GAMNYTKLILSERDRLGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRA
                      IRRIAVPVVSTLFPPAAPLAHAIGEGVDYLLGDEAQAASGTARAKL"
      misc_feature    1461..1500
                      /note="3'PCR primer N526"
      misc_feature    1501..1506
                      /note="HindIII site downstream of VP2 insert in plasmid
                      pIP201"
 BASE COUNT      405 a    402 c    379 g    320 t
 ORIGIN      large genomic segment A.

Initial Score    =     19  Optimized Score  =     26  Significance =  8.40
Residue Identity =    18%  Matches          =     31  Mismatches   =  118
Gaps             =     18  Conservative Substitutions            =    0
Translation Frame=      1

              X       10        20        30        40               50
              QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGG-------LWRLVLAQR-
                      || |         ||          ||        ||          ||   |
    IDNLMPFNLVIPTNEITQPITSIKLEIVTSKSDGQAGEQMSWSASGSLAVTIHGGNYPGALRPVTLVAYERV
          300 X      310       320       330       340       350       360
```

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        60        70        80        90       100       110       120
    WMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITR-QNFSR
          ||||     |          ||      |         |   |       |     | ||     |
    ATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDP------GAMNYTKLILSERDRLGIKTVWPTREYTDFR
        370       380       390             400       410       420

      130          140       150    X
    CLELQCQPDSSTL---PPPWSPRPLEATAPTAP
              | |             |    |
    EYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPA
  430       440       450       460 X     470
```

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5. US-08-162-407-6 (1-235)
   SCINVE       Yeast gene SUC2 encoding invertase.

 LOCUS       SCINVE       2873 bp    DNA             PLN       12-SEP-1993
 DEFINITION  Yeast gene SUC2 encoding invertase.
 ACCESSION   V01311 K00540
 KEYWORDS    invertase; signal peptide.
 SOURCE      baker's yeast.
   ORGANISM  Saccharomyces cerevisiae
             Eukaryota; Plantae; Thallobionta; Eumycota; Hemiascomycetes;
             Endomycetales; Saccharomycetaceae.
 REFERENCE   1  (bases 1 to 462)
   AUTHORS   Carlson,M., Taussig,R., Kustu,S. and Botstein,D.
   TITLE     The secreted form of invertase in Saccharomyces cerevisiae is
             synthesized from mRNA encoding a signal sequence
   JOURNAL   Mol. Cell. Biol. 3, 439-447 (1983)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 2389)
   AUTHORS   Taussig,R. and Carlson,M.
   TITLE     Nucleotide sequence of the yeast SUC2 gene for invertase
   JOURNAL   Nucleic Acids Res. 11, 1943-1954 (1983)
   STANDARD  full automatic
 REFERENCE   3  (bases 1 to 484)
   AUTHORS   Sarokin,L. and Carlson,M.
   TITLE     Comparison of two yeast invertase genes: conservation of the
             upstream regulatory region
   JOURNAL   Nucleic Acids Res. 13, 6089-6103 (1985)
   STANDARD  full automatic
 REFERENCE   4  (bases 1 to 2873)
   AUTHORS   Sarokin,L. and Carlson,M.
   TITLE     Direct Submission
   JOURNAL   Submitted (14-OCT-1985) to the EMBL/GenBank/DDBJ databases
   STANDARD  full automatic
 COMMENT     NCBI gi: 3833
 FEATURES             Location/Qualifiers
      source          1..2873
                      /organism="Saccharomyces cerevisiae"
      mRNA            745..>2581
                      /note="messenger RNA"
      CDS             785..2383
                      /note="invertase;  NCBI gi: 3834"
                      /codon_start=1
                      /translation="MLLQAFLFLLAGFAAKISASMTNETSDRPLVHFTPNKGWMNDPN
                      GLWYDEKDAKWHLYFQYNPNDTVWGTPLFWGHATSDDLTNWEDQPIAIAPKRNDSGAF
                      SGSMVVDYNNTSGFFNDTIDPRQRCVAIWTYNTPESEEQYISYSLDGGYTFTEYQKNP
                      VLAANSTQFRDPKVFWYEPSQKWIMTAAKSQDYKIEIYSSDDLKSWKLESAFANEGFL
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                      GYQYECPGLIEVPTEQDPSKSYWVMFISINPGAPAGGSFNQYFVGSFNGTHFEAFDNQ
                      SRVVDFGKDYYALQTFFNTDPTYGSALGIAWASNWEYSAFVPTNPWRSSMSLVRKFSL
                      NTEYQANPETELINLKAEPILNISNAGPWSRFATNTTLTKANSYNVDLSNSTGTLEFE
                      LVYAVNTTQTISKSVFADLSLWFKGLEDPEEYLRMGFEVSASSFFLDRGNSKVKFVKE
                      NPYFTNRMSVNNQPFKSENDLSYYKVYGLLDQNILELYFNDGDVVSTNTYFMTTGNAL
                      GSVNMTTGVDNLFYIDKFQVREVK"
      mutation        924
                      /note="mutant suc2-215 (amber)"
 BASE COUNT      855 a    578 c    537 g    903 t
 ORIGIN

Initial Score     =     19  Optimized Score   =     32  Significance =  8.40
Residue Identity =     23%  Matches           =     43  Mismatches   =    97
Gaps              =     46  Conservative Substitutions              =     0
Translation Frame=      1

              X         10        20        30        40        50
              QDCSFQ-HS-PISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL-
                 | | ||   |    |      ||           ||    |     |    ||   ||
    WLHFYXIPKEPCFSCQLHSIQRSKGVLVXTFSKMDYDGCQITRLQNXNLLLXXLEVLEARICICQRRFLRLP
           420       430       440       450       460       470       480

            60        70        80        90       100       110       120
    ---------KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITR-Q
                | |  | ||  |            ||   | || |      ||  |   |       |
    IRMSRFDXSPNXARS-FQILLGHV---------YFYQPRCTCWRFLQPIFCWILQWYSFXSVXQSIXSGRFW
         490        500                510       520       530       540

            130       140                       150    X
    NFSRCL--ELQCQPDSSTLPPPWSPR----------------PLEATAPTAP
        ||   ||  |         | |                | |      |
    XGLLCLANFLQHXP-----NLRFSIRYCLGFKLGVQCLCPNXPMEIIHVFGPQVFFEHXISS
       550            560       570       580       590       600
```

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6. US-08-162-407-6 (1-235)
   ATT13408     1474 Arabidopsis thaliana cDNA clone 39B11T7.

 ID   ATT13408   standard; RNA; EST; 374 BP.
 XX
 AC   T13408;
 XX
 DT   06-MAR-1994 (Rel. 38, Created)
 DT   06-MAR-1994 (Rel. 38, Last updated, Version 1)
 XX
 DE   1474 Arabidopsis thaliana cDNA clone 39B11T7.
 XX
 KW   EST.
 XX
 OS   Arabidopsis thaliana
 OC   Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida;
 OC   Dilleniidae; Capparales; Brassicaceae.
 XX
 RN   [1]
 RP   1-374
 RA   Newman T.;
 RT   ;
 RL   Unpublished.
 XX
 CC   Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
 CC    State University MSU-DOE-PRL, Michigan State University,Plant
 CC    Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168
 CC    Email: 22313tcn@ibm.cl.msu.edu. NCBI gi: 429777
 XX
 FH    Key              Location/Qualifiers
 FH
 FT    source           1..374
 FT                     /organism="Arabidopsis thaliana"
 FT                     /note="Thale cress"
 FT                     /clone="39B11T7"
 FT                     /strain="var columbia"
 XX
 SQ    Sequence 374 BP; 100 A; 75 C; 82 G; 101 T; 16 other;

Initial Score    =     18  Optimized Score  =      26 Significance =  7.84
Residue Identity =    23%  Matches          =      34 Mismatches   =    80
Gaps             =     31  Conservative Substitutions              =     0
Translation Frame=      1

         X  10        20        30        40             50       60
    QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRL----VLAQRWMERLKTVAGSKMQ
         |   |              ||||       |    | |   | |       ||    |
         QRFRI-------------GLLQD----LQWNXXNREQCTLCWPLFXWHWHGQRQSXXLLISXIANGV
         X                    10            20        30        40        50

    70        80           90       100        110         120       130
    GLLERVNTEIHFVTKC---AFQPPPSCLRFVQTNISRL-LQETSEQLVAL--KPWITRQNFSRCLELQCQPD
     ||        |  ||   |       |  |     || |   |  | ||      |   |         |
    LLLTGRIKQEDFXLKCYKKAYKGIDPSLXXV----FRLELVSSSKALQALGXDRNTTLKLFGESCSFFAHPL
            60        70        80            90       100       110

       140       150
    SSTLPPPWSPRPLEAT
    | |
    SNTXXK
   120   X


7. US-08-162-407-6 (1-235)
   T04557          604 Arabidopsis thaliana cDNA clone 39B11T7.

 LOCUS       T04557       374 bp ss-mRNA             EST       14-APR-1993
 DEFINITION  604 Arabidopsis thaliana cDNA clone 39B11T7.
 ACCESSION   T04557
 KEYWORDS    EST.
 SOURCE      Thale cress clone=39B11T7 library=Lambda-PRL2 strain=var columbia
             vector=lambda Zip-Lox Rsite1=Sal Rsite2=Not Lambda PRL2 is a cDNA
             library derived from equal quantities of 4 pools of mRNA.  The mRNA
             sources were 1) 7 day germinated etiolated seedlings; 2) tissue
             culture grown roots; 3) staged plants half with 24 hour light
             cycle, half on 16 hr light, 8 hour dark- rosettes;  4) same plants
             as 3 but aerial tissue (stems, flowers and siliques.  The vector is
             BRL's lambda Zip-Lox.  The cDNA inserts were directionally cloned
             with Sal-Not arms using oligo dT primed cDNA.
   ORGANISM  Arabidopsis thaliana
             Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida;
             Dilleniidae; Capparales; Brassicaceae.
 REFERENCE   1  (bases 1 to 374)
   AUTHORS   Newman,T.
   JOURNAL   Unpublished (1993)
```

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   STANDARD  full automatic
 COMMENT
             Contact: Newman,T.
             MSU-DOE Plant Research Laboratory
             Michigan State University
             MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
             Lansing,Mi
             Tel: 517-353-0854
             Fax: 517-353-9168
             Email: 22313tcn@ibm.cl.msu.edu.

             NCBI gi: 315717
 FEATURES             Location/Qualifiers
      source          1..374
                      /organism="Arabidopsis thaliana"
                      /clone="39B11T7"
                      /strain="var columbia"
                      /note="Thale cress"
 BASE COUNT      100 a      75 c      82 g     101 t      16 others
 ORIGIN

Initial Score    =     18  Optimized Score  =      26 Significance =  7.84
Residue Identity =    23%  Matches          =      34 Mismatches   =    80
Gaps             =     31  Conservative Substitutions              =     0
Translation Frame=      1

         X  10        20        30        40             50       60
    QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRL----VLAQRWMERLKTVAGSKMQ
         |   |              ||||       |    | |   | |       ||    |
         QRFRI-------------GLLQD----LQWNXXNREQCTLCWPLFXWHWHGQRQSXXLLISXIANGV
         X                    10            20        30        40        50

    70        80           90       100        110         120       130
    GLLERVNTEIHFVTKC---AFQPPPSCLRFVQTNISRL-LQETSEQLVAL--KPWITRQNFSRCLELQCQPD
     ||        |  ||   |       |  |     || |   |  | ||      |   |         |
    LLLTGRIKQEDFXLKCYKKAYKGIDPSLXWV----FRLGLVSSSKHLQALGXDRNTTLKLFGESCSFFAHPV
            60        70        80            90       100       110

       140       150
    SSTLPPPWSPRPLEAT
    | |
    STTXCK
   120   X


8. US-08-162-407-6 (1-235)
   SFIURA5A        Sordaria macrospora orotate phosphoribosyl transfe

 LOCUS       SFIURA5A     1246 bp ds-DNA             PLN       16-AUG-1994
 DEFINITION  Sordaria macrospora orotate phosphoribosyl transferase (ura5) gene,
             complete cds.
 ACCESSION   M26957
 KEYWORDS    orotate phosphoribosyl transferase; ura5 gene.
 SOURCE      Sordaria macrospora (strain FGSC 4818) ATCC 60255 DNA.
   ORGANISM  Sordaria macrospora
             Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Sordariales;
             Sordariaceae.
 REFERENCE   1  (bases 1 to 1246)
   AUTHORS   Le Chevanton,L. and Leblon,G.
   TITLE     The ura5 gene of the ascomycete Sordaria macrospora: Molecular
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             cloning, characterization and expression in Escherichia coli
  JOURNAL    Gene 77, 39-49 (1989)
  STANDARD   full automatic
COMMENT      NCBI gi: 341555
FEATURES              Location/Qualifiers
     source           1..1246
                      /organism="Sordaria macrospora"
                      /strain="FGSC 4818"
                      /sequenced_mol="DNA"
                      /tissue_type="ATCC 60255"
     CAAT_signal      199..203
                      /gene="ura5"
                      /note="putative"
     CDS              369..1067
                      /gene="ura5"
                      /note="NCBI gi: 530193"
                      /codon_start=1
                      /product="orotate phosphoribosyl transferase"
                      /translation="MAALRYKADFLKASIDGGVLKFGSFELKSKRISPYFFNAGDFYR
                      ADLLQAISTAYAKCIIEAHKSGQLDFDIVFGPAYKGIPLATAATDKLAQLDPETYGKI
                      CYSFDRKEAKDHGEGGNIVGAPLKGKRILIVDDVITAGTAKREAIAKIEKEGGIVAGI
                      VVALDRMEKLPAADGDDSKPGPSAMVSSARSTAIPIFAILTLDDIIEGMRGLASPEDV
                      KKTEEYRAKYKATD"
     polyA_signal     1086..1091
                      /gene="ura5"
BASE COUNT      279 a    370 c    300 g    297 t
ORIGIN

Initial Score     =     18  Optimized Score  =     31  Significance =  7.84
Residue Identity =     22%  Matches          =     39  Mismatches   =   109
Gaps              =     25  Conservative Substitutions           =     0
Translation Frame=       1

              X       10        20               30            40        50
              QDCSFQHSPISSDFAVKIREL-------SDYLLQDYPV-TVASN---LQDEELCGGLWRLVL
                    | |    ||     |       |   | | ||    ||            | |
    FGIFXPHIFPRGPHRAHRP-MTGFAGLAPXLAHSXPTISLTQLKDFPVXRQESNPSAPPIFYFFLILSRFLP
      30      X 40      50        60        70        80        90

           60         70        80        90       100       110
    AQRWMERLKTVAGS-KMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKP------
    |     |      |     ||         ||      |||      |  |      |    |  |
    AFFQTSRFFLWDPSISFFKLLFFYRQWPLCVTRLISSRPPS------TAASXSSAASSSSPSAFPPTSSTPA
    100       110       120       130             140       150       160

     120       130       140       150    X
    WITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAP
      |    ||   |     || |    |       ||
    TSTVPTSSRPSLLPTPSASSRLTRAASWTLTLSLAPPTRAFPSLPLPPI
        170       180       190       200 X     210

9. US-08-162-407-6 (1-235)
   RATNOSI       Rat nitric oxide synthase mRNA, complete cds.

LOCUS       RATNOSI       3595 bp ss-mRNA          ROD       09-JUN-1993
DEFINITION  Rat nitric oxide synthase mRNA, complete cds.
ACCESSION   L12562
KEYWORDS    nitric oxide synthase.
SOURCE      Rattus norvegicus (strain Sprague-Dawley) adult cDNA to mRNA.
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  ORGANISM  Rattus norvegicus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 3595)
  AUTHORS   Wood,E.R., Berger,H.Jr.., Sherman,P.A. and Lapetina,E.G.
  TITLE     Hepatocytes and macrophages express an identical cytokine inducible
            nitric oxide synthase gene
  JOURNAL   Biochem. Biophys. Res. Commun. (1993) In press
  STANDARD  full automatic
COMMENT     NCBI gi: 310187
FEATURES             Location/Qualifiers
     source          1..3595
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /cell_line="primary culture"
                     /cell_type="hepatocyte"
                     /dev_stage="adult"
                     /sequenced_mol="cDNA to mRNA"
     CDS             103..3546
                     /note="inducible form; putative;  NCBI gi: 310188"
                     /codon_start=1
                     /product="nitric oxide synthase"
                     /translation="MACPWKFLFRVKSYQGDLKEEKDINNNVEKTPGAIPSPTTQDDP
                     KSHKHQNGFPQFLTGTAQNVPESLDKLHVTPSTRPQHVRIKNWGNGEIFHDTLHHKAT
                     SDISCKSKLCMGSIMNSKSLTRGPRDKPTPVEELLPQAIEFINQYYGSFKEAKIEEHL
                     ARLEAVTKEIETTGTYQLTLDELIFATKMAWRNAPRCIGRIQWSNLQVFDARSCSTAS
                     EMFQHICRHILYATNSGNIRSAITVFPQRTDGKHDFRIWNSQLIRYAGYQMPDGTIRG
                     DPATLEFTQLCIDLGWKPRYGRFDVLPLVLQAHGQDPEVFEIPPDLVLEVTMEHPKYE
                     WFQELGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEV
                     GRRMGLETHTLASLWKDRAVTEINAAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRA
                     RGGCPADWIWLVPPVSGSITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQDEKLRPRRR
                     EIRFTVLVKAVFFASVLMRKVMASRVRATVLFATETGKSEALARDLAALFSYAFNTKV
                     VCMEQYKANTLEEEQLPLVVTSTFGNGDCPSNGQTLKKSLFMMKELGHTFRYAVFGLG
                     SSMYPQFCAFAHDIDQKLSHLGASQLAPTGEGDELSGQEDAFRSWAVQTFRAACETFD
                     VRSKHCIQIPKRYTSNATWEPEQYKLTQSPESLDLNKALSSIHAKNVFTMRLKSLQNL
                     QSEKSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGNQTALVQGILERVVDCSSPDQTV
                     CLEVLDESGSYWVKDKRLPPCSLRQALTYFLDITTPPTQLQLHKLARFATEETHRQRL
                     EALCQPSEYNDWKFSNNPTFLEVLEEFPSLRVPAAFLLSQLPILKPRYYSISSSQDHT
                     PSEVHLTVAVVTYRTRDGQGPLHHGVCSTWINNLKPEDPVPCFVRSVSGFQLPEDPSQ
                     PCILIGPGTGIAPFRSFWQQRLHDSQHRGLKGGRMTLVFGCRHRREDHLYQEEMQEMV
                     RKGVLFQVHTGYSRLPGKPKVYVQDILQKELADEVFSVLHGEQGHLYVCGDVRMARDV
                     ATTLKKLVAAKLNLSEEQVEDYFFQLKSQKRYHEDIFGAVFSYGAKKGNTLEEPKGTR
                     L"
BASE COUNT      870 a   1044 c    956 g    725 t
ORIGIN

Initial Score     =     18  Optimized Score  =     35  Significance =  7.84
Residue Identity =     24%  Matches          =     45  Mismatches   =   104
Gaps              =     35  Conservative Substitutions           =     0
Translation Frame=       1

               X       10        20           30        40          50
               QDCSFQHSPISSDFAVKIRELSDYLLQ---DYPVTVASNLQDEELCG--GLWRLVLAQRWME
                |     | |        |  |   ||       |    |  |   |   |    |
     QYKLTQSPESLDLNKALSSIHAKNVFTMRLKSLQNLQSEKSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGN
    740       750       760       770       780       790       800       810

      60        70               80                90        100       110
     RLKTVAGSKMQGLLERV-------NTEIHFV--------TKCAFQPPPSCLRFVQT-NISRLLQETSEQLVA
         |     || ||||        |    |         |    || | ||   |         |  ||
    QTALV-----QGILERVVDCSSPDQTVCLEVLDESGSYWVKDKRLPPCS-LRQALTYFLDITTPPTQLQLHK
                820       830       840        850       860       870

        120       130           140           150    X
    LKPWITRQNFSRCLELQCQP----DSSTLPPPWSPRPLE----ATAPTAP
    |    |       ||  |||    |      |     ||       | |
    LARFATEETHRQRLEALCQPSEYNDWKFSNNPTFLEVLEEFPSLRVPAAFLLSQLPILKP
     880       890       900       910       920     X 930


10. US-08-162-407-6 (1-235)
    RATNWUT      Rat mRNA.

LOCUS       RATNWUT      3614 bp ss-mRNA            ROD       14-JAN-1995
DEFINITION  Rat mRNA.
ACCESSION   D44591
KEYWORDS    .
SOURCE      Rattus norvegicus neutrophil cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 3614)
  AUTHORS   Kosuga,K., Yui,Y., Hattori,R., Sase,K., Eizawa,H., Aoyama,T.,
            Inoue,R. and Sasayama,S.
  TITLE     Cloning of an inducible nitric oxide synthase from rat
            polymorphonuclear neutrophils
  JOURNAL   Endothelium 2, 217-221 (1994)
  STANDARD  full automatic
COMMENT     Submitted (29-Dec-1994) to DDBJ by:
            Kunihiko Kosuga
            Department of Internal Medicine(3rd Division)
            Kyoto University
            54 Kawaracho, Shogoin
            Sakyo-ku
            Kyoto 606-01
            Japan
            Tel:  075-751-3200
            Fax:  075-761-4616.

            NCBI gi: 624916
FEATURES             Location/Qualifiers
     source          1..3614
                     /organism="Rattus norvegicus"
                     /cell_type="neutrophil"
                     /sequenced_mol="cDNA to mRNA"
BASE COUNT      875 a   1056 c    950 g    733 t
ORIGIN

Initial Score     =     18  Optimized Score =      35  Significance =  7.84
Residue Identity =     24%  Matches         =      45  Mismatches   =   104
Gaps             =     35  Conservative Substitutions          =     0
Translation Frame=      1

              X       10        20           30        40          50
              QDCSFQHSPISSDFAVKIRELSDYLLQ---DYPVTVASNLQDEELCG--GLWRLVLAQRWME
               |     | |        |  |   ||       |    |  |   |   |    |
    QYKLTQSPEPLDLNKALSSIHAKNVFTMRLKSLQNLQSEKSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGN
          720 X     730       740       750       760       770       780

     60        70               80                90        100        110
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    RLKTVAGSKMQGLLERV-------NTEIHFV--------TKCAFQPPPSCLRFVQT-NISRLLQETSEQLVA
        |     || ||||        |    |         |    || | ||   |         |  ||
    QTALV-----QGILERVVDCSSPDQTVCLEVLDESGSYWVKDKRLPPCS-LRQALTYFLDITTPPTQLQLHK
             790       800       810       820        830       840

        120       130           140           150    X
    LKPWITRQNFSRCLELQCQP----DSSTLPPPWSPRPLE----ATAPTAP
    |    |       ||  |||    |      |     ||       | |
    LARFATEETHRQRLEALCQPSEYNDWKFSNNPTFLEVLEEFPSLRVPAAFLLSQLPILKP
  850       860       870       880       890       900


11. US-08-162-407-6 (1-235)
    MUSINOSL     Mus musculus nitric oxide synthase (iNOS1) mRNA, c

LOCUS       MUSINOSL     3690 bp ss-mRNA            ROD       24-APR-1992
DEFINITION  Mus musculus nitric oxide synthase (iNOS1) mRNA, complete cds.
ACCESSION   M87039
KEYWORDS    cytosolic protein; nitric oxide synthase.
SOURCE      Mus musculus cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 3690)
  AUTHORS   Xie,Q.-W., Cho,H.J., Calaycay,J., Mumford,R., Swiderek,K.M.,
            Lee,T.B., Ding,A., Troso,T. and Nathan,C.
  TITLE     Cloning and characterization of inducible nitric oxide synthase
            from mouse macrophage
  JOURNAL   Science 256, 225-228 (1992)
  STANDARD  full automatic
COMMENT     NCBI gi: 198406
FEATURES             Location/Qualifiers
     source          1..3690
                     /organism="Mus musculus"
                     /cell_line="RAW 264.7"
                     /cell_type="macrophage"
                     /sequenced_mol="cDNA to mRNA"
     5'UTR           1..255
                     /gene="iNOS1"
     CDS             256..3690
                     /gene="iNOS1"
                     /EC_number="1.14.23"
                     /note="NCBI gi: 198407"
                     /codon_start=1
                     /product="nitric oxide synthase"
                     /translation="MACPWKFLFKVKSYQSDLKEEKDINNNVKKTPCAVLSPTIQDDP
                     KSHQNGSPQLLTGTAQNVPESLDKLHVTSTRPQYVRIKNWGSGEILHDTLHHKATSDF
                     TCKSKSCLGSIMNPKSLTRGPRDKPTPLEELLPHAIEFINQYYGSFKEAKIEEHLARL
                     EAVTKEIETTGTYQLTLDELIFATKMAWRNAPRCIGRIQWSNLQVFDARNCSTAQEMF
                     QHICRHILYATNNGNIRSAITVFPQRSDGKHDFRLWNSQLIRYAGYQMPDGTIRGDAA
                     TLEFTQLCIDLGWKPRYGRFDVLPLVLQADGQDPEVFEIPPDLVLEVTMEHPKYEWFQ
                     ELGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEVGRR
                     MGLETHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGG
                     CPADWIWLVPPVSGSITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQNEKLRPRRREIR
                     FRVLVKVVFFASMLMRKVMASRVRATVLFATETGKSEALARDLATLFSYAFNTKVVCM
                     DQYKASTLEEEQLLLVVTSTFGNGDCPSNGQTLKKSLFMLRELNHTFRYAVFGLGSSM
                     YPQFCAFAHDIDQKLSHLGASQLAPTGEGDELSGQEDAFRSWAVQTFRAACETFDVRS
                     KHHIQIPKRFTSNATWEPQQYRLIQSPEPLDLNRALSSIHAKNVFTMRLKSQQNLQSE
                     KSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGNQTALVQGILERVVDCPTPHQTVCLE
                     VLDESGSYWVKDKRLPPCSLSQALTYFLDITTPPTQLQLHKLARFATDETDRQRLEAL
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                      CQPSEYNDWKFSNNPTFLEVLEEFPSLHVPAAFLLSQLPILKPRYYSISSSQDHTPSE
                      VHLTVAVVTYRTRDGQGPLHHGVCSTWIRNLKPQDPVPCFVRSVSGFQLPEDPSQPCI
                      LIGPGTGIAPFRSFWQQRLHDSQHKGLKGGRMSLVFGCRHPEEDHLYQEEMQEMVRKR
                      VLFQVHTGYSRLPGKPKVYVQDILQKQLANEVLSVLHGEQGHLYICGDVRMARDVATT
                      LKKLVATKLNLSEEQVEDYFFQLKSQKRYHEDIFGAVFSYGAKKGSALEEPKATRL"
 BASE COUNT      893 a   1050 c    979 g    768 t
 ORIGIN

Initial Score    =     18  Optimized Score  =     34  Significance =  7.84
Residue Identity =    22%  Matches          =     42  Mismatches   =   108
Gaps             =     33  Conservative Substitutions           =     0
Translation Frame=      1

              X       10        20           30        40          50
              QDCSFQHSPISSDFAVKIRELSDYLLQ---DYPVTVASNLQDEELCG--GLWRLVLAQRWME
               |     | |        |  |   ||       |    |  |   |   |    |
    QYRLIQSPEPLDLNRALSSIHAKNVFTMRLKSQQNLQSEKSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGN
     790       800       810       820       830       840       850

     60        70           80                    90       100       110
    RLKTVAGSKMQGLLERV---NTEIHFV------------TKCAFQPPPSCLRFVQTNISRLLQETSEQLVAL
        |     || ||||    |    |             |    || |               |  ||  |
    QTALV-----QGILERVVDCPTPHQTVCLEVLDESGSYWVKDKRLPPCSLSQALTYFLDITTPPTQLQLHKL
   860            870       880       890       900       910       920

       120       130           140           150    X
    KPWITRQNFSRCLELQCQP----DSSTLPPPWSPRPLE----ATAPTAP
        |       ||  |||    |      |     ||       | |
    ARFATDETDRQRLEALCQPSEYNDWKFSNNPTFLEVLEEFPSLHVPAAFLLSQLPILKP
      930       940       950       960       970   X   980

12. US-08-162-407-6 (1-235)
    RNU03699     Rattus norvegicus Sprague Dawley inducible nitric

 LOCUS       RNU03699     3943 bp    mRNA            ROD       06-AUG-1994
 DEFINITION  Rattus norvegicus Sprague Dawley inducible nitric oxide synthase
             (NOS) mRNA,  complete cds.
 ACCESSION   U03699
 KEYWORDS    .
 SOURCE      rat.
   ORGANISM  Rattus norvegicus
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Rodentia; Myomorpha; Muridae; Rattus.
 REFERENCE   1  (bases 1 to 3943)
   AUTHORS   Galea,E., Reis,D.J. and Feinstein,D.L.
   TITLE     Cloning and expression of inducible nitric oxide synthase from rat
             astrocytes
   JOURNAL   J. Neurosci. Res. 37, 406-414 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 3943)
   AUTHORS   Feinstein,D.L.
   TITLE     Direct Submission
   JOURNAL   Submitted (23-NOV-1993) Douglas L. Feinstein, Neurobiology, Cornell
             University Medical College, 411 East 69th Street, New York, NY
             10021, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 430718
 FEATURES             Location/Qualifiers
      source          1..3943
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                      /clone="pAstNOS1-4"
                      /clone_lib="Lambda Zap II-LPS treated astrocytes"
                      /strain="Sprague Dawley"
                      /organism="Rattus norvegicus"
                      /tissue_type="astrocytes"
      mRNA            1..3939
      CDS             4..3447
                      /standard_name="NOS"
                      /note="NCBI gi: 430719"
                      /codon_start=1
                      /product="nitric oxide synthase"
                      /translation="MACPWKFLFRVKSYQGDLKEEKDINNNVEKTPGAIPSPTTQDDP
                      KSHKHQNGFPQFLTGTAQNVPESLDKLHVTPSTRPQHVRIKNWGNGEIFHDTLHHKAT
                      SDISRKSKLCMGSIMNSKSLTRGPRDKHTPVEELLPQAIEFINQYYGSFKEAKIEEHL
                      ARLEAVTKEIETTGTYQLTLDELIFATKMAWRNAPRCIGRIQWSNLQVFDARSCSTAS
                      EMFQHICRHILYATNSGNIRSAITVFPQRTDGKHDFRIWNSQLIRIAGYQMPDGTIRG
                      EPATLEFTQLCIDLGWKPRYGRFDVLPLVLQAHGQDPEVFEIPPDLVLEVTMEHPKYE
                      WFQELGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEV
                      GRRMGLETHTLASLWKDRAATEINAAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRA
                      RGGCPADWIWLVPPVSGSITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQDEKLRPRRR
                      EIRFTVLVKAVFFASVLMRKVMASRVRATVLFATETGKSEALARDLAALFSYAFNTKV
                      VCMEQYKANTLEEEQLLLVVTSTFGNGDCPSNGQTLKKSLFMMKELGHTFRYAVFGLG
                      SSMYPQFCAFAHDIDQKLSHLGASQLAPTGEGDELSGQEDAFRSWAVQTFRAACETFD
                      VRSKHCIQIPKRYTSNATWEPEQYKLTQSPESLDLNKALSSIHAKNVFTMRLKSLQNL
                      QSEKSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGNQTGLVQGILERVVDCSSPDQTV
                      CLEVLDESGSYWVKDKRLPPCSLRQALTYFLDITTPPTQLQLHKLARFATEETHRQRL
                      EALCQPSEYNDWKFSNNPTFLEVLEEFPSLRVPAAFLLSQLPILKPRYYSISSSLDHT
                      PSEVHLTVAVVTYRTRDGQGPLHHGVCSTWINNLKPEDPVPCFVRSVSGFQLPEDPSQ
                      PCILIGPGTGIAPFRSFWQQRLHDSQHRGLKGGRMTLVFGCRHPEEDHLYQEEMQEMV
                      RKGVLFQVHTGYSRLPGKPKVYVQDILQKELADEVFSVLHGEQGHLYVCGDVRMARDV
                      ATTLKKLVAAKLNLSEEQVEDYFFQLKSQKRYHEDIFGAVFSYGAKKGNTLEEPKGTR
                      L"
      3'UTR           3448..3939
      polyA_signal    one-of(3474..3479,3902..3907)
      misc_signal     one-of(3769,3792,3804,3878)
                      /function="cis-regulation of mRNA stability"
      polyA_site      3943
 BASE COUNT      949 a   1154 c   1001 g    839 t
 ORIGIN

Initial Score    =     18  Optimized Score  =     35  Significance =  7.84
Residue Identity =    24%  Matches          =     45  Mismatches   =   104
Gaps             =     35  Conservative Substitutions           =     0
Translation Frame=      1

              X       10        20           30        40          50
              QDCSFQHSPISSDFAVKIRELSDYLLQ---DYPVTVASNLQDEELCG--GLWRLVLAQRWME
               |     | |        |  |   ||       |    |  |   |   |    |
    QYKLTQSPESLDLNKALSSIHAKNVFTMRLKSLQNLQSEKSSRTTLLVQLTFEGSRGPSYLPGEHLGIFPGN
      710     X 720       730       740       750       760       770

     60        70               80                90        100       110
    RLKTVAGSKMQGLLERV-------NTEIHFV--------TKCAFQPPPSCLRFVQT-NISRLLQETSEQLVA
        |     || ||||        |    |         |    || | ||   |         |  ||
    QTGLV-----QGILERVVDCSSPDQTVCLEVLDESGSYWVKDKRLPPCS-LRQALTYFLDITTPPTQLQLHK
    780            790       800       810       820        830       840

        120       130           140           150    X
    LKPWITRQNFSRCLELQCQP----DSSTLPPPWSPRPLE----ATAPTAP
    |    |       ||  |||    |      |     ||       | |
    LARFATEETHRQRLEALCQPSEYNDWKFSNNPTFLEVLEEFPSLRVPAAFLLSQLPILKP
        850       860       870       880       890  X    900


13. US-08-162-407-6 (1-235)
    MUSRGEETS    Mouse 18S ribosomal RNA gene 5' end, and 5' extern

 LOCUS       MUSRGEETS    4194 bp ds-DNA            ROD       15-JUN-1989
 DEFINITION  Mouse 18S ribosomal RNA gene 5' end, and 5' external transcribed
             spacer (5'ETS).
 ACCESSION   M20154
 KEYWORDS    18S ribosomal RNA; external transcribed spacer.
 SOURCE      Mouse DNA.
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 4194)
   AUTHORS   Bourbon,H.-M.M., Michot,B., Hassouna,N., Feliu,J. and
             Bachellerie,J.-P.P.
   TITLE     Sequence and secondary structure of the 5' external transcribed
             spacer of mouse pre-rRNA
   JOURNAL   DNA 7, 181-191 (1988)
   STANDARD  full automatic
 COMMENT     NCBI gi: 200733
 FEATURES             Location/Qualifiers
      source          1..4194
                      /organism="Mus musculus"
      rRNA            4175..>4194
                      /note="18S ribosomal RNA"
 BASE COUNT      375 a   1373 c   1375 g   1071 t
 ORIGIN

Initial Score     =      18 Optimized Score  =      30 Significance =  7.84
Residue Identity  =     24% Matches          =      38 Mismatches   =    98
Gaps              =      22 Conservative Substitutions              =     0
Translation Frame=       1

              X       10         20        30         40        50        60
              QDCSFQHSPIS-SDFAVKIRELSDYLLQDYP-VTVASNLQDEELCGGLWRLVLAQRWMERLK
                |    |  | |      | |        |   |   |    |   |   |   |  ||
    RCIPFPSGVCTRCFLXASRCSWSVPGLSPRCLLLSWWWRSPFPGVPPVL---RLAVCLPVCVXEAR--ERGV
           390       400       410       420          430       440

            70        80        90       100       110       120       130
    TVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQ
             || ||         ||          |     ||       |  |     |        ||
    EERRRGKTPLLRRVRRPPRDXYACAXGWCXAVAAGVGKFLERLIAFPWGALRGLAFGGDR--------LQ--
    450       460       470       480       490       500

         140        150    X
    PDSSTLPPPWSPR-PLEATAPTAP
         || |   | |||   | |
    ----GLPCPRMLRMPLEENLPVAADPPARSPACW
      510       520       530


14. US-08-162-407-6 (1-235)
    T35584       EST87799 Homo sapiens cDNA 5' end similar to None.

 LOCUS       T35584       319 bp ss-mRNA            EST       04-JAN-1995
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 DEFINITION  EST87799 Homo sapiens cDNA 5' end similar to None..
 ACCESSION   T35584
 KEYWORDS    EST.
 SOURCE      human library=Human Lung primer=M13 Reverse.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 319)
   AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
             Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
             White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
             Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
             FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
             Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,
             Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
             Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T.,
             Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
             Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
             Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
             Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
             Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
             Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
             Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
             Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
             Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
   TITLE     Initial Assessment of Human Gene Diversity and Expression Patterns
             Based Upon 52 Million Basepairs of cDNA Sequence
   JOURNAL   Unpublished (1995)
   STANDARD  full automatic
 COMMENT     Other_ESTs: THC9516
             Contact: Venter, JC
             The Institute for Genomic Research
             932 Clopper Rd, Gaithersburg, MD 20878
             Tel: 3018699056
             Fax: 3018699423
             Email: tdbinfo@tdb.tigr.org
             For clone availability, additional sequence and expression
             information related to this EST, please contact the TIGR Database
             (tdbinfo@tdb.tigr.org).

             NCBI gi: 617682
 FEATURES             Location/Qualifiers
      source          1..319
                      /organism="Homo sapiens"
                      /note="human"
 BASE COUNT       73 a     97 c     89 g     58 t      2 others
 ORIGIN

Initial Score     =      17 Optimized Score  =      23 Significance =  7.28
Residue Identity  =     25% Matches          =      28 Mismatches   =    74
Gaps              =       6 Conservative Substitutions              =     0
Translation Frame=       1

    X        10        20         30          40        50        60
    QDCSFQHS-PISSDFAVKIRELSDY-LLQDYPVTVASNL--QDEELCGGLWRLVLAQRWMERLKTVAGSKMQ
        |  | |     ||       |  |         ||    ||| | |  |||              | |
    GAAGFSSSGPAATSGAVLQAATGMYEQLKGEWNRKSPNLSKCGEEL-GRL-KLVLLELNFLPTTGTKLTKQQ
    X       10        20        30        40           50        60        70

    70        80        90       100   X   110
    GLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVAL
      | |   ||           ||  |        ||
    LILARNILEIGAQWSILRKDIPSFERYMAQLKCLLL
            80        90       100     X


15. US-08-162-407-6 (1-235)
    CHKRERYF1    Chicken erythroid-specific transcription factor er

 LOCUS       CHKRERYF1    1068 bp ss-mRNA            VRT       15-DEC-1989
 DEFINITION  Chicken erythroid-specific transcription factor eryf1 mRNA,
             complete cds.
 ACCESSION   M26209
 KEYWORDS    DNA-binding transcription factor; globin.
 SOURCE      Chicken (White Leghorn) 9 day embryonic blood, cDNA to mRNA, clone
             E120-1.
   ORGANISM  Gallus gallus
             Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
             Neognathae; Galliformes; Phasianidae.
 REFERENCE   1  (bases 1 to 1068)
   AUTHORS   Evans,T. and Felsenfeld,G.
   TITLE     The erythroid-specific transcription factor Eryf1: A new finger
             protein
   JOURNAL   Cell 58, 877-885 (1989)
   STANDARD  full automatic
 COMMENT     Draft entry and computer-readable sequence for [1] kindly submitted
             by T.R.Evans, 17-JUL-1989.

             NCBI gi: 212628
 FEATURES             Location/Qualifiers
      source          1..1068
                      /organism="Gallus gallus"
      CDS             41..955
                      /note="Eryf1 protein;  NCBI gi: 212629"
                      /codon_start=1
                      /translation="MEFVALGGPDAGSPTPFPDEAGAFLGLGGGERTEAGGLLASYPP
                      SGRVSLVPWADTGTLGTPQWVPPATQMEPPHYLELLQPPRGSPPHPSSGPLLPLSSGP
                      PPCEARECVNCGATATPLWRRDGTGHYLCNACGLYHRLNGQNRPLIRPKKRLLVSKRA
                      GTVCSNCQTSTTTLWRRSPMGDPVCNACGLYYKLHQVNRPLTMRKDGIQTRNRKVSSK
                      GKKRRPPGGGNPSATAGGGAPMGGGGDPSMPPPPPPPAAAPPQSDALYALGPVVLSGH
                      FLPFGNSGGFFGGGAGGYTAPPGLSPQI"
 BASE COUNT      206 a    371 c    342 g    149 t
 ORIGIN

Initial Score     =     17  Optimized Score =     31  Significance =  7.28
Residue Identity =     24%  Matches         =     42  Mismatches   =    86
Gaps             =     45  Conservative Substitutions     =     0
Translation Frame=      1

              X        10           20        30        40        50
              QDCSFQHS-PISS---DFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMER
                |   || |  |     |   ||       |     |         | |  |
    PPHGVRGAGGAGCGLPHSVPXXSRSLPGAGGGRE-------DGGGGAA---------GLLPPLRPRVPGAVG
           20 X      30        40               50                 60

    60        70        80           90       100       110         120
    LKTVAGSKMQGLLERVNTEIHFVTKCA---FQPPPSCLRFVQTNISRLLQETSEQLVA--LKPWITRQNFS-
         |    |     |         |    ||||| ||            |  |  |  |     ||  |
    RHGYFGDPPVGAARHPNGAPPLPGAAATPPGQPPPSLLR----------APTATQQRAPTLRGPXVRQLRSD
     70       80        90       100                 110       120
```

```
               130       140       150    X
    --------RCLELQCQPDSSTLPPPWSPRPLEATAPTAP
            |   |  |     ||||  | |       ||
    GNAAVAPGRHRALPVQ-RLRALPPPQRPEPPAHPPQKAPAGEXARRHSV
  130       140        150       160       170
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file sq6nsqna.res made by  on Wed 5 Apr 95 18:27:19-PDT.


Query sequence being compared:US-08-162-407-6 (1-235)
Number of sequences searched:                 57621
Number of scores above cutoff:                 4182

      Results of the initial comparison of US-08-162-407-6 (1-235) with:
   Data bank : N-GeneSeq 17, all entries

100000-
      -
N     -
U50000-
M     -
B     -     *
E     -
R     -
      -
O     -
F10000-
      -         *
S     -            *  *
E 5000-                  *
Q     -
U     *
E     -                     *
N     -
C     -
E     -                        *
S 1000-
      -                            *
      -
   500-  *
      -
      -                               *
      -
      -
      -
      -                                   *
   100-
      -
      -
    50-                                      *
      -
      -
      -                                         *   *
      -
      -
      -
    10-                                                 *
      -
      -
     5-
      -
      -
      -                                                              *
      -
      -
     0----------------------------------------------------------------------
      ||     |   |  |  |   |  |   |  |   |  |   | |    | |    | |    |
SCORE 0|     2   |  4  |   6  |   8  |  11  |  13 |   15 |   17 |   19
STDEV -1     0   1     2      3      4      5     6      7      8

                              PARAMETERS

Similarity matrix       Unitary    K-tuple                        2
Translation Frame             1
Mismatch penalty              1    Joining penalty               20
Gap penalty                1.00    Window size                   32
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

Initial scores to save       45    Alignments to save        15
Optimized scores to save      0    Display context           10

                              SEARCH STATISTICS

Scores:                  Mean        Median       Standard Deviation
                           3            3              2.00

Times:                    CPU                     Total Elapsed
                      00:01:15.09                 00:01:16.00

Number of residues:                  8098565
Number of sequences searched:          57621
Number of scores above cutoff:          4182

Cut-off raised to 2.
Cut-off raised to 3.
Cut-off raised to 4.
Cut-off raised to 5.
Cut-off raised to 6.
Cut-off raised to 7.
Cut-off raised to 8.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name      Description                    Length Score Score  Sig. Frame
---------------------------------------------------------------------------------
                     ****  8 standard deviations above mean ****
   1. Q14896        E/DEL-2 clone .                  490   19    26   8.01   1
   2. Q45441        Sequence of wild type Delawar   1060   19    26   8.01   1
                     ****  6 standard deviations above mean ****
   3. Q26710        Gene regulating lipase expres    282   15    24   6.01   1
   4. Q10571        Lipase modulating factor gene    344   15    27   6.01   1
   5. Q05980        Sequence encoding Aleuria aur    456   15    28   6.01   1
   6. Q44282        Lipase/lipase modulator fusio    706   15    27   6.01   1
   7. Q06332        Murine IL-2R beta chain.         768   15    28   6.01   1
   8. Q05873        Sequence encoding murine inte    768   15    29   6.01   1
   9. Q41331        pMV206 - cassette contg. seq'   1373   15    31   6.01   1
  10. Q57710        Neurocan DNA.                   1730   15    30   6.01   1
                     ****  5 standard deviations above mean ****
  11. N80626        Bovine Bone Morphogenic Prote    137   14    20   5.51   1
  12. N92199        Region of clone bP-819 which     137   14    20   5.51   1
  13. N81258        Encodes recombinant human pre    293   14    26   5.51   1
  14. N71341        Sequence encoding rotavirus i    452   14    27   5.51   1
  15. N90612        CD19 cDNA.                       640   14    31   5.51   1
  16. Q12071        T-PA with -ve charged finger     699   14    31   5.51   1
  17. Q38723        AII/AVPv2 receptor coding seq    750   14    34   5.51   1
  18. Q04339        Aquaricine I gene                757   14    17   5.51   1
  19. Q53061        Human thyroid peroxidase.       1016   14    21   5.51   1
  20. N90606        piH3M vector (ATCC 67,633) DN   1117   14    30   5.51   1
  21. Q06313        Sequence of plasmid p267BGL.    1142   14    29   5.51   1
  22. Q21166        Expression vector piH3M.        1300   14    30   5.51   1
  23. Q06312        Sequence of plasmid p264BGL.    1326   14    29   5.51   1
  24. Q05397        Secretion Vector pSEC-BP1 enc   1396   14    31   5.51   1
  25. Q46823        pLISC-SE vector.                1505   14    31   5.51   1
  26. Q51730        Plasmid pRK5.1 for huHGF site   1577   14    31   5.51   1
  27. Q05590        Insert sequence encoding sign   1698   14    30   5.51   1
  28. Q20732        pAD-CMV19 expression vector.    2020   14    30   5.51   1
  29. Q20765        pAD-CMV19.                      2020   14    30   5.51   1
  30. Q20733        pAD-CMV1 expression vector.     2138   14    30   5.51   1
  31. Q20766        pAD-CMV1.                       2138   14    30   5.51   1
  32. Q06283        pAD-CMV1 contg. a Tumour Necr   2138   14    30   5.51   1
  33. N70996        Sequence encoding N-terminal    2749   14    30   5.51   1
  34. Q55003        Humanised anti-CD18 Ab 60.3 v   3067   14    29   5.51   1
  35. Q20907        DNA encoding the chimeric pro   3143   14    30   5.51   1
  36. Q60158        Human brain Expressed Sequenc     88   13    22   5.01   1
  37. N90627        Sequence encoding PB1rf HIV f    229   13    30   5.01   1
  38. N81409        Beta chain gene of DP antigen    368   13    32   5.01   1
  39. N80251        H-env probe for detection of     410   13    28   5.01   1
  40. N70693        N-myc 1 proto-oncogene C-term    428   13    22   5.01   1
  41. Q04459        N-myc 1 clone                    428   13    22   5.01   1
  42. N70450        Rotavirus SA-11 gene 6.          452   13    26   5.01   1
  43. N90416        DNA sequence encoding methylt    626   13    27   5.01   1
  44. Q47790        Bilirubin oxidase gene.          653   13    30   5.01   1
  45. Q26657        glut4 promoter/enhancer .        773   13    28   5.01   1


1. US-08-162-407-6 (1-235)
   Q14896        E/DEL-2 clone .

  ID   Q14896 standard; DNA; 1471 BP.
  AC   Q14896;
  DT   24-FEB-1992  (first entry)
  DE   E/DEL-2 clone .
```

```
 KW   Infectious bursal disease virus; IBDV; vaccine; poultry; ss.
 OS   Chicken infectious bursal disease virus.
 FH   Key             Location/Qualifiers
 FT   CDS             19..1470
 FT   /*tag=  a
 FT   /note= "polypeptide encoded by E/DEL-2 clone"
 PN   WO9116925-A.
 PD   14-NOV-1991.
 PF   30-APR-1991;  U03056.
 PR   04-MAY-1990;  US-519202.
 PA   (UYMA-) UNIV MARYLAND COL.
 PI   Vakharia V.
 DR   WPI; 91-353531/48.
 DR   P-PSDB; R15053.
 PT   Infectious bursal disease virus nucleic acids - useful as
 PT   vaccines against IBDV in poultry
 PS   Example; Page 28; 45pp; English.
 CC   The sequence is that of a clone of variant Delaware type E of
 CC   infectious bursal disease virus (IBDV). It can be used in broad
 CC   spectrum IBDV poultry vaccines, administration is ophthalmically,
 CC   by injection, nasally or orally, at any time after hatching and as a
 CC   booster at other times. Poultry treated include chickens, roosters,
 CC   broilers, roasters, breeders, layers, turkeys and ducks. See also
 CC   Q14897.
 SQ   Sequence   1471 BP;    403 A;    389 C;    366 G;    313 T;

Initial Score    =     19  Optimized Score  =     26  Significance =  8.01
Residue Identity =    20%  Matches          =     34  Mismatches   =   113
Gaps             =     22  Conservative Substitutions            =     0
Translation Frame=      1

              X       10        20        30        40               50
              QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGG-------LWRLVLAQR-
                      || |         ||          ||        ||          ||   |
    IDNLMPFNLVIPTNEITQPITSIKLEIVTSKSDGQAGEQMSWSASGSLAVTIHGGNYPGALRPVTLVAYERV
         310  X    320       330       340       350       360       370

        60        70        80        90       100        110        120
    WMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRL-LQETSEQLVALK-PWITR-QNF
          ||||     |          ||      |         |   | | |     |  |  | ||
    ATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDP------GAMNYTKLILSE--RDRVGIKTVWPTREYTD
       380       390       400             410       420         430

        130          140       150    X
    SRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP
     |          | |             |    |
    FREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPA
   440       450       460       470  X    480

2. US-08-162-407-6 (1-235)
   Q45441          Sequence of wild type Delaware infectious bursal d

 ID   Q45441 standard; DNA; 3180 BP.
 AC   Q45441;
 DT   07-OCT-1994  (first entry)
 DE   Sequence of wild type Delaware infectious bursal disease virus
 DE   (IBDV).
 KW   Infectious bursal disease virus; IBDV; vaccine; monoclonal antibody
 KW   Mab 67; assay; ss.
```

```
 OS   Delaware infectious bursal disease virus.
 FH   Key             Location/Qualifiers
 FT   CDS             64..3102
 FT   /*tag=  a
 PN   WO9406475-A.
 PD   31-MAR-1994.
 PF   01-SEP-1993;  U08033.
 PR   15-SEP-1992;  US-944525.
 PA   (UYMA-) UNIV MARYLAND BALTIMORE.
 PI   Luetticken HD,  Snyder DB,  Vakharia V;
 DR   WPI; 94-118171/14.
 DR   P-PSDB; R51171.
 PT   Attenuated live vaccine for Delaware strain infectious bursal
 PT   disease virus - is produced by screening with a monoclonal
 PT   antibody and used for immunising poultry against IBDV
 PS   Claim 9; Fig 1A-1K; 24pp; English.
 CC   The applicants have developed a Mab, designated Mab 67, which
 CC   neutralises wild-type Delaware strain IBDV. It was developed
 CC   according to the method set forth in US Patent 4,956,452. The
 CC   hybridoma cell line expressing Mab 67 has been deposited under ATCC-
 CC   HB111222. Bps 1-1404 of Q45441 is the nucleotide sequence of the
 CC   gene responsible for the expression of Delaware IBDV structural
 CC   protein(s) recognised by Mab 67. Mab 67 can be used in an assay to
 CC   determine the presence of Delaware type IBDV and can be employed to
 CC   prepare a vaccine conferring challenge protection against Delaware-
 CC   type IBDV.
 SQ   Sequence   3180 BP;    864 A;    880 C;    822 G;    614 T;

Initial Score    =     19  Optimized Score  =     26  Significance =  8.01
Residue Identity =    18%  Matches          =     31  Mismatches   =   118
Gaps             =     18  Conservative Substitutions            =     0
Translation Frame=      1

              X       10        20        30        40               50
              QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGG-------LWRLVLAQR-
                      || |         ||          ||        ||          ||   |
    IDNLMPFNLVIPTNEITQPITSIILEIVTSKSDGQAGEQMSWSASGSLAVTIHGGNYPGALRPVTLVAYERV
     310       320       330       340       350       360       370

        60        70        80        90       100       110       120
    WMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITR-QNFSR
          ||||     |          ||      |         |   |       |     | ||     |
    ATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDP------GAMNYTKLILSERDHLGIKTVWPTREYTDFR
   380       390       400       410             420       430       440

      130          140       150    X
    CLELQCQPDSSTL---PPPWSPRPLEATAPTAP
              | |             |    |
    EYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPA
       450       460       470       480

3. US-08-162-407-6 (1-235)
   Q26710          Gene regulating lipase expression.

 ID   Q26710 standard; DNA; 846 BP.
 AC   Q26710;
 DT   18-JAN-1993  (first entry)
 DE   Gene regulating lipase expression.
 KW   Fatty acid; fat; oil; ester; detergents; ss.
 OS   Pseudomonas.
 PN   J04169184-A.
 PD   17-JUN-1992.
 PF   31-OCT-1990; 294558.
 PR   31-OCT-1990; JP-294558.
 PA   (KURK ) KURITA WATER IND LTD.
 DR   WPI; 92-253390/31.
 DR   P-PSDB; R25719.
 PT   Gene regulating expression of lipase - useful in prodn. of fatty
 PT   acid from fats and fatty oils, prodn. of ester and addn. to
 PT   detergents
 PS   Claim 1; Fig 3; 9pp; Japanese.
 CC   The gene regulating lipase expression was obtd. from a Pseudomonas
 CC   clone, esp. from Pseudomonas KWI-56(FERM P-9659).  Lipase is useful
 CC   for the prodn. of fatty acid from fats and oils, the prodn. of
 CC   esters, and for addition to biological detergents.  Transformants
 CC   contg. the lipase structural gene together with its regulatory gene
 CC   can be used to produce 20-300 times greater lipase activity than
 CC   transformants contg. the lipase structural gene alone.
 SQ   Sequence   846 BP;    141 A;    296 C;    302 G;    107 T;

Initial Score     =    15  Optimized Score   =     24  Significance =  6.01
Residue Identity  =   24%  Matches           =     32  Mismatches   =    77
Gaps              =    22  Conservative Substitutions          =     0
Translation Frame=      1

           30 X      40        50        60        70        80         90
    SDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKC-AFQPPPS-
                ||         ||    ||     ||   ||    | |        |   |   |   |
              VPAS--------TGL-PPSLAGSSAPRLPLDAG----GHLAKSRAVRDFFDYCLTAQSDLSA
              X                10        20            30        40

            100       110          120       130       140       150    X
    --CLRFVQTNISRLLQETSEQLVALKPW---ITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAP
         ||   |   |  |  |  ||  |            |      | | |        |   |  |
    AGLDAFVMREIAAQLDGTVAQAEALDVWHRYRAYLDALAKLRDAGAADKSDL--GALQLALDQRASIAYRTL
   50        60        70        80        90       100         110     X

    GDWSQPF
  120


4. US-08-162-407-6 (1-235)
   Q10571       Lipase modulating factor gene, lim.

 ID   Q10571 standard; DNA; 1032 BP.
 AC   Q10571;
 DT   15-APR-1991  (first entry)
 DE   Lipase modulating factor gene, lim.
 KW   Food; detergent; ss.
 OS   Pseudomonas cepacia SB10.
 PN   WO9100908-A.
 PD   24-JAN-1991.
 PF   24-JAN-1991; DK0170.
 PR   07-JUL-1989; DK-003368.
 PA   (NOVO ) NOVO NORDISK A/S.
 PI   Jorgensen S;
 DR   WPI; 91-051335/07.
 DR   P-PSDB; R10864.
 PT   DNA encoding lipase modulating factor acting in trans - used in
```

```
 PT   prodn. of lipase derived from Pseudomonas cepacia, for increased
 PT   prodn. of lipase.
 PS   Claim 4; Fig 1; 57pp; English.
 CC   The lim gene encodes a lipase modulating factor which acts in trans
 CC   to modulate prodn. of P.cepacia lipase.  It is used to improve prodn.
 CC   of recombinant lipase for use in e.g. the food industry or in
 CC   detergents.    Chromosomal DNA from P. cepacia SB10 was used to
 CC   prepare a library in phage lambda.   A positive phage, SJ150 was
 CC   found to harbour plasmid pSJ150 contg. 6 kb of the lipase gene and
 CC   the lipase modulating gene.  Sequencing showed that the codon TCG
 CC   separates the lim start codon (ATG) from the lipase stop codon (TAA).
 CC   See also Q10573.
 SQ   Sequence   1032 BP;    150 A;    357 C;    401 G;    124 T;

Initial Score     =    15  Optimized Score   =     27  Significance =  6.01
Residue Identity  =   20%  Matches           =     33  Mismatches   =   114
Gaps              =    15  Conservative Substitutions          =     0
Translation Frame=      1

              X       10        20        30        40        50        60
              QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTV
                                 |  |      |   |   |            ||     ||
    VYGAVGLAAIAGVAMWSGAGRHGGTGASGEPPDASAARGP--AAAPPQAAVPASTSLPPSLAGSSAPRLPLD
       20     X  30        40        50          60        70        80

          70        80         90          100       110          120
    AGSKMQGLLERVNTEIHFVTKC-AFQPPPS---CLRFVQTNISRLLQETSEQLVALKPW---ITRQNFSRCL
    ||    | |        |   |   |   |      ||   |   |  |  |  ||  |            |
    AG----GHLAKARAVRDFFDYCLTAQSDLSAAGLDAFVMREIAAQLDGTVAQAEALDVWHRYRAYLDALAKL
           90       100       110       120       130       140       150

    130       140       150    X
    ELQCQPDSSTLPPPWSPRPLEATAPTAP
          | | |        |   |  |
    RDAGAVDKSDL--GALQLALDQRASIAYRWLGDWSQPF
        160         170       180


5. US-08-162-407-6 (1-235)
   Q05980       Sequence encoding Aleuria aurantia lectin.

 ID   Q05980 standard; cDNA; 1370 BP.
 AC   Q05980;
 DT   14-JAN-1991  (first entry)
 DE   Sequence encoding Aleuria aurantia lectin.
 KW   Lectin; cancer; sugar chains; ss.
 OS   Aleuria aurantia.
 FH   Key             Location/Qualifiers
 FT   CDS             80..1021
 FT   /*tag=  a
 FT   /label=A.aurantia lectin
 PN   EP-387861-A.
 PD   19-SEP-1990.
 PF   14-MAR-1990; 104854.
 PR   14-MAR-1989; JP-061280.
 PA   (NICH-) NICHIREI CORP.
 PI   Kobata A, Kochibe N, Fukumori F, Takeuchi N;
 DR   WPI; 90-284100/38.
 DR   P-PSDB; R06870.
 PT   Cloned cDNA encoding Aleuria aurantia lectin - used for producing
PT   lectin for diagnosing cancer or sepg. or analysing sugar chains
PS   Disclosure; fig 1; 15pp; English.
CC   This cDNA encodes A.aurantia lectin which has a binding affinity
CC   for fucosyl linkages.  It recognises the change of oligosaccharide
CC   chains in cell surface glycoproteins and hence can be used as a
CC   diagnostic agent for e.g. cancer, where the oligosaccharide chains
CC   are modified.  It can also be used for sepg. or analysing various
CC   sugar chains.
SQ   Sequence   1370 BP;    312 A;    365 C;    373 G;    320 T;

Initial Score     =     15  Optimized Score   =     28  Significance =  6.01
Residue Identity =    22%  Matches           =     39  Mismatches   =    91
Gaps              =     47  Conservative Substitutions              =     0
Translation Frame=      1

          X        10        20        30        40        50        60
          QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTV
            |       ||     |        | |   ||  |   || |    |         |  |
LLAERXGGIVRGCLWRFMEHSSSDQGRI--------QAY-ALVARHLYCCELLGEHRHLCVLPSXRRLLAAV
   260    X  270       280               290       300       310

      70                      80        90       100           110
AGSKMQGLLER-----------VN---TEIHFVTKCAFQPPPSCLRFVQTNISRL----LQETSEQLVALKP
|    |||  |           ||      | |       | |  |      |||             | |
AMDLRQGLVHRRGCSHWHSRGMVNGDQIRPHGV-------PTSVRRERLRHVSRLFYFCFLFSPYHAYAEK-
320       330       340       350              360       370       380

 120          130       140       150   X
WITRQNFSRCLEL----QCQPDSSTLPPPWSPRPLEATAPTAP
        | | |     |      |   |          |
------DGRKLSLFIWFICCVYGDFL--GWRSQGFFSVLGTWFILRLSLPWHT
            390       400          410     X 420


6. US-08-162-407-6 (1-235)
   Q44282        Lipase/lipase modulator fusion gene.

ID   Q44282 standard; DNA; 2118 BP.
AC   Q44282;
DT   09-DEC-1993  (first entry)
DE   Lipase/lipase modulator fusion gene.
KW   Lipase; LipA; LipD; lipase modulator; LimA; LimD; renaturation;
KW   chaperone molecule; lipolysis; detergent; denaturation; ss.
OS   Pseudomonas cepacia.
PN   WO9313200-A.
PD   08-JUL-1993.
PF   18-DEC-1992; DK0391.
PR   20-DEC-1991; WO-DK0402.
PA   (NOVO ) NOVO-NORDISK AS.
PI   Buckley CM,  Diderichsen BK,  Hobson A,  Joergensen ST;
PI   McConnell DJ;
DR   WPI; 93-227318/28.
PT   Prepn. of active lipase in high quantities - by subjecting to
PT   denaturation and restructuring in presence of chaperone molecule
PS   Claim 26; Page 47-48; 78pp; English.
CC   A DNA construct is claimed comprising a lipase coding sequence
CC   fused to a sequence coding for a chaperone molecule. One fusion
CC   construct is specifically claimed where the lip and lim coding
CC   sequences are both from Pseudomonas cepacia. The SEQ ID number for
CC   the specifically claimed fusion does not correspond to a nucleotide
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CC   sequence so Q44282 (the only fusion gene sequence in the
CC   specification) is taken to be the intended fusion gene. Production
CC   of active lipase is enhanced by denaturation followed by
CC   renaturation in the presence of a lipase modulator chaperone
CC   protein.
SQ   Sequence   2118 BP;    336 A;    718 C;    772 G;    292 T;

Initial Score     =     15  Optimized Score   =     27  Significance =  6.01
Residue Identity =    20%  Matches           =     33  Mismatches   =   114
Gaps              =     15  Conservative Substitutions              =     0
Translation Frame=      1

          X        10        20        30        40        50        60
          QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTV
                             |  |      |   |   |            ||     ||
VYGAVGLAAIAGVAMWSGAGRHGGTGASGEPPDASAARGP--AAAPPQAAVPASTSLPPSLAGSSAPRLPLD
 380       390       400       410         420       430       440

      70        80         90          100       110          120
AGSKMQGLLERVNTEIHFVTKC-AFQPPPS---CLRFVQTNISRLLQETSEQLVALKPW---ITRQNFSRCL
||    | |        |   |   |   |      ||   |   |  |  |  ||  |            |
AG----GHLAKARAVRDFFDYCLTAQSDLSAAGLDAFVMREIAAQLDGTVAQAEALDVWHRYRAYLDALAKL
     450       460       470       480       490       500       510

130       140       150    X
ELQCQPDSSTLPPPWSPRPLEATAPTAP
      | | |        |   |  |
RDAGAVDKSDL--GALQLALDQRASIAYRWLGDWSQPF
   520         530       540       550


7. US-08-162-407-6 (1-235)
   Q06332        Murine IL-2R beta chain.

ID   Q06332 standard; cDNA; 2306 BP.
AC   Q06332;
DT   07-FEB-1991  (first entry)
DE   Murine IL-2R beta chain.
KW   Interleukin; receptor; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             375..1994
FT   /*tag=  a
FT   misc_difference 1182..1184
FT   /*tag=  b
FT   /label=ggc, tgc
PN   AU9050726-A.
PD   13-SEP-1990.
PF   06-MAR-1990; 050726.
PR   07-MAR-1989; EP-104023.
PR   29-MAY-1989; EP-109656.
PR   20-JUL-1989; EP-113310.
PA   (BOEH ) BOEHRINGER INGELHEI.
PI   Taniguchi T, Hatakeyama M, Minamoto S, Kono T, Doi T;
PI   Miyasaka M, Tsudo, Karasuyma H;
DR   WPI; 90-327673/44.
DR   P-PSDB; R07507.
PT   Recombinant interleukin-2 receptor beta chain - useful for
PT   diagnosis and therapy by immune suppression or activation.
PS   Claim 4; Fig 8; 65pp; English.
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CC   The sequence was obtd. from clones isolated from a cDNA library
CC   prepd. from RNA extracted from Concanavalin A-stimulated mouse
CC   spleen cells.  The clones were selected using a probe derived from
CC   the human sequence.  The sequence encodes a soluble portion of the
CC   IL-2R beta chain.
CC   See also Q06331.
SQ   Sequence   2306 BP;    487 A;    685 C;    580 G;    550 T;
SQ   4 Others;

Initial Score     =     15  Optimized Score  =     29  Significance =  6.01
Residue Identity  =    20%  Matches          =     35  Mismatches   =   114
Gaps              =     24  Conservative Substitutions          =     0
Translation Frame=      1

              X       10        20                    30        40
              QDCSFQHSPISSDFAVKIRE---------LSDYLL---QDYPVTVASNLQDEELCGG----L
                |        |    |  |          |   |   |  |    |       | |
    ASSRDRRGSSWRCXSLVPHMRSRXGSKLNETIPGPGVPGASPXPLGQGQQIPXRRSS------PCHGSDTFC
           320       330       340       350       360             370

      50          60        70        80        90       100       110
    WRLV--LAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKP
    | ||  ||           |    |                    ||          ||    |   |||
    WSLVVFLASSPASTFWSRHGTLGHGXRQFSSATSQILLSSSPSXAPSMGETFRNGSPRLSPCPSSAPVALPL
     380       390       400       410       420       430       440

     120       130       140       150    X
    WITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAP
       |   |      |         |  |||     | |
    RSLRWKCSTEIPRPCSCSCYRRTLPLYPRPAATHRPAASPTRATSSSIC
   450       460       470       480       490

8. US-08-162-407-6 (1-235)
   Q05873         Sequence encoding murine interleukin-2 receptor be

 ID   Q05873 standard; DNA; 2306 BP.
 AC   Q05873;
 DT   07-JAN-1991  (first entry)
 DE   Sequence encoding murine interleukin-2 receptor beta-chain.
 KW   IL-2R beta; pIL-2R beta 9; ss;
 OS   Mus musculus.
 FH   Key             Location/Qualifiers
 FT   CDS             375..1994
 FT   /*tag=  a
 PN   EP-386304-A.
 PD   12-SEP-1990.
 PF   29-MAY-1989; 109656.
 PR   07-MAR-1989; EP-104023.
 PR   29-MAY-1989; EP-109656.
 PA   (OSAU ) OSAKA UNIVERSITY.
 PI   Taniguchi T;
 DR   WPI; 90-276456/37.
 DR   P-PSDB; R06647.
 PT   Recombinant interleukin-2 receptor beta chain - used for studying
 PT   IL-2 system and producing antibodies for diagnosis and therapy.
 PS   Claim 6; Fig 8; 37pp; English.
 CC   IL-2 receptor beta chains are useful in studying the biochemistry of
 CC   interleukin, and in diagnosis and therapy by immune suppression and
 CC   activation.
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 SQ   Sequence    2306 BP;    482 A;    688 C;    585 G;    551 T;

Initial Score     =     15  Optimized Score  =     29  Significance =  6.01
Residue Identity  =    19%  Matches          =     34  Mismatches   =   117
Gaps              =     20  Conservative Substitutions          =     0
Translation Frame=      1

              X       10        20        30                  40
              QDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVAS----------NLQDEELCGG----LWR
                |        |    |  |          |  ||                 | |     |
    ASSRDRRGSSWRCXSLVPHMRSRXGSKLNE----TIPGPGVPGASPXPFGQGQQIPXRRSSPCHGSDTFCWS
           320       330       340           350       360       370

    50          60        70        80        90       100       110
    LV--LAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWI
    ||  ||          ||    |                    ||          ||    |   |||
    LVVFLASSPASTFWSSAGTLGHGXRQFSSATSQILLSSSPSXAPSMGETFRNGSPRLSPCPSSAPVALPLRS
   380       390       400       410       420       430       440       450

   120       130       140       150     X
    TRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAP
     |   |      |         |  |||     | |
    LRWKCSTEIPRPCSCSCYRRTLPLYPRPAATHRPAASPTRATSSSIC
           460       470       480       490

9. US-08-162-407-6 (1-235)
   Q41331          pMV206 - cassette contg. seq's necessary for repli

 ID   Q41331 standard; DNA; 4119 BP.
 AC   Q41331;
 DT   04-JUN-1993  (first entry)
 DE   pMV206 - cassette contg. seq's necessary for replicn. in mycobacteria.
 KW   cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG;
 KW   Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV;
 KW   pertussis; malaria; influenza virus; CTL; herpes virus.
 OS   Mycobacterium.
 FH   Key             Location/Qualifiers
 FT   misc_feature    122..125
 FT   /*tag=  a
 FT   /codon= kan start codon
 FT   misc_feature    935..937
 FT   /*tag=  b
 FT   /codon= kan stop codon.
 PN   WO9307897-A.
 PD   29-APR-1993.
 PF   21-OCT-1992; U09075.
 PR   21-OCT-1991; US-780261.
 PA   (MEDI-) MEDIMMUNE INC.
 PI   Stover CK;
 DR   WPI; 93-152187/18.
 PT   Expression vector for expressing protein or polypeptide in
 PT   mycobacterium - contg DNA sequences encoding lipoprotein
 PT   secretion signal and peptide heterologous to bacteria expressing
 PT   fusion protein of lipoprotein heterologous to bacteria
 PS   Example 1; Fig 12; 86pp; English.
 CC   This sequence represents that of plasmid pMV206. This is a plasmid
 CC   containing sequences necessary for replication in mycobacteria.
 CC   It contains a synthetic multiple cloning site to facilitate
 CC   versatile molecular cloning and manipulations for foreign gene
CC   expressions in mycobacteria and for integration into the
CC   mycobacterial chromosome.
SQ   Sequence   4119 BP;     922 A;     1129 C;     1163 G;     904 T;
SQ   1 Others;

Initial Score     =     15  Optimized Score  =     31  Significance =  6.01
Residue Identity  =    22%  Matches          =     44  Mismatches   =    91
Gaps              =     58  Conservative Substitutions             =     0
Translation Frame=       1

              X       10        20                    30        40        50
              QDCSFQHSPISSDFAVKIREL----------SDYL--LQDYPVTVASNLQDEELCGGLWRLV
                  |    |          |            ||  |   ||  ||      | |   |
    PDQELPTLFPKVTGFSRAQIPNTVLLVXPXLGHHFKNSVAPPTYLALLILLPVAAAS-GDKSCLTGLDSRRX
   450       460       470       480       490       500        510

               60        70         80        90         100
    L---AQRWMERLKTVAGSKMQGLLER-VNTEIHFVTKCAFQPPPSCLRFVQ--TNISRLLQE----------
    |   ||    |    |||  |  |||   ||               ||  |     |  | |
    LPDKAQ----RSGXTAGSCTQPSLERTTYTE---------------LRYLQREHXESATLPEGRKADRYPVS
  520           530       540                     550        560       570

         110       120             130       140       150    X
    ----TSEQLVALKPWITRQNFS----RCL--ELQCQPDSSTLPPPWSPRPLEATAPTAP
        | |    |         |    | |  |      ||     |      |     |
    GRVRTGERTRELPGGNAWYLYSPVGFRHLXLERRFLXCSSGGRSLWKNASNAAFLRSWPFAGLLLTCSF
         580       590       600       610       620       630       640


10. US-08-162-407-6 (1-235)
    Q57710         Neurocan DNA.

 ID  Q57710 standard; DNA; 5191 BP.
 AC  Q57710;
 DT  11-AUG-1994  (first entry)
 DE  Neurocan DNA.
 KW  Neurocan; cell adhesion; leukocyte-endothelial cell recognition;
 KW  tissue-related inflammation allergy; cellular; humoural;
 KW  hypersensitivity; trauma; neuronal development; cell transport;
 KW  infection; diagnosis; lectin; versican; aggrecan; gelsolin;
 KW  receptor; cell recognition; membrane cytoplasmic protein; lipid;
 KW  carbohydrate; saccharide; nucleoside; enzyme; ion; ss.
 OS  Homo sapiens.
 FH  Key             Location/Qualifiers
 FT  CDS             77..3850
 FT  /*tag=  a
 FT  /product= Neurocan
 PN  WO9403601-A.
 PD  17-FEB-1994.
 PF  03-AUG-1993; U07306.
 PR  03-AUG-1992; US-922911.
 PA  (UYNY ) UNIV NEW YORK STATE.
 PI  Margolis RK,  Margolis RU,  Rauch U;
 DR  WPI; 94-065690/08.
 DR  P-PSDB; R46627.
 PT  Eukaryotic neurocan polypeptide(s) with epidermal growth factor,
 PT  lectin or complement binding activity - used in the diagnosis,
 PT  treatment or research of hypersensitivity and allergic diseases
 PS  Claim 1; Page 69-75; 105pp; English.
 CC  This sequence encodes a neurocan polypeptide.  This protein has
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 CC  several biological activities, including cell adhesion, leukocyte-
 CC  endothelial cell recognition, tissue-related inflammation allergies,
 CC  cellular and/or humoural hypersensitivity, trauma, neuronal
 CC  development, and cell transport and/or infection.  Compositions
 CC  containing them can be used as modulators of these conditions, and
 CC  may be used as therapeutic, diagnostic, and/or research tools.
 CC  Neurocan peptides can be used to mimic proteins, such as lectins,
 CC  cell adhesion molecules, versicans, aggrecans or gelsolins, as
 CC  receptor or effector subtypes.  The protein can be used to treat
 CC  diseases involving a qualitative or quantitative pathological
 CC  abnormality of cell adhesion or leukocyte-endothelial cell recognition,
 CC  or a functionally associated molecule such as a membrane cytoplasmic
 CC  protein, lipid, carbohydrate, saccharide, nucleoside, enzyme or ion.
 SQ  Sequence    5191 BP;    1104 A;    1534 C;    1457 G;    1096 T;

Initial Score     =     15  Optimized Score  =     30  Significance =  6.01
Residue Identity  =    23%  Matches          =     40  Mismatches   =    90
Gaps              =     40  Conservative Substitutions             =     0
Translation Frame=       1

              X       10        20           30        40           50
              QDCSFQHSPISSDFAVKIRELSDYLLQ---DYPVTVASNLQDEEL---CGGLWRLVLAQRWM
                 |    | ||        ||    |     |   |       |   ||           |
    LXLQPPLRLQEGYSAVWAPSSS-----GECLSCWCAQGQVQCPCHCAIPVXXRILPAPCG--------YHPM
     1170      1180           1190      1200      1210      1220

      60        70        80        90       100        110       120
    ERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQET-SEQLVALKPWITRQNFSRCL
         |      |           ||  |  ||||      |      ||| |  |        |
    PKQWEV------GPASDCVHQAQAVTSDASTPPPSTPASQATQGAQKTQETPSGRL----GERXRGFLLTIQ
      1230            1240      1250      1260      1270          1280

    130       140               150    X
    ELQCQPDSSTLPPPWSPRPLE---------ATAPTAP
      | |    | ||  ||   |           | ||
    TNQAQ--APTPPPEHSPGDPEPRQPPERGWGHPAAPHPCSRSSVQS
    1290        1300      1310      1320      1330


11. US-08-162-407-6 (1-235)
    N80626         Bovine Bone Morphogenic Protein-3 in bp-819 detect

 ID  N80626 standard; DNA; 413 BP.
 AC  N80626;
 DT  08-OCT-1990  (first entry)
 DE  Bovine Bone Morphogenic Protein-3 in bp-819 detected by probe #2.
 KW  Bone morphogenic protein; bBMP-3; probes; cartilage formation;
 KW  bone formation; osteogenic cpds.;  prodontal disease; ss.
 OS  Bos taurus.
 FH  Key             Location/Qualifiers
 FT  CDS             41..374
 FT  /*tag=  a
 FT  /product=bBMP-3
 FT  misc_RNA        274..298
 FT  /*tag=  b
 FT  /product=tryptic fragment 12
 FT  misc_RNA        322..352
 FT  /*tag=  C
 FT  /product=tryptic fragment 10
 PN  WO8800205-A.
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PD   14-JAN-1988.
PF   30-JUN-1987; U01537.
PR   26-MAR-1987; US-031346,
PA   (GENE-) Genetics Inst Inc.
PI   Wozney JM, Rosen VA;
DR   WPI; 88-021565/03.
DR   P-PSDB; P81515.
PT   Bone morphogenic proteins - obtd. using recombinant DNA and used
PT   for inducing cartilage and bone formation.
PS   Disclosure; 7pp; English.
CC   This region of bp-819 hybridises to probe #2. The Bp-819 clone
CC   encodes the bovine bone growth factor bBMP-3.
CC   BBMP-3 is characterised by the sequences of clone bp-819  of N80626
CC   and N80627. The peptide is 175 amino acids long.
CC   This sequence is also used to screen a human genomic library to
CC   detect  the BMP-3 human bone inductive factor which is significantly
CC   homologous to the bovine factor.
CC   See also N80619-N80636 and N81963-64.
SQ   Sequence   413 BP;   119 A;   95 C;   111 G;   88 T;

Initial Score     =     14  Optimized Score  =     20  Significance =  5.51
Residue Identity  =    22%  Matches          =     25  Mismatches   =    61
Gaps              =     23  Conservative Substitutions              =     0
Translation Frame=       1

              X       10              20          30                40
              QDCSFQHSPISSDFA------VKIRE-LSDYLLQDYPV--------TVASNLQDEELCGGLW
              ||        ||| |       |  |        | ||                 |||
    GXSMGGEEALQD--------SSDSAPXXEXEQKETEEGTSAEESDAPVXXTDPEEGKKKAMDXTPELCQTVP
      30      X         40        50        60        70        80        90

     50        60        70        80        90   X   100
    RLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLL
       |   | ||           || |     |      |   ||
    XSGLRRYWLERMDYFPQVLRCLLLLRSVPVPHAKGSHCFLSCPSHFH
           100       110       120       130      X

12. US-08-162-407-6 (1-235)
    N92199        Region of clone bP-819 which hybridzes with bovine

ID   N92199 standard; cDNA; 413 BP.
AC   N92199;
DT   06-APR-1990  (first entry)
DE   Region of clone bP-819 which hybridzes with bovine BMP-3 probe.
KW   BMP-3 protein; lambda bP-819; bone formation; tissue repair;
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             41..373
FT   /*tag=  a
PN   WO8910409-A.
PD   02-NOV-1989.
PF   07-APR-1989; U01464.
PR   08-APR-1988; US-179197.
PA   (GENE-) Genentic Institute, Inc.
PI   Wang EA, Wozney JM, Rosen V;
DR   WPI; 89-339971/46.
DR   P-PSDB; P93233.
PT   Isolated DNA sequence and purified BMP-3 protein prepn. - by culturing
PT   cell transformed with defined DNA and recovery of 96 amino acid protein.
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PS   Disclosure; page 20; 37pp; English.
CC   The sequence encodes part of a BMP-3 protein . The CDS is joined to the
CC   CDS of N92200. The sequence was isolated from clone lambda bP-819 by
CC   hybridization to a probe (N93420). Purified BMP-3 may be used to induce
CC   bone and/or cartilage formation and to promote wound healing and tissue
CC   repair.
SQ   Sequence   413 BP;   119 A;   95 C;   111 G;   88 T;

Initial Score     =     14  Optimized Score  =     20  Significance =  5.51
Residue Identity  =    22%  Matches          =     25  Mismatches   =    61
Gaps              =     23  Conservative Substitutions              =     0
Translation Frame=       1

              X       10              20          30                40
              QDCSFQHSPISSDFA------VKIRE-LSDYLLQDYPV--------TVASNLQDEELCGGLW
              ||        ||| |       |  |        | ||                 |||
    GXSMGGEEALQD--------SSDSAPXXEXEQKETEEGTSAEESDAPVXXTDPEEGKKKAMDXTPELCQTVP
      30      X         40        50        60        70        80        90

     50        60        70        80        90   X   100
    RLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLL
       |   | ||           || |     |      |   ||
    XSGLRRYWLERMDYFPQVLRCLLLLRSVPVPHAKGSHCFLSCPSHFH
           100       110       120       130      X

13. US-08-162-407-6 (1-235)
    N81258        Encodes recombinant human preproapoprotein A1

ID   N81258 standard; cDNA; 881 BP.
AC   N81258;
DT   24-OCT-1990  (first entry)
DE   Encodes recombinant human preproapoprotein A1
KW   human preproapoprotein A1; high density lipoprotein deficiency; ss.
OS   synthetic.
FH   Key             Location/Qualifiers
FT   misc_RNA        20..73
FT   /*tag=  a
FT   /note="encodes precursor peptide"
FT   misc_RNA        74..94
FT   /*tag=  b
FT   /note="encodes propeptide"
FT   misc_RNA        95..823
FT   /*tag=  c
FT   /note="encodes mature apoprotein A1"
FT   misc_difference 74..136
FT   /*tag=  d
FT   /note="replaces wild type sequence to eliminate hairpins"
PN   EP-293357-A.
PD   30-NOV-1988.
PF   24-MAY-1988; 870095.
PR   28-MAY-1987; GB-012540.
PA   (UNIO) UCB SA.
PI   Bollen A, Gobert J, Wulfert E;
DR   WPI; 88-339891/48.
DR   P-PSDB; P80668.
PT   New DNA encoding human preproapoprotein A1 -
PT   modified to eliminate hairpin structures
PS   Claim 1; page 12; 25pp; French.
CC   The DNA fragment used to replace the wild-type sequence encoding
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 CC   amino acids -6 to +14 (= nucleotides 74 to 136) includes an
 CC   additional ATG start codon and modifies codons corresponding to
 CC   wild-type amino acids -6, -1, 1, 3, 4, 5, 6, 7, 10, 11 and 14.
 CC   The changed codons still encode the same amino acids as in the
 CC   wild-type protein but reduce formation of secondary structures in
 CC   mRNA.
 CC   See also N82064 for wild-type sequence.
 SQ   Sequence   881 BP;   200 A;   269 C;   280 G;   132 T;

Initial Score    =      14  Optimized Score  =      26  Significance =  5.51
Residue Identity =     23%  Matches          =      34  Mismatches   =    79
Gaps             =      29  Conservative Substitutions              =     0
Translation Frame=       1

           20 X      30        40         50        60        70        80
    SDFAVKIRELSDYLLQDYPVTVASNLQDEELCG-GLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT
              |   |||            | ||  | |              ||      |       | |
              SPTALQD------------ESCGADLGRALPDGEPGYETFLAAGRTSTISLGXSXGLGHCVR
              X                   10        20        30        40        50

          90       100       110       120       130              140
    KCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQ------CQPDSSTL-PPPWSPRPL
     || |     |  |     ||           ||    |   | | ||         |   |  |    |
    GCA-QRQRQRL-CVPVXRLRL-------GKTAKPKAPXQLGQRDLHLQQAARTARPCDPGVLGXPGKGDRGP
             60                70        80        90       100       110

    150    X
    EATAPTAP
    ||
    EAGDEQGSGGGEGQGAAL
        120       130

14. US-08-162-407-6 (1-235)
    N71341        Sequence encoding rotavirus inner shell protein VP

 ID   N71341 standard; DNA; 1357 BP.
 AC   N71341;
 DT   24-MAY-1991  (first entry)
 DE   Sequence encoding rotavirus inner shell protein VP6 serotype SAII.
 KW   Diarrhoea; gastrointestinal disorder; RNA virus; vaccine; ss.
 OS   Rotavirus.
 FH   Key                Location/Qualifiers
 FT   CDS                24..1217
 FT   /*tag=  a
 PN   AU8666987-A.
 PD   02-JUL-1987.
 PF   23-DEC-1986; 017981.
 PR   26-DEC-1985; US-813661.
 PR   03-SEP-1986; US-903325.
 PA   (UYSA-) UNIV OF SASKATCHEWA.
 PI   Sabara MIJ, Frenchick PJ, Potter AA, Ijaz MK, Gilchrist JE;
 DR   WPI; 87-228567/33.
 DR   P-PSDB; P71563.
 PT   New peptide fragments of rota:viral proteins - useful conjugates
 PT   in vaccines for protecting against gastrointestinal disorders and
 PT   diarrhoea
 PS   Disclosure; Fig 2; 84pp; English.
 CC   The peptide fragments of glycoprotein VP7 and proteins VP6 and VP3
 CC   of rotaviruses are useful when attached to carriers as vaccines for
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 CC   birds and mammals, including man. The vaccines confer protection
 CC   against gastrointestinal disorders and diarrhoea produced by the
 CC   rotaviruses. For use in vaccines the peptides are covalently linked
 CC   to e.g., keyhole limpet haemocyanin, BSA, ovalbumin, poly-L-lysine,
 CC   or VP6 bovine rotavirus protein. An adjuvant may be included.
 SQ   Sequence   1357 BP;   449 A;   257 C;   267 G;   384 T;

Initial Score    =      14  Optimized Score  =      27  Significance =  5.51
Residue Identity =     18%  Matches          =      31  Mismatches   =   124
Gaps             =      10  Conservative Substitutions              =     0
Translation Frame=       1

              X       10          20        30        40            50
              QDCSFQHSPISSDFAVK--IRELSDYLLQDYPVTVASNLQDEEL----CGGLWRLVLAQ--R
                 |     |      |  |    |             |    |       |     ||
    LNQTPXESCQPLNSKEXILIIRRNTXKTGICKIEDRGQVSLFINQTFFLIQHHLHXIDHNPLMIIXWAQCGX
   120       130       140       150       160       170       180       190

        60        70        80        90         100       110       120
    WMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR--FVQTNISRLLQETSEQLVALKPWITRQNFS
       |           ||            |        ||  | ||      || | || |       | ||
    TQDRKFKSLDLTTHVLLTHQPIYNNLSILCHSDECXLQLRXLFYQTRKGLVFQEXSIQLTAQLHGFSTQXFS
           200       210       220       230       240       250       260

       130       140       150    X
    RCLELQCQPDSSTLPPPWSPRPLEATAPTAP
        |                 ||
    GRITLKWSFYXMDRXXTLIKQDLELSXLEILILLDYHSSXX
         270       280       290  X    300

15. US-08-162-407-6 (1-235)
    N90612        CD19 cDNA.

 ID   N90612 standard; cDNA; 1921 BP.
 AC   N90612;
 DT   20-DEC-1989  (first entry).
 DE   CD19 cDNA.
 KW   Tyrosine suppressor gene; ASV LTR; human cytomegalovirus AD169 enhancer;
 KW   HIV box; immunoselection; immune deficiency diseases;  vasculitis;
 KW   systemic lupus erythematosus; rheumatoid arthritis; neoplasms;
 PN   EP-330191-A.
 PD   30-AUG-1989.
 PF   23-FEB-1989; 103127.
 PR   25-FEB-1988; US-160416.
 PA   (GEHO) Gen. Hospital Corp.
 PI   Seed B, Allen J, Aruffo A, Camerini D, Lauffer L, Oquendo CP,
 PI   Simmons D, Stamenkovic I, Stengelin S;
 DR   WPI; 89-250302/35.
 PT   Rapid immuno:selection cloning - used to clone genes encoding
 PT   cell surface antigens associated with mammalian T lymphocytes.
 PS   Disclosure; fig. 12; 69pp; English.
 CC   CD19 encodes a cell surface antigen involved in cell mediated immunity.
 CC   This DNA can be expressed in a vector which transforms COS cells. The
 CC   vector can isolate any protein, and clones are easy to manipulate.
 SQ   Sequence   1921 BP;   402 A;   566 C;   567 G;   386 T;

Initial Score    =      14  Optimized Score  =      31  Significance =  5.51
Residue Identity =     21%  Matches          =      39  Mismatches   =   115
Gaps             =      26  Conservative Substitutions              =     0
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Translation Frame=      1

          X       10        20                30        40        50
          QDCSFQHSPISSDFAVKIREL--------SDYLLQDYPVTVASNLQDEELCGGLWRLVLAQR
           |    ||       |    |                |   |  ||     |||
GRXRCAAVPQGDLRWPHSAADLVSGVPAXTLLKTQPGAARPGNPHEAPGHLAFHLQRLSTDGGLLPVPAGAP
   40     X  50        60        70        80        90       100

    60        70        80        90       100       110        120
WMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV-ALKPWITRQNFSR
  | |     |   |    |  |          |    ||  |    |   |     |    |       |
LXEGLAAWLDSQCGGQRGAVPVECFGPRWPGLWPEEQVLRGPQ-LPFREAHEPQAVCVGQRPPXDLGGRASV
110       120       130       140       150        160       170

    130         140         150               X
 C-LELQCQPDSSTLP--PPW--SPRPLEAT-----------APTAP
 |  | |  |     |   ||      |  |            | ||
 CPTEGQPEPEPQPGPHHGPWLHTLAVLWGTPXLCVQGPPLLDPCAPQGAXVIAEPR
180       190       200       210       220   X   230
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maryh@stic **stdin**

NeWSprinter20

Thu Apr 06 10:25:06 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

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> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file trans_nsq.res made by root on Thu 6 Apr 95 9:58:03-PDT.


Query sequence being compared:US-08-162-407-6 (1-705)
Number of sequences searched:                 57621
Number of scores above cutoff:                 4419

      Results of the initial comparison of US-08-162-407-6 (1-705) with:
   Data bank : N-GeneSeq 17, all entries

100000-
      -
N     -
U50000-
M     -
B     -
E     -
R     -
      -
O     - *
F10000-  *
      -
S     -    *
E 5000-     *
Q     -   *
U     -      *     *
E     -
N     -        ***
C     -              **
E     -                  *
S 1000-       *   * *  ** *
      -                     *
      -                      *
   500-*                   *  * *
      -
      -
      *                        *  * *
      -
      -                          *
      -                            *   *
   100-                              **
      -                                *  *
      -                                 **
    50-
      -
      -
      -                                     * *
      -                                      * * *
      -                                       *    *
      -
    10-
      -
      -                                          *
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     5-                                           * *   *
      -
      -
      -                                                *   *
      -
      -
      -                                                  **       *  *
     0---------------------------------------------------------------------
      |    | |    | |    | |    | |    | |    | |    | |    | |    | |
SCORE 0    |16    |33    |49    |65    |82    |98    114    131    147
STDEV      0      1      2      3      4      5      6      7      8

                              PARAMETERS

Similarity matrix       Unitary     K-tuple                   4
Mismatch penalty              1     Joining penalty          30
Gap penalty                1.00     Window size              32
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                              SEARCH STATISTICS

Scores:                   Mean        Median      Standard Deviation
                           19           14           15.88

Times:                    CPU                     Total Elapsed
                       00:03:44.07                00:03:45.00

Number of residues:                24347505
Number of sequences searched:         57621
Number of scores above cutoff:         4419


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                       Init. Opt.
Sequence Name     Description                   Length Score Score   Sig. Frame
-------------------------------------------------------------------------------
                    ****  8 standard deviations above mean ****
   1. N91235        DNA sequence of prepropasmol   1368   147   368    8.06   0
                    ****  7 standard deviations above mean ****
   2. Q43249        Sequence of AtT20 murine proh  2012   138   373    7.49   0
                    ****  6 standard deviations above mean ****
   3. Q45334        Human TLE-2 gene.              2271   122   368    6.48   0
   4. Q62176        Human TLE-2 gene.              2271   122   368    6.48   0
   5. Q11127        Sequence encoding P450SU2 and  1998   121   365    6.42   0
   6. Q27764        Adrenodoxin reductase gene (p  5089   118   351    6.23   0
   7. Q56917        Glutamic acid receptor.        3717   117   369    6.17   0
   8. N60554        Sequence encoding bovine male  5783   117   366    6.17   0
   9. Q06233        Bovine male-specific insert o  4414   116   367    6.11   0
  10. Q02830        cDNA to HIV-2 RNA.             9360   116   348    6.11   0
                    ****  5 standard deviations above mean ****
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 11. Q46249       Construct EC2L (Contains catR  8528   114   360   5.98   0
 12. Q31999       Encodes eimeria antigen Eam45  1631   113   372   5.92   0
 13. Q40697       B. burgdorferi strain Ip90 Os  1005   110   346   5.73   0
 14. Q14687       Factor XIII subunit a.         2350   110   261   5.73   0
 15. N82401       A and A' subunits of human Fa  2350   110   262   5.73   0
 16. Q25893       Human Factor XIII coding sequ  3905   110   261   5.73   0
 17. N70461       Sequence encoding human facto  3905   110   259   5.73   0
 18. Q58719       Human gamma-1 chain second me   838   109   230   5.67   0
 19. Q55783       Segment of human gamma-1 chai   838   109   230   5.67   0
 20. Q58990       Mutant human creatine kinase   1568   109   362   5.67   0


1. US-08-162-407-6 (1-705)
   N91235        DNA sequence of preprospasmolysin.

 ID   N91235 standard; DNA; 1368 BP.
 AC   N91235;
 DT   07-FEB-1990  (first entry)
 DE   DNA sequence of preprospasmolysin.
 KW   Preprospasmolysin; Xenopus laevis.
 OS   Xenopus laevis
 FH   Key             Location/Qualifiers
 FT   CDS             28..1230
 FT   /*tag=  a
 PN   DE3808456-A.
 PD   28-SEP-1989.
 PF   14-MAR-1988; 808456.
 PR   14-MAR-1988; DE-808456.
 PA   (PLAC) Max-Plank Ges. Wissensch.
 PI   Weickmann H, Fincke K, Weickmann F, Huber B, Liska H, Prechtel J,
 DR   WPI; 89-286097/40. P-PSDB; P91941.
 PT   New polypeptide preprospasmolysin and its fragments- derived from Xenopus
 PT   laevis, with spasmolytic and neurotransmitter activities.
 PS   Disclosure; Fig. 2; 8pp; german.
 CC   The DNA or mRNA corresp. to the peptides are derived from the skin of
 CC   Xenopus laevis. The DNA sequence is inserted into a vector and used to
 CC   transform eukaryotic cells, esp. COS cells, or the DNA is converted into
 CC   mRNA and microinjected into eukaryotic cells, esp. X. laevis oocytes.
 SQ   Sequence   1368 BP;   511 A;   332 C;   234 G;   291 T;

Initial Score     =    147  Optimized Score   =    368  Significance =  8.06
Residue Identity =    26%  Matches           =    338  Mismatches   =   340
Gaps              =     81  Conservative Substitutions              =     0

          X       10        20        30        40         50        60
          ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNACNTAYYTNYTNY-TNYTNYTNYTNYTNW
          ||| | |  ||    || |  |  |   | || |  |  |  || | |  | |  |  |  |
GAGCAGTAGGATG-CTGCTTTGATTCCAGTATCCTTAAC-ACTAAATGGTGCTTCTATAATGCAACAGC--A
160       170        180       190        200       210       220

       70           80            90       100          110       120
SNWSNGGNY---TNWSNGGNACNCA----RGAYTGYWSNTTYCARCAYWS---NCCNATNWSNWSNGAYTTY
| ||    |     ||  | |  ||    ||||  ||| |   || ||||    |  ||  | |   ||  |
GGTCCAATCAAGAAACTCGAATGCAGTGGGGATCCTAC-TAAGAGAATAGACTGCGGATTCCCAAGAATAAC
  230       240       250       260        270       280       290

    130       140          150         160       170          180
GCNGTNAARATNMGNGARYTNWS-NGA--YTAYYT--NYTNCARGAYTAYCCNG---TNACNGTNGCNWSNA
   |  | |||  |    || ||  ||  || |||   || ||| ||| ||| |   | |  |  || ||
AGAGAAACAAT--GCATTCTAAGAGGATGCTGTTTTGATTCCAGTATT-TCCGGTGTTAAATGGTGCTACGC
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   300         310       320        330       340        350       360

   190       200        210       220       230       240       250
   AYYTNCARGAYGARGARYT-NTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNY--
   || | |||    || ||||   ||    | |     |  ||    ||    ||||    ||   |||  |
   ACGTACAGTTATAACAACTCCAGCACCAGAT----ACAACTACAGCTTCAACAACTGCAGAAACAACTACAG
    370        380       390           400       410       420       430

    260       270           280       290       300       310       320
   TNAARACNGTNGCNGGNWSNA----ARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTN
   |   |||     | |  || |    || | |||   || |   |||   |  |||     |   ||| |
   TTCCAACAACTCCAGAAACAACTACAGTTCCAACAACTCCAGAAACAACT--ACAGTTCCAACAACTCCAGA
       440       450       460       470       480         490       500

      330       340       350       360       370         380       390
   ACNAARTGYGCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCAR-ACNA-AYATNWSNMGNYTNYTNC
   |  || | |   |||||||  |  |  |     || |  |||   |||  | | | |  || |  |  || |
   AACAACTAC-AGTTCCAACAACTCCAGAAACAACTACAGTTCCAACAACTCCAGAAACAACTA--CAGTTCC
       510        520       530       540       550       560         570

       400       410         420       430       440           450
   ARGAR-ACNWSNGARCARYT--NGTNGCNYTNAARCCNTGGATNACNMGNCAR----AAYTTYWSNMGNTGY
   || ||  | ||  |||||||   ||  |    |  ||    |  || |  |||    |||  ||| ||   |
   AACAACTCCAG-AAACAACTACAGTTCCAACAACTCCAGAAACAACTA--CAGTTCCAACAACTCCAGAAAC
        580        590       600       610         620       630       640

460        470            480       490        500       510       520
   YTNGARYTNCARTGYCAR-----CCNGAYWSNWSNAC-NYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGA-
       |||| |||| ||||     || || || || ||  || |  |  |    ||  |  |  |  ||  |
   ----AACTACAGTTCCAACAACTCCAGAAACAACTACAGTTCCAACAACTCCAGAAACAACTACAGTTCCAA
             650       660       670       680       690       700

       530       540        550       560       570       580       590
   -RGCNACNGCNCCNACNGC-NCCNCARCCNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYTN
    | |  | |   | ||  |  |  ||||  |  |     |  || |  || |  |   |       |  ||
   CAACTCCAGAAACAACTACAGCTTCAACAACTGCAGAAACAACTACAGTTCCAACAACTCCAGAAACAACTA
710        720       730       740       750       760       770       780

      600        610        620       630       640        650       660
   YTNGCNGCNGC-NTGGTGYYTNC-AYTGGCARMGNACNMGNMGNMGNA-CNCCNMGNCCNGGNGARCARGTN
   |  |   |  |       ||  | || |  |    || |  |  |  | | || |  || |   ||||| |
   C-AGAACCGACTACAACACCAACAACAGATACTACACCACCAACACTACCACCAACACCAG--AAACAACTA
         790       800        810       820       830       840         850

         670          680        690       700.    X
   C---CNCCNGTNCCNW---SNCCNCARGAYYTNYTNYTNGTNGARC-AY
   |     |   | |  |     |  ||| | |  || |      ||| ||
   CAGAAACAACTACAGAAACAACTACAGAAACAACTACAGAAACAACTACAGAAACAACT
         860       870        880       890       900


2. US-08-162-407-6 (1-705)
   Q43249        Sequence of AtT20 murine prohormone convertase 2 c

 ID   Q43249 standard; cDNA; 2012 BP.
 AC   Q43249;
 DT   24-SEP-1993  (first entry)
 DE   Sequence of AtT20 murine prohormone convertase 2 cDNA.
 KW   Prohormone convertase; enzyme; cleavage; ss.
 OS   Mus musculus.
 FH   Key             Location/Qualifiers
 FT   CDS             6..2012
 FT   /*tag=  a
 PN   WO9311247-A.
 PD   10-JUN-1993.
 PF   04-DEC-1992; U10621.
 PR   06-DEC-1991; US-803631.
 PR   22-MAY-1992; US-887265.
 PA   (GETH ) GENENTECH INC.
 PI   Gorman CM,  Groskreutz DJ,  Marriott D;
 DR   WPI; 93-197065/24.
 DR   P-PSDB; R37618.
 PT   Heterologous polypeptide factor prepn. - by introducing into
 PT   polypeptide factor dependent host cell nucleic acid, and then
 PT   culturing host cell, etc.
 PS   Disclosure; Fig 2; 134pp; English.
 CC   The inventors describe the production of mammalian cells expressing
 CC   prohormone convertase which facilitates the processing of prohormone
 CC   precursors to active hormones. More specifically the cleavage site
 CC   is the prohormone convertase cleavage site given in R37632-35. The
 CC   mouse pituitary tumour cell line, AtT20, was used as the source for
 CC   candidate prohormone convertase mRNA's from which cDNA was generated.
 CC   Amplification using PCR of candidate prohormone convertase targets
 CC   was carried out. The primer sequences were based on the conserved
 CC   aspartate and serine catalytic residues of KEX2, PC2, Proprotease B,
 CC   and subtilisin BPN. The forward primer used was Q43250 and the
 CC   reverse primer was Q43251. A cDNA pool was prepared as a source of
 CC   template for the cloning of full length sequences of the candidate PC
 CC   enzymes. Mouse AtT-20 total RNA was denatured and added to a first
 CC   strand cDNA synthesis reaction containing adapter primer Q43252.
 CC   Aliquots of the cDNA pool were used for amplification of unknown 3'
 CC   and 5' regions by Q43253  and 5' RACE primer Q43254 and the inner
 CC   adapter Ri PCR primer Q43255.
 SQ   Sequence   2012 BP;    520 A;    516 C;    565 G;    411 T;

Initial Score     =    138  Optimized Score  =    373  Significance =  7.49
Residue Identity =    28%  Matches          =    350  Mismatches   =   313
Gaps              =     88  Conservative Substitutions            =     0

              X       10           20          30        40        50
              ATGACNGTNYTNGCNC---CNGCNTG--GWSNCCNACNACNTAYYTNYTNYTNYTNYTN
              || ||  | ||  | |     || ||   || || |  |   |    |  |  || |  |
    GAAGGCCTGTATCAC--TTTATCACAATGGGCTTGCAAAGGCCAA--AAGAAGACGCAGC--CTACACC--
     270       280         290       300       310         320         330

     60        70        80        90       100       110       120
    YTNWSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTN
     | ||  |  | |  || |  || | ||  |  || |    || |||  | |  || || |||||  | ||
    ATAAGCGGCAGCTAGAGAGAGACCCCAGGATAAAGAT---GGCGCTG--CAACAAGAAG-GATTTGACCGT-
           340       350       360          370         380        390

  130       140       150       160          170           180       190
    AARATNMGNGARYTNWSNGAYTAYYTNYTNCA---RGAYTAYCCNG--TNA--CNGTNGCNWSNAAYY--TN
    ||||  || | ||  || ||| |||  |   |   | || | |  |  | |  |  |    || || |  |
    AAAAAGAGAGGGTACAGGGAC-ATCAATGAGATTGACATCAACATGAATGATCCTCTCTTTACAAAGCAATG
      400       410        420       430       440       450       460

         200       210       220        230        240       250       260
    CARGAYGARGARYTNTGYGGNGGNYTNTGG-MGNYTNGTNYTNG-CNCARMGNTGGATGGARMGNYTNAARA
      |  ||   |||  || |   | |  ||| |  |  |  || | |   ||  |||  |  ||| ||   |
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    GTACCTGTTCAACACTGGGCAAGCCGATGGAACTCCTGGGCTAGACTTGAACGTGGCCG--AAGCCTGGGAG
     470       480       490       500       510       520         530

         270       280       290       300       310        320        330
    CNGTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYT-TYGTNAC-NAARTG
    | |        || |||| | || | |  || | ||   |  ||   | |||  ||| ||   ||  | |
    CTGGGATACACAGGAAAA-GGAGTGACCATT-GGAATTATGGATGATGGAATTGACTATCTCCACCCAGACC
     540       550        560        570       580       590       600

         340       350       360         370       380       390       400
    YGCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYG--TNCARACNAAYATNWSNMGNYTNYTNCARGARACN
    ||   | ||||  |  |  || |||   || | ||  | |||   | ||  || |  || |  | | |  |
    TGGCCTACAACTACAACGCTGATGC--AAGTTATGACTTCAG--CAGCA-ATGACCCCTAC--CCATACCCT
     610       620       630         640         650        660         670

          410        420       430       440               450       460
    WSNGA-RCA-RYTNGTNGCNYTNAARCCNTGGATNACNMG----NCA----RAAYTTYWSNMGNTGYYTNGA
     |  | ||| ||   | |  |   |||| ||||  || ||     ||    || ||||||  |  |||   |
    CGATACACAGATGACTGGTTCAACAGCCATGGA--ACTAGGTGTGCAGGAGAAGTTTCTGCTGCAGCC---A
          680       690       700         710       720       730

       470       480       490       500       510       520         530
    RYTNCARTGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGC--NAC-NGC
    ||  |||| || |   || ||  |    |   |  | ||  |||| |  ||    |  || ||   ||  ||
    GCAACAATATCTG-TGGAGTCGGCGTAGCATACAACTCCAAGGTGGC--AGGGATCCGGATGCTGGACCAGC
   740       750        760       770       780         790       800

            540       550       560       570          580       590
    NC----CNACNGCNCCNCARCCNCCNYTNYTNYTNYTNY-TNYTNC--CNGTNGGNYTNYTNYTNYTNG
     |      || |  |  || |     || || |  |  |  | | |  |  | |   | |  || |  |  |
    CCTTTATGACAG-ACATCATCGAAGCCTCCTCCATCAGCCACATGCCTCAACTGATCGACATCTACAGT--G
    810        820       830       840       850       860       870

   600       610       620        630         640        650       660
    CNGCNGCNTGGTGYYTNCAYTGGCAR-MGNACNM--GNMGNMGNACNCCNMG-NCCNGGNGARCARGTNCCN
    |    || ||| |||  ||| | |||  | |  |  |  |  |  |  | || ||  |        ||||
    C--AAGC-TGGGGCC-CCACAGACAATGGGAAGACGGTTGATGGGCCCCGAGAGCTCACACTCCAGGCCATG
       880         890       900       910       920       930       940

     670        680        690       700    X
    CCNG-TNCCNWSNCCNCARGAY-YTNYTNYTNGTNGARCAY
     | | |  | ||  |   || | |     |      |||||
    GCTGATGGCGTGAACAAGGGCCGTGGGGGCAAAGGCAGCATCTATGTGTGG
       950       960       970       980    X  990


3. US-08-162-407-6 (1-705)
   Q45334         Human TLE-2 gene.

 ID   Q45334 standard; cDNA; 2271 BP.
 AC   Q45334;
 DT   10-SEP-1994  (first entry)
 DE   Human TLE-2 gene.
 KW   TLE-2; transducin-like enhancer of split protein; cell fate;
 KW   differentiation; cervix cancer; breast cancer; psoriasis; baldness;
 KW   ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             26..2257
 FT   /*tag=  a
```

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PN   WO9407522-A.
PD   14-APR-1994.
PF   30-SEP-1993; U09339.
PR   30-SEP-1992; US-954813.
PA   (UYYA ) UNIV YALE.
PI   Artavanis-tsakonas S,  Stifani S;
DR   WPI; 94-135221/16.
DR   P-PSDB; R51110.
PT   Transducin-like enhancer or split proteins and nucleic acids- -
PT   are for treatment of disorders of cell fate or differentiation
PT   e.g. cervical cancer, breast cancer, psoriasis, baldness etc.
PS   Disclosure; Page 91-94; 147pp; English.
CC   The nucleotide and deduced aa sequences of human transducin-like
CC   enhancer of split proteins TLE-1 (Q45333, R51109), TLE-2 (Q45334,
CC   R51110), TLE-3 (Q45335, R51111) and TLE-4 (Q45336, R52953) were
CC   determined.  The aa sequences were compared with that of
CC   Drosophila E(spl) m9/10 (R52955).  Comparison of the WD-40 domains
CC   of these proteins defined the consensus residues shown in R52954.
CC   The CcN motifs of the proteins were compared with those of SV40 T
CC   antigen, human c-myc, human p53, human A-myb and dorsal protein with
CC   respect to nuclear localization site, and casein-kinase and cd2-
CC   kinase phosphorylation sites (sequences R52956-70).
SQ   Sequence   2271 BP;    437 A;    751 C;    672 G;    411 T;

Initial Score     =    122  Optimized Score  =     368  Significance =  6.48
Residue Identity =    27%  Matches          =     338  Mismatches   =   333
Gaps              =     75  Conservative Substitutions               =     0

             X       10        20          30        40        50        60
             ATGACNGTNYTNGCNCCNGC--NTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYTN
              ||||       ||  | ||    ||||  | |   | ||       |        |  |
   TATCCCCTTCCTGAC-CCAGGAGCATCAGCAGCAGGTGCTCCAGGCCGTAGAACGCGCCAAGCAGGTCACCG
   300       310        320       330       340       350       360

           70        80        90        100       110        120
   WSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCAR-CAYWSNCCNATNW-SNWSNGAYTTYG-CNGTN
   ||  |  | |  || |   |   || | ||||  ||||| | ||| || |  | | ||   || || |  |
   TGGGGGAGCTGAACAGCCTCATCGGGCAGCAG-CTCCAGCCGCTGTCCCACCACGCACCCCCTGTGCCCCTG
  370       380       390       400        410       420       430

 130        140       150       160           170       180       190
   AARATNMG-NGARYTNWSNGAYTAYYTNYTNCARGAYTAY----CCNGTNACNGTNGCNWSNAAYYTNCARG
   |     ||   |||   | | |  |   |  |||  ||||    |   |  |  |  |  |   |||    |
   ACCCCCCGCCCAGC--CGGGCTGGTGGGCGGCAGTGCTACGGGGCTGCTTGCTCTGTCTGGAGCCCTGGCTG
 440       450         460       470       480       490       500

    200          210       220       230       240       250        260
   AYGARG---ARYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARM-GNYTNAARACN
    | |||   ||||  |||| || || |  ||    |  |  ||   ||| |||| |  || |  |  |||
   CCCAGGCTCAGCT-GGCGGCGG-CTGTCAAG-GAGGACCGTGC-GGGCG-TGGAGGCCGAGGGGTCCAGAGT
 510       520        530          540        550        560       570

      270       280       290       300       310       320       330
   GTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCN
   |  |   |  |  ||  | || | |  ||    ||      | | ||||    | ||||     || | ||
   GGAGAGAGCCCCGAGCAGGAGTG-CATCTCCCTCG----CCCCCTGAGA---GTCTCGTGGAGGAG-GAGCG
    580       590        600       610           620          630

    340       350         360       370       380         390       400
   TTYCARCCNCCNCCNWSNTGYY--TNMGNTTYGTNCARACNAAYATNWSNMGNY--TNYTNCARGARA-CNW
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     | ||   ||    || || |    ||    |  ||||  |  |  || |  |    |   | |||| | |
   ACCGAGTGGCCCTGGTGGTGGCGGGAAGCAGAGAGCAGATGAGAAGGAGCCATCAGGACCTTATGAAAGCGA
 640       650       660       670       680       690       700       710

       410       420        430        440       450       460          470
   SNGARCARYTNGTNGCNYTNAARC-CNTGGATNACNM-GNCARAAYTTYWSNMGNTGYYTNG---ARYTNCA
   |  ||  |   || |  |  || |   |||   || | | | || | |||| ||   ||  |    ||| |
   CGAAGACAAGAGT-GATTACAATCTGGTGGTGGACGAGGACCAACCCTCAG-AGCCCCCAGCCCGGCTACC
         720        730       740       750       760        770       780

          480       490       500       510       520       530       540
   RTGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGC
   |  ||   | || ||  | || |  |  |   | ||  | |  ||    || | ||  || |  ||  |  |
   ACCCCCTGCGGAAAG--GTACCCATCTGCATTCCTG--CCCGTCGGGACCTGGTGG--ACAG-TCCAGC--C
         790         800       810         820       830          840

        550         560       570       580       590             600
   NCCNCARCCNC--CNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYT------NYTNGCNG-CNGC
    ||   ||| |    || |  |  || |      |    |  ||  | ||       ||  | | | ||
   TCCTTGGCCTCTAGCTTGCGGTCACCGCTGCCTAGAGCCAAGGAGCTCATCCTGAATGACCTTCCCGCCAGC
      850       860       870       880       890       900       910

      610           620        630       640         650       660
   -NTGGTGYYTNCA----YTG-GCARMGNACNMGNMGNMGNACNC--CNMGNCCNGGNGARCARGTNCCNCCN
     |  ||||| ||     || |   |   | || |  || || |  | |  || || |  ||| | |  ||
   ACTCCTGCCTCCAAATCCTGTGACTCCTCCCCGCCCCAGGACGCTTCCACCCCCGG-GCCCAGCT-CGGCCA
    920       930       940       950       960       970        980

 670       680       690       700    X
   GTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
   ||  | ||  | |||  ||| |  |      |||||
   GTCACCTCTGC-CAG--CTTGCGCTCAAGCCAGCACCTTCCACGGA
    990      1000        1010      1020


4. US-08-162-407-6 (1-705)
   Q62176          Human TLE-2 gene.

 ID   Q62176 standard; cDNA; 2271 BP.
 AC   Q62176;
 DT   10-SEP-1994  (first entry)
 DE   Human TLE-2 gene.
 KW   TLE-2; transducin-like enhancer of split protein; differentiation;
 KW   protein transport; cervix cancer; dysplasia; malignancy;
 KW   ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   CDS             26..2257
 FT   /*tag=  a
 PN   WO9408037-A.
 PD   14-APR-1994.
 PF   30-SEP-1993; U09333.
 PR   30-SEP-1992; US-955011.
 PA   (MEDI-) MEDICAL RES COUNCIL.
 PA   (UYYA ) UNIV YALE.
 PI   Artavanis-tsakonas S,  Hill RE,  Redhead NJ,  Stifani S;
 DR   WPI; 94-135597/16.
 DR   P-PSDB; R51477.
 PT   New human transducin-like enhancers of split protein - and
 PT   associated multi-protein complexes, chimeric proteins,
PT   antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic
PT   protein transport
PS   Disclosure; Page 58-61; 112pp; English.
CC   The nucleotide and deduced aa sequences of human transducin-like
CC   enhancer of split proteins TLE-1 (Q62175, R51476), TLE-2 (Q62176,
CC   R51477), TLE-3 (Q62177, R51478) and TLE-4 (Q62178, R51479) were
CC   determined.  The aa sequences were compared with that of Drosophila
CC   E(spl)m9/10 protein (R51481).  Comparison of the WD-40 domains of
CC   these proteins defined the consensus residues shown in R51480.  The
CC   CcN motifs of the proteins were compared with those of the SV40 T
CC   antigen, human c-myc, human p53, human A-myb and dorsal proteins
CC   with respect to nuclear localization site, and casein-kinase II and
CC   cdc2-kinase phosphorylation sites (sequences R51482-96).  TLE can be
CC   used to treat or diagnose (pre)neoplastic conditions, or
CC   to study cell differentiation.
SQ   Sequence   2271 BP;    437 A;    751 C;    672 G;    411 T;

Initial Score     =    122  Optimized Score =    368  Significance =  6.48
Residue Identity =    27%  Matches         =    338  Mismatches   =   333
Gaps              =     75  Conservative Substitutions         =     0

              X       10        20          30        40        50        60
              ATGACNGTNYTNGCNCCNGC--NTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYTN
               ||||       ||  | ||    ||||  | |   | ||       |        |  |
    TATCCCCTTCCTGAC-CCAGGAGCATCAGCAGCAGGTGCTCCAGGCCGTAGAACGCGCCAAGCAGGTCACCG
    300       310        320       330       340       350       360

            70        80        90        100       110        120
    WSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCAR-CAYWSNCCNATNW-SNWSNGAYTTYG-CNGTN
    ||  |  | |  || |   |   || | ||||  ||||| | ||| || |  | | ||   || || |  |
    TGGGGGAGCTGAACAGCCTCATCGGGCAGCAG-CTCCAGCCGCTGTCCCACCACGCACCCCCTGTGCCCCTG
   370       380       390       400        410       420       430

  130       140       150       160           170       180       190
    AARATNMG-NGARYTNWSNGAYTAYYTNYTNCARGAYTAY----CCNGTNACNGTNGCNWSNAAYYTNCARG
    |     ||   |||   | | |  |   |  |||  ||||    |   |  |  |  |  |   |||    |
    ACCCCCCGCCCAGC--CGGGCTGGTGGGCGGCAGTGCTACGGGGCTGCTTGCTCTGTCTGGAGCCCTGGCTG
  440     450         460       470       480       490       500

     200          210       220       230       240       250        260
    AYGARG---ARYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARM-GNYTNAARACN
     | |||   ||||  |||| || || |  ||    |  |  ||   ||| |||| |  || |  |  |||
    CCCAGGCTCAGCT-GGCGGCGG-CTGTCAAG-GAGGACCGTGC-GGGCG-TGGAGGCCGAGGGGTCCAGAGT
  510     520        530         540        550        560       570

       270       280       290       300       310       320       330
    GTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCN
    |  |   |  |  ||  | || | |  ||    ||      | | ||||    | ||||     || | ||
    GGAGAGAGCCCCGAGCAGGAGTG-CATCTCCCTCG----CCCCCTGAGA---GTCTCGTGGAGGAG-GAGCG
     580       590        600       610           620          630

     340       350         360       370       380         390       400
    TTYCARCCNCCNCCNWSNTGYY--TNMGNTTYGTNCARACNAAYATNWSNMGNY--TNYTNCARGARA-CNW
      | ||   ||    || || |    ||    |  ||||  |  |  || |  |    |   | |||| | |
    ACCGAGTGGCCCTGGTGGTGGCGGGAAGCAGAGAGCAGATGAGAAGGAGCCATCAGGACCTTATGAAAGCGA
  640     650       660       670       680       690       700       710

        410       420        430        440       450       460          470
    SNGARCARYTNGTNGCNYTNAARC-CNTGGATNACNM-GNCARAAYTTYWSNMGNTGYYTNG---ARYTNCA
    |  ||  |   || |  |  || |   |||   || | | | || | |||| ||   ||  |    ||| |
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    CGAAGACAAGAGT-GATTACAATCTGGTGGTGGACGAGGACCAACCCTCAG-AGCCCCCCAGCCCGGCTACC
          720        730       740       750       760        770       780

           480       490       500       510       520       530       540
    RTGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGC
    |  ||   | || ||  | || |  |  |   | ||  | |  ||    || | ||  || |  ||  |  |
    ACCCCCTGCGGAAAG--GTACCCATCTGCATTCCTG--CCCGTCGGGACCTGGTGG--ACAG-TCCAGC--C
          790         800       810         820       830          840

         550         560       570       580       590             600
    NCCNCARCCNC--CNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYT------NYTNGCNG-CNGC
     ||   ||| |    || |  |  |  || |      |    |  ||  | ||       ||  | | | ||
    TCCTTGGCCTCTAGCTTGCGGTCACCGCTGCCTAGAGCCAAGGAGCTCATCCTGAATGACCTTCCCGCCAGC
       850       860       870       880       890       900       910

       610           620        630       640         650       660
    -NTGGTGYYTNCA----YTG-GCARMGNACNMGNMGNMGNACNC--CNMGNCCNGGNGARCARGTNCCNCCN
      |  ||||| ||    ||| |   |   | || |  || || |  | |  || || |  ||| | |  ||
    ACTCCTGCCTCCAAATCCTGTGACTCCTCCCCGCCCCAGGACGCTTCCACCCCCGG-GCCCAGCT-CGGCCA
     920       930       940       950       960       970        980

  670     680       690       700    X
    GTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
    ||  | ||  | |||  ||| |  |      |||||
    GTCACCTCTGC-CAG--CTTGCGCTCAAGCCAGCACCTTCCACGGA
     990       1000        1010      1020


5. US-08-162-407-6 (1-705)
   Q11127       Sequence encoding P450SU2 and FeS-A.

ID   Q11127 standard; DNA; 1998 BP.
AC   Q11127;
DT   05-JUN-1991  (first entry)
DE   Sequence encoding P450SU2 and FeS-A.
KW   Cytochrome P450; P450SU1; P450SU2; herbicide resistance; ds.
OS   Streptomyces griseolus.
FH   Key             Location/Qualifiers
FT   misc_RNA        195..1403
FT   /*tag=  a
FT   /product= P450SU2
FT   misc_RNA         1452..1643
FT   /*tag=  b
FT   /product= FeS-A protein
PN   WO9103561-A.
PD   21-MAR-1991.
PF   27-AUG-1990; U04785.
PR   11-SEP-1989; US-405605.
PR   12-JAN-1990; US-464499.
PR   23-AUG-1990; US-569781.
PA   (DUPO ) DU PONT DE NEMOURS CO.
PI   Dean C, Harder PA, Leto KJ, Lichtner FT, Odell JT;
PI   O'Keefe DP, Omer CA, Romesser JA;
DR   WPI; 91-102077/14.
DR   P-PSDB; R11350, R11804.
PT   DNA encoding cytochrome P450 enzymes - and electron donating
PT   iron-sulphur proteins, used to confer herbicide resistance to
PT   plants and microorganisms
PS   Claim 15; page 158; 224pp; English.
CC   This sequence contains the coding information for (a) the cytochrome
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 CC   P450 enzyme, P450SU2; and (b) the electron donor iron sulphur
 CC   protein FeS-A.  It is contained in a recombinant plasmid which is
 CC   used to transform host Streptomyces species which in turn are used
 CC   to coat a plant seed to transform the plant.  The resultant trans-
 CC   formants are resistant to herbicides.
 CC   See also Q11126.
 SQ   Sequence   1998 BP;    272 A;    839 C;    620 G;    267 T;

Initial Score    =    121  Optimized Score   =    365 Significance =  6.42
Residue Identity =    28%  Matches           =    331 Mismatches   =   346
Gaps             =     65  Conservative Substitutions             =     0

              X       10        20         30        40       50        60
              ATGACNGTNYTNGCNCCNGCNTGGWSNCC-NACNACNTAYYTNYTNYTNYTNYTNYTNW
              | | | |      |  | || ||  | ||  |  ||  |||  | |  |  |  |  |
    TAATTAGCTCACG-CGGAAGGACCGGCCGCATGACGACCGCAGAACGCACCGCTCCCCCGACGCCCTCACC
      170     X  180       190       200       210      220       230

           70        80        90       100        110       120       130
    SNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAY-WSNCCNATNWSNWSNGAYTTYG-CNGTNAA
    |  | || |  ||  |  | |  | |||| | ||| | | |  | || |  || || ||    | | |
    GTCCCGGCC--AGCCGCGCCCCCGGCTGCCCCTTCGACCCCGCGCCCGACGTC-ACCGAGGCGGCCCGCACC
     240         250       260       270       280        290       300

          140       150       160        170        180       190        200
    RATNMGNGARYTNWSNGAYTAYYTNYTNCA-RGAYTAYCCNG-TNACNGTNGCNWSNAAYYTNCARGAYG-A
    ||  ||   ||   | | |  ||| |   | || |  ||| | |  |  | |  ||   ||  |||||||
    GAACCGGTCAC-CCGGGCCACCCTCTGGGACGGCTCCTCCTGCTGGC--TGGTGACGCGCCATCAGGACGTC
      310        320       330       340       350         360       370

             210       220        230           240       250       260
    RGARY--TNTGYGGNGGNYTNTGGMGNYT-NGTNY--TNGCNCA--RMGNTGGATGGARMGNYTNAARACNG
     | || |   ||| |  |    ||| ||  |  |    || ||  ||   || |    |  ||   ||| |
    CGCGCGGTCCTCGGCGACC---CGCGCTTCAGCGCCGACGCCCACCGCACCGGCT--TCCCCTTCCTGACCG
       380       390          400       410       420         430       440

      270       280         290        300       310        320       330
    TNGCNGGNWSNAARAT--GCARGGNYTNYTNGARM-GNGTNAAYACNGA-RATNCAYTTYGTNACNAARTGY
      |  ||  |  ||||   | |   |  |  || |    |   ||  || ||  |    |    |  | |||
    CCGGCGGCCGCGAGATCATCGGCACCAACCCGACCTTCCTGCGCATGGACGACCCGGAGCACGCCCGACTGC
          450       460       470       480       490       500       510

           340       350       360       370       380       390       400
    GC---NTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACN
    ||    | |  | | ||  | || | | | |     ||  || |  ||    | ||     | |||
    GCCGGATGCTCACCGCCGACTTCAT-CGTCAAGAAGGTCGAGGC-GATGCGCCCCG--AGGTGCAGCGCCTC
        520       530        540       550        560         570       580

         410       420         430         440       450       460       470
    WSNGARCARYTNGTNGCNYTNA--ARCCNTGGA-TNAC-NMGNCARAAYTTYWSNMGNTGYYTNGARYTNCA
     | ||  | || || |  |  |  | |   |||   ||  |  | || ||  || |   | || | ||| |
    GCCGACGACCTGGTCGACCGGATGACCACCGGACGCACCTCCGCCGACCTGGTCACCGAG-TTCGCGCTGCC
          590       600       610       620       630       640        650

            480       490       500       510       520        530
    R-TGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARG-CNAC-NGCNCCNAC
    | ||||  ||   ||| ||    || ||  |  |  || | |     || |  |||| | ||  |  |   |
    GCTGCCGTCC---CTGGTG--ATCTGCCTGCTGCTCGGCGTC-----CCCTACGAGGACCACGCGTTCTTCC
         660            670       680            690       700       710
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540       550        560        570        580       590          600
  NGCNCCNCARCC-NCCNYTNYTNYTNYTNY-TNYTNYTNCC-NGTNGGNYTNYTNYTNYTNG---CNGCNGC
   |   | |||||     || ||    || |   |  || ||  |   | |     |  |  |     |  ||
  AGGAGCGCAGCCGGGTCCTGCTCACCCTGCGGTCCACTCCCGAGGAAGTCCGGGCCGCCCAGGACGAGTTGC
     720       730       740       750       760       770       780

     610       620          630       640       650       660       670
  NTG-GTGYYTNCAYTGGC-ARM--GNACNMGNMGNMGNACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNC
    | || |||   | |||  ||  | || |  ||  |  |  |  | |   |  | ||    || || |  |
  TGGAGTACCTCGCCCGGCTCGCCCGGACCAAGCG-GGAGCGGCCGGACGACGCCATCATCAGCCGCCTGGTC
   790       800       810       820        830       840       850

      680       690       700    X
  CNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
     | |  | || ||  |  |     || | |
  GCCCGCGGCGAGCTCGACGACACCCAGATCGCCACCATGGA
  860       870       880       890


6. US-08-162-407-6 (1-705)
   Q27764        Adrenodoxin reductase gene (part 2).

 ID   Q27764 standard; DNA; 5089 BP.
 AC   Q27764;
 DT   19-NOV-1992  (first entry)
 DE   Adrenodoxin reductase gene (part 2).
 KW   Ad Red; unsequenced intron; cholesterol side chain cleavage system;
 KW   adrenodoxin; alternate splicing; ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   intron          ..706
 FT   /*tag=  a
 FT   /number= 2
 FT   /label= "Intron continued from Q25050; see comments"
 FT   exon            707..799
 FT   /*tag=  b
 FT   /number= 3
 FT   intron          800..1012
 FT   /*tag=  c
 FT   /number= 4
 FT   exon            1013..1135
 FT   /*tag=  d
 FT   /number= 4
 FT   intron          1136..1336
 FT   /*tag=  e
 FT   /number= 4
 FT   exon            1337..1450
 FT   /*tag=  f
 FT   /number= 5
 FT   intron          1451..1757
 FT   /*tag=  g
 FT   /number= 5
 FT   exon            1758..1859
 FT   /*tag=  h
 FT   /number= 6
 FT   intron          1860..2623
 FT   /*tag=  i
 FT   /number= 6
 FT   exon            2624..2749
 FT   /*tag=  j
FT   /number= 7
FT   intron          2750..3005
FT   /*tag=  k
FT   /number= 7
FT   exon            3006..3090
FT   /*tag=  l
FT   /number= 8
FT   intron          3091..3218
FT   /*tag=  m
FT   /number= 8
FT   exon            3219..3418
FT   /*tag=  n
FT   /number= 9
FT   intron          3419..3498
FT   /*tag=  o
FT   /number= 9
FT   exon            3499..3670
FT   /*tag=  p
FT   /number= 10
FT   intron          3671..4319
FT   /*tag=  q
FT   /number= 10
FT   exon            4320..4490
FT   /*tag=  r
FT   /number= 11
FT   intron          4491..4617
FT   /*tag=  s
FT   /number= 11
FT   exon            4618..4748
FT   /*tag=  t
FT   /number= 12
FT   3'UTR           4749..5048
FT   /*tag=  u
FT   mat_peptide     ..4745
FT   /*tag=  v
FT   /note= "Peptide continued from Q25050; see comments"
FT   misc_signal     2641
FT   /*tag=  w
FT   /label= Alternative_splice_site
PN   WO9207865-A.
PD   14-MAY-1992.
PF   30-OCT-1991; U08081.
PR   31-OCT-1990; US-606876.
PA   (REGC ) UNIV CALIFORNIA.
PI   Lin D, Miller WL;
DR   WPI; 92-183618/22.
PT   Human adrenodoxin reductase gene and related polypeptide(s) - for
PT   diagnosis and treatment of diseases and genetic disorders causing
PT   high cholesterol levels
PS   Disclosure; Fig 2; 36pp; English.
CC   The sequence shows the second portion of the sequence of the human
CC   adrenodoxin reductase (Ad Red) gene.  A region of approx. 5kb of
CC   unsequenced DNA is represented by 50 n's.  The first portion of
CC   this sequence is given in Q25050.  There are a total of 12 exons and
CC   the whole sequence covers 6905 bp, excluding the unsequenced intron
CC   sequence.
CC   Ad Red is involved in the cholesterol side chain cleavage system
CC   and is loosely associated with the inner mitochondrial membrane.
CC   It recieves electrons from NADPH and then passes these electrons
CC   to adrenodoxin, which functions as an indiscriminate electron shuttle.
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CC   Ad Red mRNA undergoes alternate splicing to produce two different
CC   forms, with the less abundant form containing 18 nucleotides
CC   encoding 6 amino acids in the middle of the protein.  The
CC   alternative splicing site occurs at the begining of exon 7 (see
CC   feature table).
SQ   Sequence   5089 BP;    902 A;    1401 C;    1633 G;    1100 T;
SQ   53 Others;

Initial Score    =    118 Optimized Score   =    351  Significance =  6.23
Residue Identity =    25% Matches           =    322  Mismatches   =   350
Gaps             =     72 Conservative Substitutions                 =     0

              X       10        20        30        40        50         60
              ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYT-NW
                |   |      | || || ||||      | ||  |||| |  |   | |  |  ||  |
    TCTTACTCTTCAGTAAGCCACATCCCCTGCTTGGATCATCCCCACTCACCTCCCACCAGT-TAACAGTTAAA
   2080      2090      2100      2110      2120      2130       2140

           70        80        90          100        110       120
    SNWSNGGNYTNWSNGGNACNCARGAYTGYWSNT---TYCARCAY-WSNCCNATNWSNWSNGAYTTYGCNGTN
    | ||    || ||       |  | |||| | |   ||||| || || |  |  || ||  ||| | |  |
    GTTCATCTTTGAGATCTTGGCTCGGTTGTCCCTTCCTCCAGGACTTCCCTGAATTGGTC-CACTCCCCCATC
  2150      2160      2170      2180      2190      2200       2210

  130        140       150       160       170       180         190
    AAR-ATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNW--SNAAYYTNCARGAY
      |  | |    ||  ||   || ||| || | |  | |||   | |   | || |  | |||||   | ||
    GTGCCTCCTCCCATAGAC---CTGTCTACTTCTGTTTCACCGCAT-ATCATCGCCACGGCAATTT--TACAC
 2220      2230         2240      2250      2260       2270      2280

   200       210       220       230        240       250       260
    GARGARYTNTGYGGNGGNYTNTGGMGNYTNGTNYT-NGCNCARMGNTGGATGGARMGNYTNAARACNG-TNG
         ||  ||  | |  || ||  |  |  | ||   | ||||    |||   ||| |   |||  |   |
    -----ACATTGATGAGTATT-TGATGAGTATTTCTCTCCCCAGC---AGATCACAAGCTCTGAGAGGGCCTG
          2290      2300       2310      2320         2330      2340

   270       280       290         300       310       320       330
    CNGGNWSNAARATGCARGGNYTNYTNGA--RMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTT
    |    ||     |       |  || ||  ||       | |  || | | || | |      | || | |
    CTCCTTGTCTCTTTTCCTCACCATT-GACCACCCCGCCCCTCCAAGCT-CTTTGCATGGGGGTGAGCACATG
  2350      2360      2370       2380      2390       2400      2410

   340       350       360       370       380        390        400
    YCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMG-NYTNYT-NCARGARACNWSNGAR
      ||   ||  | || | |||  | |   |  ||         ||  |  || ||    |||| | |  | |
    GTAGAGGCCCACTACATACTT--GTTGAATGAAAGTGTGGGCCTGGTGTGCTATTAGTTGGAGCCATTTGCA
  2420      2430        2440      2450      2460      2470      2480

   410       420       430       440       450       460       470
    CARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCAR---TGYCAR
     |||| |  ||  |    |    |   || ||   || |   || ||   ||| ||||  | |     ||||
    GAGTTGGCAGCAATGCTCCATCTGGCCACCAGGGGGAGC-AGTGGCGCAATTT-GAGCCGCCAGCTCTCCAG
  2490      2500      2510      2520       2530      2540       2550

    480       490       500         510       520       530       540
    CCNGAYWSNWSNACNYTNCCNCCNCCNTG--GWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCNC
     |  || |  | || |  ||       ||  ||| || |   | || | | | |  |  |  |   | ||
    GCCCACGGTGGGACATGACC----AAATGGAGAGTCCCCTTTC-CTCG-GTC-AGTG-TCTGATGACTCCAA
  2560      2570          2580      2590       2600         2610      2620
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8. US-08-162-407-6 (1-705)
   N60554       Sequence encoding bovine male specific sequence.

 ID   N60554 standard; DNA; 5783 BP.
 AC   N60554;
 DT   24-MAY-1991  (first entry)
 DE   Sequence encoding bovine male specific sequence.
 KW   Plasmid pES8; PstI fragment; ss DNA; probe; sex determination;
 OS   Bos sp.
 PN   WO8607095-A.
 PD   04-DEC-1986.
 PF   30-MAY-1986; U01169.
 PR   31-MAY-1985; US-739817.
 PR   05-JUN-1986; US-871111.
 PA   (SALK ) SALK INST FOR BIOL STUD.
 PI   Ellis SB;
 DR   WPI; 86-332096/50.
 PT   Nucleic acid probes - for prenatal sexing of bovine species
 PS   Disclosure; page 36-7; 75pp; English.
 CC   The nucleic acid hybridises to a greater extent with total
 CC   DNA of a breed of the genus Bos than with total DNA of females of the
 CC   breed.  An embryo or foetus of the Bos species may be sexed by
 CC   contacting cellular DNA with the labelled probe.  The probe provides
 CC   rapid, 100% accurate sexing of bovine embryos using the small amt. of
 CC   DNA obtd. from 4 embryonic cells.  Kits may be assembled.
 SQ   Sequence   5783 BP;    745 A;    1627 C;    1029 G;    753 T;
 SQ   1629 Others;

Initial Score    =    117  Optimized Score  =    366  Significance =  6.17
Residue Identity =    27%  Matches          =    341  Mismatches   =   334
Gaps             =     88  Conservative Substitutions           =     0

           X        10          20        30        40        50
           ATGA-CNGTNYTNGCNCCNG--CNTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYT
            ||| |    || || || |  |  ||||     |     |    || |     |  || |
 GGTGTCTGCACTGATCCAGGCTGGCTCCTGCCCTCGGTCAAGACCCTGGCAAACACTCCAGAGCCCACTCC-
5030      5040      5050      5060      5070      5080      5090

60        70        80            90        100        110       120
 NWSNWSNGGNYTNWSNGGNACNCARG--AYTG--YWSNTTYCARCA-YWSNCCNATNWSNWSNGAYTTYGCN
   | ||    |   |  | |  | ||   |||  ||| ||| |||| ||| |  |  |  || | |
 -GGATCCCTGCACCGAAGCAGGCTGGCTCCTGCCTTCGTTCAAGCACCTGGCAAAGTA--ACCGCCGGGAGA
5100      5110      5120      5130      5140      5150        5160

  130       140       150       160         170        180       190
 GTNAARATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYT--AYCCNGTNACNGT-NGCNWSNAAYYTNCAR
  |  || | ||    ||  | | | ||||      |  ||  ||   ||  |  |  || || || ||   |
 CTCCAGCT-CGCTCCCTGCCCGTCCACTTCGCTGTGTCCTGCATTTGGTCCCTCTCCGCGACAAAGCT-GTG
5170       5180      5190      5200      5210      5220      5230

   200       210       220            230       240          250
 GAYGARGARYTNTGYGGNGGNYTNTGGMG-----NYTNGTNYTNGCNCARM-GNTGGA--TGGARMGNYTNA
   |  | ||||   |   || |  || ||      || |  || |  | ||     ||    ||||  |  |
 ATCCCGCAGCTCACTCCCGG-CACTGAAGCCACCTCTGGGGCTTGGCCTGCTTCAAGACCCCGAGAAATACA
5240      5250       5260      5270      5280      5290      5300

260      270       280            290        300       310        320
 ARACNGTNGCNGGNWSNAARATGC-----ARGGNYT-NYTNGARMGNGTNAAYACNGARATNCAY-TTYGTN
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    | || |  |     |||| ||     |||| ||  ||    ||    | | | | ||  |||  || |
 TCTCGGTCGGCGCACTGAAGAAGCAGTCTAGGGCCTGCCTTCTTCG----ATTCCCGCGACACACACTCCTG
5310     5320      5330      5340      5350          5360      5370

     330       340          350         360       370       380       390
 A-CNAARTGYGCNTTYCARCC---NCCNCCNW--SNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTN
 | | | |  ||| | |  |||     | |  |  | ||||  |   |||  ||| |   |   || |  ||
 AGCCACAGCTGCGTGCGCGCCCTGAACTCGGATGGATGCTGCC--CTTGGGCAACC--CCCCCACCCTCCTC
 5380      5390      5400      5410        5420      5430        5440

        400      410         420            430          440       450
 YTNCARGARACNWSNGARCARYTNGT-NGCNYTNA-----ARCCNTG-GATNA--CNMGNCARAAYTTYWSN
 |  | |  ||  ||  ||  |||  |  || || |       || || | | |  | ||   |  || |||
 CCCCCACCAAACACACAAACACTCCTGAGCGTTCATCTCGGTCCCTGAGCTCAACCACGGTGG--TTCCTGC
   5450      5460      5470      5480      5490      5500        5510

     460       470       480       490         500       510       520
 MGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNY--TNCCNCCNCCNTGGWSNCCNMGNCCNYTNG
 |  || |  |||   |   | ||| |  | || ||  | |    |   | || ||| | ||  | ||
 CTCTGGC--GAAGGCCCCCGACAAAC--AATCCTGAGCCCAAACCTGGCCCCCTGGCCCCCTGGCCCCGAAC
   5520        5530        5540      5550      5560      5570      5580

       530       540       550       560        570       580       590
 A--RGCNACNGCNCCNACNGCNCCNCARCCNCCNYTNYTNYTNYTNY-TNYTNYTNCCNGTNGGNYTNYTNY
 |  ||  |   | ||    |  ||  | || ||    |  || || |   ||  |  |    |     ||
 AATGGTGAGTCCTCCCCTTGTTCC-AACCCCCCGGAATCACTGCTGTGCCCTCATCTCACGCGCTGAACTAA
     5590      5600       5610      5620      5630      5640      5650

      600       610       620        630       640           650
 TNYTNGCNGCNGCNTGGTGYYTNCAYTGGCA-RMGNACNMGNMGNMGNAC----NCCNMGNCCNGG----NG
   |  ||  | |  | |||||    ||  || |||  | || |  |   |     || || |  ||     |
 ACCAAGC-ACGG--TCGTGCC----CTTCCAGAAGAGCCCGTCTAAATTCCTGAGCCCCGTCTCGGTCACTG
    5660         5670          5680      5690      5700      5710

   660         670       680        690       700    X
 ARCARGTNCC--NCCNGTNCCNWSNCCNCAR-GAYYTNYTNYTNGTNGARCAY
 ||| ||  ||   |  |  ||  | |    | || |  ||  |  | || | |
 AAC-GGAACCAGTCGAGGTCCTGCCCTTGTGCGAGCGCCTAGTCCTTGACCGTAAGACATGAA
5720      5730      5740      5750      5760      5770      5780


9. US-08-162-407-6 (1-705)
   Q06233       Bovine male-specific insert of lambda ES6.0 genome

 ID   Q06233 standard; DNA; 4414 BP.
 AC   Q06233;
 DT   28-JAN-1991  (first entry)
 DE   Bovine male-specific insert of lambda ES6.0 genome.
 KW   Bovine male-specific insert; lambda ES6.0 embryo sexing;
 KW   embryo transfer; ss.
 OS   Bos taurus.
 FH   Key             Location/Qualifiers
 FT   misc_RNA        466..469
 FT   /*tag=  a
 FT   /note="best guess from ambiguous sequence info."
 FT   misc_RNA        957..962
 FT   /*tag=  b
 FT   /note="best guess from ambiguous sequence info."
 FT   misc_RNA        1246..1252
 FT   /*tag=  c
 550       560       570       580           590       600       610
AR-CCNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGG----NYTNYTNYTNYTNGCNGCNGCNTGGTGYYT
 | || || ||  | |           |  |  |  ||     ||     | || |  || |  | | ||
GGCCCTCCTTTGTGCCAGAGAACGGACATCACGAAGGCAGCCCTGGGTGTACT-GAGGCAGAGTCGAGTGA
     2630      2640      2650      2660      2670       2680      2690

       620        630       640           650         660          670
NCAY----TGGC-ARMGNACNMGNMGNMGNACNC--CNMG--NCCNGGNGAR--CARGTNC---CNCCNG-T
  ||    |||| || |  | || ||  |  | |  | ||   ||      |   |||| |     || |
AGACAGTGTGGCTAGTGGGC-CGGCGTGGCNCCCTGCAAGTGGCCTTCACCATTAAGGTGCTGGGGCCAGAG
   2700      2710       2720      2730      2740      2750      2760

      680       690       700    X
NCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
    ||    |||| ||     |     | || |
TGGGAGGAGCCAGGGTTCCAGGTGGAGGGGCCTCTCCTTAAGG
  2770      2780      2790      2800


7. US-08-162-407-6 (1-705)
   Q56917        Glutamic acid receptor.

ID   Q56917 standard; DNA; 3717 BP.
AC   Q56917;
DT   08-AUG-1994  (first entry)
DE   Glutamic acid receptor.
KW   Glutamic acid receptor; synaptic signal translation; diagnosis;
KW   brain disease; nerve signal; gene therapy; NMDA; cerebellum; ICR;
KW   mouse; nerve cell necrosis; ds.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   CDS             1..3717
FT   /*tag=  a
FT   /product= glutamic_acid_receptor
PN   J06014783-A.
PD   25-JAN-1994.
PF   30-JUN-1992; 173155.
PR   30-JUN-1992; JP-173155.
PA   (MITU ) MITSUBISHI KASEI CORP.
DR   WPI; 94-061478/08.
DR   N-PSDB; Q56916.
PT   New glutamic acid receptor and gene - for use in analysis of
PT   synaptic signal translation, and diagnosis of brain disease
PS   Claim 1; Page 21-24; 35pp; Japanese.
CC   The sequence codes for a glutamic acid receptor. The receptor is
CC   useful for the analysis of nerve signal translation; within the
CC   synapse, expresssion of synapse plasticity, nerve cell necrosis,
CC   brain structure and brain disease. It can also be used in gene
CC   therapy.
SQ   Sequence   3717 BP;    675 A;    1199 C;    1120 G;    723 T;

Initial Score     =    117  Optimized Score =    369  Significance =  6.17
Residue Identity  =    29%  Matches         =    351  Mismatches   =   312
Gaps              =     96  Conservative Substitutions            =     0

          X       10          20        30        40        50        60
          ATGACNGTNYT-NGCNC-CNGCNTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYTN
            | | |  ||  || |   ||  ||||  | |   | |  |  |  |   |  | ||
CCTTGGTGCTTGGGCAGGGCTGGGCGCAGGGCAGGGAGAAC-AGGCCGTGACCGTGGC-GGTGGTGTTTGGC
       50 X      60        70        80         90        100       110
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          70         80          90       100       110       120
  WSNWSNGGNYTNWSNG-GNACNCARGAYTG--YWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTN
  || || || |  || |    | |||| | |  ||| | || || | |    |  || || |||||  |  |
  AGCTCTGGGC-CACTGCAGGCCCAGGCCCGGACTCGTCTC-ACCCCGCAGAACTTCCTG-GACTTGCCTCTG
        120        130       140       150        160        170       180

130       140       150       160       170       180       190       200
  AARATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGAR
   |||| |   |||  ||  || |||     ||| | ||||     ||    || || | ||| ||   | |
  GAGATCC---AGC-CACTCACCATCGGGGTCAACAATACC----AACCCCAGC-AGCATCCT-CA--CCCA-
            190        200       210           220        230

        210         220        230       240         250       260
  GARYTNTGYGGNGGNYT--NTGGMG-NYTNGTNYTNGCNCARMG--NTGGATGGARMGNYTNAARACNGTNG
   |||  |||||    ||   || ||  |  || |  |  || ||   | || ||| |   |  | || |  |
  -AAT-CTGTGGGCTCCTGGGTGCCGCCCGAGTCCACG-GCATCGTCTTTGA-GGACAACGTGGACACTGAGG
 240        250       260       270        280        290       300

 270       280       290       300       310       320         330
  CNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNA--ARTGYGCNTT
  | |   |  || ||| ||  ||  |    |   |  | ||  |  | | | || | |  |  |||| |   |
  CCGTGGCTCAGCTGCTGGATTTCGT--CTCCTCT-CAGACCCACGTGCCCATCCTCAGCATCAGTG-GAGGT
  310       320       330          340       350       360       370

 340             350       360       370       380       390       400
  YCARC---------CNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARAC
  || ||         | || || ||  |||  ||  ||   |   |  |||  ||  |  | |  | ||||
  TCTGCTGTGGTCCTCACCCCCAAGGAGCC--AGGCTCCGCCTTTC-TACAGCTG-GGCGTGTCCCTGGAG--
    380       390       400         410        420        430       440

        410       420        430        440       450       460
  NWSNGARCARYTNGTNGCNYTNAA-RCCNTGGA-TNACNMGNCARAAYTTYWSNMGNTGYYTNGA----RYT
   ||  ||| ||  ||    || || |   ||||   |  || | | |   |   || ||||   |     ||
  CAG-CAGCTGCAGGTGCTGTTCAAGGTGCTGGAGGAATACGACTGGAGCGCGTTCGCTGTCATCACCAGCCT
         450       460       470       480       490       500       510

  470              480       490       500       510           520
  NCA---RTGYCA-RC---CNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCC-NMGNCC---NYTNGARGCN
   ||   | |||| ||   |   ||| ||  | |   | ||  |   ||| ||  |  ||    || | |||
  GCACCCGGGCCACGCGCTCTTCCTCGAGGGCGTGCGCGCCGTCGCCGACGCCAGCTACCTGAGCTGGCGGCT
       520       530       540       550       560       570       580

 530        540       550           560       570       580       590
  ACNGCNCCNAC-NGCNCCNCARC----CNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYTNY
   | |  |   |   | |   |||    | ||  |    |     |     ||  | |   | || || |  |
  GCTGGACGTGCTCACGCTGGAGCTGGGCCCCGGTGGGCCGCGAGCGCGCACT--CAG--CGCTTACTGCGCC
     590       600       610       620       630           640       650

    600              610        620        630        640       650
  TNGCNGCNGC-------NTGGT-GYYTNCAYTGGCARMG-NACNMGNMGNM-GNACNCCNMGNCCNGG-NGA
    |  |  ||        |||| ||||  ||||    ||  |  || || | |  | |  ||    ||  |
  AGGTCGACGCCCCGGTGCTGGTGGCCT--ACTGCTCCCGTGAAGAGGCGGAGGTGCTCTTCGCGGAGGCTGC
         660       670         680       690       700       710       720

   660       670       680       690       700    X
  RCARGTNCCNCCNGTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
  |||||  |   |  |     | ||     || | |  || ||     ||
  ACAGG--CTGGC-TTGGTGGGACCCGGTCACGTGTGGTTAGTACCTAATCTGGCGCTGG
         730        740       750       760       770
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FT   /note="best guess from ambiguous sequence info."
FT   misc_RNA        2912..3032
FT   /*tag=  d
FT   /note="only appears in about 50% of lambda ES6.0"
FT   misc_RNA        3080..3087
FT   /*tag=  e
FT   /note="best guess from ambiguous sequence info."
PN   US4960690-A.
PD   02-OCT-1990.
PF   05-JUN-1986; 871111.
PR   31-MAY-1985; US-739817.
PR   05-JUN-1986; US-871111.
PA   (SALK ) SALK INST FOR BIOL STUD.
PI   Ellis SB, Harpold MM;
DR   WPI; 90-319822/42.
PT   Bovine male-specific nucleic acid probes - used for sexing bovine
PT   embryos at the time of embryo transfer with high accuracy
PS   Example; Fig 1; 22pp; English.
CC   Lambda clone ES6.0 was isolated from a bovine liver-derived
CC   library. Filters were assayed for male-specific clones by comparing
CC   those that were pre-hybridised with sheared female bovine DNA and
CC   those that were not. Nine possible male-specific clones were
CC   identified for further analysis. In 2 of the 9 clones, bands
CC   corresponding to 4.0kb and 2.2kb, indicative of male-specific
CC   clones, were observed. ES6.0 was one of the clones. It was partially
CC   sequenced. Some bases could not be unambiguously identified. The long
CC   rows of 60 "N" residues within the sequence represent breaks in the
CC   6.2kb insert. The actual numbering of the blocks of sequence are
CC   420-716, 1089-1747, 2540-3560, 4000-6203.
CC   See also Q06234 and Q06235.
SQ   Sequence   4414 BP;    742 A;    1625 C;    1030 G;    756 T;
SQ   261 Others;

Initial Score     =    116  Optimized Score  =    367  Significance =  6.11
Residue Identity  =    28%  Matches          =    344  Mismatches   =   329
Gaps              =     92  Conservative Substitutions              =     0

              X        10          20        30        40        50
              ATGA-CNGTNYTNGCNCCNG--CNTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYT
               ||| |    || || || |  |  ||||     |     |    || |     |  || |
    GGTGTCTGCACTGATCCAGGCTGGCTCCTGCCCTCGGTCAAGACCCTGGCAAACACTCCAGAGCCCACTCC-
  3660      3670      3680      3690      3700      3710      3720

   60        70        80            90       100         110           120
    NWSNWSNGGNYTNWSNGGNACNCARG--AYTG--YWSNTTYCARCA-YWSNCCNA-TNWS----NWSNGAYT
      | ||    |   |  | |  | ||   |||  ||| ||| |||| ||| |  | | ||      | ||||
    -GGATCCCTGCACCGAAGCAGGCTGGCTCCTGCCTTCGTTCAAGCACCTGGCAAAGTAACCGCCGGGAGACT
  3730      3740      3750      3760      3770      3780      3790      3800

           130       140       150       160           170       180
    TY-GCNGTNAARATNMGNGARYTNWSNGAYTAYYTNYTNCA---RGAYTAYC-CNGTNACNGTNGCNWSNAA
     | ||        | |  |  |  |  | || | | || ||   || |  || | |  ||    ||    |
    CCAGCTCGCTCCCTGCCCGTCCACTTCG-CTGTGTCCTGCATTTGGTCCCTCTCCGGGAC-AAAGCTGTGAT
          3810      3820       3830      3840      3850       3860      3870

   190         200       210       220       230       240       250
    YYTNCAR--GAYGARGARYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTN
    ||  |||   ||     ||  ||  |    || ||| | || |  |  ||   |||       ||||  |
    CCCGCAGCTCACTCCCGGCACTGAAGCCACCTCTGGGGCTTGG--CCTGCTTCAAG--ACCCCGAGAAATAC
          3880      3890      3900      3910        3920        3930
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   260       270       280            290        300       310        320
    AARACNGTNGCNGGNWSNAARATGC-----ARGGNYT-NYTNGARMGNGTNAAYACNGARATNCAY-TTYGT
    |   | || |  |     |||| ||     |||| ||  ||    ||    | | | | ||  |||  || |
    ATCTCGGTCGGCGCACTGAAGAAGCAGTCTAGGGCCTGCCTTCTTCG----ATTCCCGCGACACACACTCCT
  3940      3950      3960      3970      3980          3990      4000

         330       340          350         360       370       380
    NA-CNAARTGYGCNTTYCARCC---NCCNCCNW--SNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYT
     | | | |  ||| | |  |||     | |  |  | ||||  |   |||  ||| |   |   || |  ||
    GAGCCACAGCTGCGTGCGCGCCCTGAACTCGGATGGATGCTGCC--CTTGGGCAACC--CCCCCACCCTCCT
    4010      4020      4030      4040      4050        4060        4070

  390       400       410        420       430       440         450
    NYTNCARGARACNWSNGARCARYTNGT-NGCNYTNAARCCNTGGATNACNMG-NCAR-AAYTTYWSNMGNTG
     |  | |  ||  ||  ||  |||  |  || ||   | |  ||      ||  |||  ||  | |    ||
    CCCCCCACCAAACACACAAACACTCCTGAGCGTT--CATCTCGGTCCCTGAGCTCAACCACGGTGGTTCCTG
      4080      4090      4100        4110      4120      4130      4140

   460       470       480       490        500       510       520
    YYTNGARYTNCARTGYCARCCNGAYWSNWSNA-CNYTNCCNCCNCCNTGGWSNCCNMGNCCNYT-----NGA
    |||   ||  ||| |||  || ||||  || | | |   | |   | ||| | ||  | || ||      ||
    CCTCTGGC--CAAGGCC--CCCGACA-AACAATCCTGAGCCCAAACCTGGCCCCCTGGCCCCCTGGCCCCGA
      4150          4160       4170      4180      4190      4200      4210

            530       540       550       560        570       580       590
    R-----GCNACNGCNCCNACNGCNCCNCARCCNCCNYTNYTNYTNYTNY-TNYTNYTNCCNGTNGGNYTNYT
    |     |  |   | ||    |  ||  | || ||    |  || || |   ||  |  |    |     ||
    ACAATGGTGAGTCCTCCCCTTGTTCC-AACCCCCCGGAATCACTGCTGTGCCCTCATCTCACGCGCTGAACT
         4220      4230       4240      4250      4260      4270      4280

           600       610       620        630       640           650
    NYTNYTNGCNGCNGCNTGGTGYYTNCAYTGGCA-RMGNACNMGNMGNMGNAC----NCCNMGNCCNGG----
        |  ||  | |  | |||||    ||  || |||  | || |  |   |     || || |  ||
    AAACCAAGC-ACGG--TCGTGCC----CTTCCAGAAGAGCCCGTCTAAATTCCTGAGCCCCGTCTCGGTCAC
        4290         4300          4310      4320      4330      4340

        660         670       680        690       700    X
    NGARCARGTNCC--NCCNGTNCCNWSNCCNCAR-GAYYTNYTNYTNGTNGARCAY
     |||| ||  ||   |  |  ||  | |    | || |  ||  |  | || | |
    TGAAC-GGAACCAGTCGAGGTCCTGCCCTTGTGCGAGCGCCTAGTCCTTGACCGTAAGACATGAA
   4350       4360      4370      4380      4390      4400      4410


10. US-08-162-407-6 (1-705)
    Q02830        cDNA to HIV-2 RNA.

 ID   Q02830 standard; cDNA; 9360 BP.
 AC   Q02830;
 DT   29-MAY-1989  (first entry)
 DE   cDNA to HIV-2 RNA.
 KW   HIV; AIDS; Vaccine; pUC-HIV-2(GH-1).
 OS   HIV-2.
 FH   Key             Location/Qualifiers
 FT   CDS             544..2109
 FT   /*tag=  a
 FT   /label=Gag reading frame
 FT   CDS             1830..4934
 FT   /*tag=  b
 FT   /label=Pol gene reading frame.
FT   CDS               4867..5511
FT   /*tag=  c
FT   /label=Q gene reading frame
FT   CDS               5342..5677
FT   /*tag=  d
FT   /label=X gene reading frame
FT   CDS               5680..5994
FT   /*tag=  e
FT   /label=R gene reading frame
FT   CDS               6148..8703
FT   /*tag=  f
FT   /label=Env gene reading frame.
FT   CDS               8540..9304
FT   /*tag=  g
FT   /label=F gene reading frame.
PN   J01289486-A.
PD   21-NOV-1989.
PF   16-MAY-1988; 119024.
PR   16-MAY-1988; JP-119024.
PA   Toa Nenryo Kogyo KK,  Fuji Kebio KK.
DR   WPI; 90-005177/01.
DR   P-PSDB; R04024-30.
PT   DNA indicating complement to RNA gene -
PT   of Human Immunodeficiency Virus type 2 used for new vaccine or
PT   diagnostic for AIDS virus.
PS   Claim 2; Fig.4; 12pp; Japanese.
CC   cDNA to novel HIV-2 (GH-1) has been integrated into plasmid
CC   pUC HIV-2(GH-1). Useful for diagnosis and vaccination against the virrus.
CC   Carries 7 overlapping genes in varrious reading frames, includding Gag,
CC   Pol and Env.
SQ   Sequence   9360 BP;   3211 A;   1944 C;   2317 G;   1888 T;

Initial Score    =    116  Optimized Score   =    348  Significance =  6.11
Residue Identity =    26%  Matches           =    318  Mismatches   =   355
Gaps             =     67  Conservative Substitutions               =     0

              X       10          20          30         40        50
              ATGACNGTNY--TNGCNCCNGCNTGG--WSNCCNACNACNT-AYYTNYTNYTNYTNYTNYTN
              ||||   | |  | ||    |   ||  ||    |   | | ||    |  | || |  ||
    CAATACATGGATGATATTTTAATAGCTAGTGACAGGACAGGTTTAGAGCATGACAAAGTAGTCCTGCAGCT-
         2930 X    2940      2950      2960      2970      2980      2990

     60        70        80        90       100           110       120
    YTNWSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAY----WSNCCNATNWSNWSNGAYTTYGC
       || ||    || |  ||  |  ||| || |||   || | ||    ||  | |  |  ||   || |||
    AAAAGAAC--TTCTGAATGG--CCTAGGGTT-CTCTACCCCAGATGAGAAGTTCCA--AAAAGACCCTCCGC
        3000        3010         3020      3030      3040        3050

      130         140       150       160        170       180       190
    NGTNAA--RATNMGNGARYTNWSNGAYTAYYTNYTNCARGAY-TAYCCNGTNACNGTNGCNWSNAAYYTNCA
      | ||  |||    | ||| ||  |||||   |  | | ||  |  | |   | |     || | |   |
    -TTCAATGGAT----GGGCTATG-AACTATGGCCAACTAAATGGAAGCTG---CAGAAATTACAACTGCCCC
    3060          3070       3080      3090      3100         3110      3120

       200       210       220        230        240       250       260
    RGAYGARGARYTNTGYGGNGGNYTNTGGMGNYTNG-TNYTNG-CNCARMGNTGGATGGARMGNYTNAARACN
    |||  ||||| | || |   | |   | |  |  |   || |    ||   |  || | ||| |  ||| |
    AGA--AAGAAATATG-GACAGTCAACGACATCCAGAAGCTGGTGGGAGTCTTAAATTGGGCGGCACAAATCT
            3130       3140      3150      3160      3170      3180
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       270       280       290       300       310        320       330
    GTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARAT-NCAYTTYGTNACNAARTGYGC
     |  | || |  ||||   ||   || |    ||   | ||     ||||  ||||     |  ||||||
    AT-CCAGGAATAAAAACCAAACATTTGTGTAGGCTAATCAAAGGAAAAATGACACTCACAGAAGAAGTGCAG
 3190       3200      3210      3220      3230      3240      3250      3260

      340       350       360       370         380       390       400
    NTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAA--YATNWSNMGNYTNYTNCARGARACNWSN
        |||      |  ||  | |  || |      |||| ||  ||| |  || |     ||||||   |
    TGGACAGAGTTAGC--AGAAG-CAGAGCTAGAAGAAAACAAAATTATCTTAAGCCAGGAACAAGAAGGATAC
          3270         3280      3290      3300      3310      3320

      410       420       430         440        450        460       470
    GARCARYTNGTNGCNYTNAARCCNTGGA--TNACNMGNC-ARAAYTTYW-SNMGNTGYYTNGARYTNCARTG
     |  | |  |  |     |||   | ||    || |  | ||||  ||| | |  |   | ||  | |||
    TATTACCAAGAAG--AAAAAGAATTAGAGGCAACAATCCAAAAAAATCAAGACAATCAGTGGACATACAAAA
 3330      3340        3350      3360      3370      3380      3390

        480       490       500         510       520       530       540
    YCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGG--WSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCN
    |  ||| |  || || |  |  ||        ||  |     |     |   ||    |    || |  |
    TACACCAGGAAG-AGAAAAT--CCTAAAAGTAGGGAAATATGCAAAGATAAAAAATACCCATACCAATGGGG
 3400      3410         3420      3430      3440      3450      3460

          550       560       570       580       590       600        610
    CCNCA--RCCNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYTNYTNGCNGCNG-CNTGGTGY
     |  |  ||   | |   |  | |      |       |  |  ||  | |  || |   | |
    TCAGATTACTAGCACAGGTAGTTCAGAAAATAGGAAAAGAAGCACTAGT-CATCTGGGGACGGATACCAAAA
  3470      3480      3490      3500      3510       3520      3530

         620       630       640       650        660        670        680
    YTNCAYTGGCARMGNACNMGNMGNMGNACNCCNMGNCCNGG-NGARCARGTNC-CNCCNGTNCCNW-SNCCN
    || ||||  | |      || || ||  |    ||    ||  | | || | |   |  ||  | | |  |
    TTCCACTTACCGGTGGAGAG-AG-AGACCTGGGAGCAGTGGTGGGATAACTACTGGCAAGTGACATGGATCC
 3540      3550       3560       3570      3580      3590      3600

                690       700    X
    CA-----RGAYYT-NYTNYTNGTNGARCAY
    ||     ||||||  |  ||     | |||
    CAGAGTGGGACTTCGTATCTACCCCACCACTAGTCAGGTT
 3610      3620      3630      3640
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file transl.res made by root on Thu 6 Apr 95 9:53:08-PDT.


Query sequence being compared:US-08-162-407-6 (1-705)
Number of sequences searched:                   313646
Number of scores above cutoff:                    4021

      Results of the initial comparison of US-08-162-407-6 (1-705) with:
   Data bank : EMBL-NEW 1, all entries
   Data bank : GenBank 86, all entries
   Data bank : GenBank-NEW 1, all entries
   Data bank : UEMBL 41_86, all entries
```

```
1000000-
      -
N     -
U00000-
M     -
B     -
E     -
R     -
      -
O     - *
F00000-
      -  *
S     -
E50000-*  *
Q     -
U     -
E     -
N     -    *
C     -
E     *
S10000-
      -
      -     *
  5000-
      -
      -
      -      *
      -
      -
      -
  1000-       *
      -
      -
   500-
      -        *
      -
      -
      -
      -         *
      -
   100-
      -
      -
    50-
      -          *
      -
      -           *
      -
      -
      -
    10-
      -
      -
     5-            **
      -
      -              *
      -
      -
      -
```

```
      -                                        **                       *
     0------------------------------------------------------------------------
      | |  | |||   |||      |      |       |      |      |      |       |
SCORE 0 |  |77||   154    232    309     386    463    541    618     695
STDEV  -1  2   5     9


                        PARAMETERS

Similarity matrix      Unitary     K-tuple                    4
Mismatch penalty             1     Joining penalty           30
Gap penalty               1.00     Window size               32
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                          SEARCH STATISTICS

Scores:                 Mean        Median       Standard Deviation
                         33           33           13.99

Times:                  CPU                      Total Elapsed
                    00:39:05.03                  00:39:16.00

Number of residues:             288682119
Number of sequences searched:      313646
Number of scores above cutoff:       4021


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                     Init. Opt.
Sequence Name    Description                  Length Score Score   Sig. Frame
-----------------------------------------------------------------------------
                  **** 47 standard deviations above mean ****
  1. HSU03858     Human flt3 ligand mRNA, compl   1080   695   705  47.31   0
  2. HSU04806     Human FLT3/FLK2 ligand mRNA,     859   693   704  47.16   0
                  **** 29 standard deviations above mean ****
  3. MUSLIGAND    Mouse flt3 ligand mRNA, compl    829   442   586  29.23   0
                  **** 28 standard deviations above mean ****
  4. MMU04807     Mus musculus FLT3/FLK2 ligand   1152   427   578  28.15   0
                  **** 10 standard deviations above mean ****
  5. SCMIG1       S.cerevisiae MIG1 gene for a    2622   173   368  10.00   0
                  ****  9 standard deviations above mean ****
  6. TAGLUIN1     Wheat Glu-Aly sublocus with W    794   164   296   9.36   0
  7. TAGLU1AG     Wheat gene for HMW-glutenin s   2915   164   362   9.36   0
  8. HSCOL16A     Homo sapiens alpha-1 type XVI   5387   160   306   9.08   0
                  ****  8 standard deviations above mean ****
  9. SCBYP13CS    S.cerevisiae gene for bypl-3    4100   156   368   8.79   0
 10. WHTGLIABF    Wheat (T.aestivum) alpha-/bet    950   153   227   8.58   0
 11. DUKMTTGRA    Anas platyrhyncos mitochondri   2046   153   364   8.58   0
 12. SQDSKLC      Loligo pealii kinesin light c   2043   152   371   8.50   0
 13. A10377       Artificial sequence for prepr   1368   147   368   8.15   0
 14. XELSPAA      X.laevis spasmolysin mRNA.      1378   147   368   8.15   0
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                **** 7 standard deviations above mean ****
 15. ADRE3FIBES     Adenovirus 11 E3 region encod   2481    143    324    7.86    0
 16. MMOCT2710      M.musculus Oct-2 gene.          1246    140    382    7.65    0
 17. HUMDSP         Human duhydrolipoamide succin   3012    139    397    7.57    0
 18. HUMCOL16A      Homo sapiens alpha-1 type XVI   5387    139    306    7.57    0
 19. HUMCOL16A      Homo sapiens alpha-1 type XVI   5387    139    306    7.57    0
 20. SCYKR007W      S.cerevisiae chromosome XI re    950    138    364    7.50    0


1. US-08-162-407-6 (1-705)
  HSU03858     Human flt3 ligand mRNA, complete cds.

 LOCUS       HSU03858     1080 bp    mRNA             PRI       19-JUL-1994
 DEFINITION  Human flt3 ligand mRNA, complete cds.
 ACCESSION   U03858
 KEYWORDS    .
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 1080)
   AUTHORS   Lyman,S.D., James,L., Johnson,L., Brasel,K., de Vries,P.,
             Escobar,S.S., Downey,H., Splett,R.R., Beckmann,M.P. and
             McKenna,H.J.
   TITLE     Cloning of the human homologue of the murine flt3 ligand: a growth
             factor for early hematopoietic progenitor cells
   JOURNAL   Blood 83, 2795-2801 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1080)
   AUTHORS   Lyman,S.D.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-NOV-1993) Stewart D. Lyman, Immunex Research and
             Development Corporation, 51, University St., Seattle, WA 98101, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 494978
 FEATURES             Location/Qualifiers
      source          1..1080
                      /clone_lib="expression, cDNA"
                      /organism="Homo sapiens"
                      /cell_line="clone 22 (T cell)"
      5'UTR           1..83
      CDS             84..791
                      /standard_name="FMS-like tyrosine kinase-3 ligand"
                      /note="ligand for the flt3/flk-2 tyrosine kinase receptor;
                       NCBI gi: 494979"
                      /codon_start=1
                      /function="stimulates proliferation of early hematopoietic
                      cells"
                      /product="flt3 ligand"
                      /translation="MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVK
                      IRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVN
                      TEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
                      DSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPG
                      EQVPPVPSPQDLLLVEH"
      sig_peptide     84..161
      misc_feature    162..629
                      /note="extracellular domain"
      misc_feature    630..698
                      /note="transmembrane domain"
      misc_feature    699..788
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                      /note="cytoplasmic domain"
      3'UTR           792..1080
      misc_feature    1015..1080
                      /note="ATTTA mRNA instability motif"
      polyA_signal    1059..1064
      polyA_site      1080
                      /note="32 A residues"
 BASE COUNT      204 a    384 c    290 g    202 t
 ORIGIN

Initial Score    =    695  Optimized Score  =    705  Significance = 47.31
Residue Identity =    54%  Matches          =    545  Mismatches   =   160
Gaps             =      0  Conservative Substitutions                =     0

            X       10        20        30        40        50        60
            ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYTNWS
            ||||| || || || || || ||||| || || || ||||| || || || || || || ||
  CCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAG
       80   X     90       100       110       120       130       140

        70        80        90       100       110       120       130
  NWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARAT
   || || || || || || ||||||||||| ||||||||||| || || || || |||||||| || |||||
  CTCGGGACTCAGTGGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAAT
    150       160       170       180       190       200       210

     140       150       160       170       180       190       200
  NMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYT
   || ||||| || |||||||| || ||||||||||| || || || || || ||||| ||||||||||||||
  CCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCT
  220       230       240       250       260       270       280

   210       220       230       240       250       260       270
  NTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAA
   ||||| || || ||||| || || || || ||||| ||||||||||| || ||||| || || || || ||
  CTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAA
290       300       310       320       330       340       350       360

 280       290       300       310       320       330       340       350
  RATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCC
  ||||||||| || || ||||| || ||||| ||||| |||||||| || |||||||| |||||||| || ||
  GATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCC
        370       380       390       400       410       420       430

         360       370       380       390       400       410       420
  NWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYT
   || ||||| || ||||| ||||| ||||| || || || || |||||||| || |||||||| || || ||
  CAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCT
      440       450       460       470       480       490       500

       430       440       450       460       470       480       490
  NAARCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNYT
   ||||| ||||| || || ||||||||||| || ||||| ||||| ||||||||||| ||||| || || ||
  GAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCT
    510       520       530       540       550       560       570

     500       510       520       530       540       550       560
  NCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCNCARCCNCCNYTNYTNYTNYT
   || || || ||||| || || || || ||||| || || || || || || ||||| || || || || ||
  GCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTGCTCCTCCT
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    580       590       600       610       620       630       640

     570       580       590       600       610       620       630
    NYTNYTNYTNCCNGTNGGNYTNYTNYTNYTNGCNGCNGCNTGGTGYYTNCAYTGGCARMGNACNMGNMGNMG
     || || || || || || || || || || || || || |||||||| ||||||||||| || || || ||
    ACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCGGAG
  650       660       670       680       690       700       710       720

   640       650       660       670       680       690       700    X
    NACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
     || || || || || |||||||| || || || || || || |||||||| || || || ||||||
    GACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCACTGACC
          730       740       750       760       770       780       790

    TGGCC


2. US-08-162-407-6 (1-705)
   HSU04806     Human FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS       HSU04806      859 bp    mRNA            PRI       11-MAY-1994
 DEFINITION  Human FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION   U04806
 KEYWORDS    .
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 798)
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 859)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483844
 FEATURES             Location/Qualifiers
      source          1..859
                      /clone="human Flt3/Flk2 ligand S86"
                      /clone_lib="SV48 cDNA"
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                      /cell_line="SV48 thymic stroma"
      CDS             93..800
                      /note="NCBI gi: 483845"
                      /codon_start=1
                      /product="FLT3/FLK2 ligand"
                      /translation="MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVK
                      IRELSDYLLQDYPVTVASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVN
                      TEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
                      DSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPG
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                      EQVPPVPSPQDLLLVEH"
 BASE COUNT      147 a    318 c    246 g    148 t
 ORIGIN

Initial Score    =    693  Optimized Score   =   704  Significance = 47.16
Residue Identity =    54%  Matches           =   544  Mismatches   =   161
Gaps             =      0  Conservative Substitutions              =     0

              X       10        20        30        40        50        60
              ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNACNTAYYTNYTNYTNYTNYTNYTNYTNWS
              ||||| || || || || || ||||| || || || ||||| || || || || || || ||
    CCCGGCCGAAATGACAGTGCTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAG
          90  X    100       110       120       130       140       150

          70        80        90       100       110       120       130
    NWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARAT
     || || || || || || ||||||||||| ||||||||||| || || || || |||||||| || |||||
    CTCGGGACTCAGTGGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAAT
       160       170       180       190       200       210       220

       140       150       160       170       180       190       200
    NMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYT
     || ||||| || |||||||| || ||||||||||| || || || || || ||||| ||||||||||||||
    CCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCT
     230       240       250       260       270       280       290

     210       220       230       240       250       260       270
    NTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAA
     ||||| |  || ||||| || || || || ||||| ||||||||||| || ||||| || || || || ||
    CTGCGGGGCGCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAA
   300       310       320       330       340       350       360       370

   280       290       300       310       320       330       340       350
    RATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCC
    ||||||||| || || ||||| || ||||| ||||| |||||||| || |||||||| |||||||| || ||
    GATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCC
           380       390       400       410       420       430       440

           360       370       380       390       400       410       420
    NWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYT
     || ||||| || ||||| ||||| ||||| || || || || |||||||| || |||||||| || || ||
    CAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCT
         450       460       470       480       490       500       510

         430       440       450       460       470       480       490
    NAARCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNYT
     ||||| ||||| || || ||||||||||| || ||||| ||||| ||||||||||| ||||| || || ||
    GAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCT
       520       530       540       550       560       570       580

       500       510       520       530       540       550       560
    NCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCNCARCCNCCNYTNYTNYTNYT
     || || || ||||| || || || || ||||| || || || || || || ||||| || || || || ||
    GCCACCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTGCTCCTCCT
     590       600       610       620       630       640       650

     570       580       590       600       610       620       630
    NYTNYTNYTNCCNGTNGGNYTNYTNYTNYTNGCNGCNGCNTGGTGYYTNCAYTGGCARMGNACNMGNMGNMG
     || || || || || || || || || || || || || |||||||| ||||||||||| || || || ||
    ACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCACTGGCAGAGGACGCGGCGGAG
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660       670       680       690       700       710       720       730

640       650       660       670       680       690       700    X
  NACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
   || || || || || |||||||| || || || || || || |||||||| || || || ||||||
  GACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGTCCCCAGGACCTGCTGCTTGTGGAGCACTGACC
         740       750       760       770       780       790       800

  TGGCC


3. US-08-162-407-6 (1-705)
   MUSLIGAND    Mouse flt3 ligand mRNA, complete cds.

 LOCUS       MUSLIGAND     829 bp ss-mRNA            ROD       04-JAN-1994
 DEFINITION  Mouse flt3 ligand mRNA, complete cds.
 ACCESSION   L23636
 KEYWORDS    ligand.
 SOURCE      Mus musculus (strain SJL/J) cDNA to mRNA.
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 829)
   AUTHORS   Lyman,S.D., James,L., VandenBos,T., deVries,P., Brasel,K.,
             Gliniak,B., Hollingsworth,L., Picha,K.S., McKenna,H.J.,
             Splett,R.R., Fletcher,F.A., Maraskovsky,E., Farrah,T.,
             Foxworthe,D., Williams,D.E. and Beckmann,M.P.
   TITLE     Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
             receptor -- a proliferative factor for primitive hematopoietic
             cells
   JOURNAL   Cell 75, 1157-1167 (1993)
   STANDARD  full automatic
 COMMENT     NCBI gi: 439441
 FEATURES             Location/Qualifiers
      source          1..829
                      /organism="Mus musculus"
                      /strain="SJL/J"
                      /sequenced_mol="cDNA to mRNA"
      sig_peptide     32..109
                      /codon_start=1
      CDS             32..727
                      /note="NCBI gi: 439442"
                      /codon_start=1
                      /product="flt3 ligand"
                      /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                      KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                      NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQ
                      CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR
                      GELHPGVPLPSHP"
      mat_peptide     110..724
                      /codon_start=1
 BASE COUNT      163 a    265 c    221 g    180 t
 ORIGIN

Initial Score    =    442  Optimized Score  =    586  Significance = 29.23
Residue Identity =    44%  Matches          =    465  Mismatches   =   239
Gaps             =     20  Conservative Substitutions             =     0

             X       10        20        30            40        50
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            ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNACNTAY---YTNYTNYTNYTNYTNYT
            ||||| || || || || || ||||| || |   | | |   || || || || || || ||
  CCCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCT
         30 X       40        50        60        70        80        90

  60        70        80        90       100       110       120       130
  NWSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAA
   ||  |  | ||  | || || |  |||||||  |||   ||||| || || || ||  |||||   || ||
  GAGTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAA
      100       110       120       130       140       150       160

        140       150       160       170       180       190       200
  RATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGA
  | | || ||||| || ||| |||| ||  |||||||||| || || || ||    ||||| ||||||||| |
  GTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAA
    170       180       190       200       210       220       230

      210       220       230       240       250       260       270
  RYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWS
  ||  |||   |  || ||||| ||  | || || ||||| ||||| ||||  || ||||| || || || ||
  GCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTC
  240       250       260       270       280       290       300

    280       290       300       310       320       330       340
  NAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCC
   |||||||||   || || |||   || ||||| ||||| |||||||| ||   |||| | |||||||| |
  TAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCT
310       320       330       340       350       360       370       380

  350       360       370       380       390       400       410
  NCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGC
   ||    ||||| || ||||| ||||| ||||| || |  || ||  |||| || ||   ||||||  | ||
  ACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGC
        390       400       410       420       430       440       450

420       430             440       450       460       470       480
  NYTNAARCCNT------GGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWS
   || ||||| |      |||   |  | ||||||||||| || ||||| ||| | ||||||||||| |||||
  TCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTC
      460       470       480       490       500       510       520

    490       500       510       520       530            540        550
  NWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNAC--NGCNCCNA---CNGCNCCNCA-RCC
   || || || |  || ||  |||| || |   | || ||||| ||   || || |   |  |  | || ||
  CTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCA
    530       540       550       560       570       580       590

        560       570       580       590       600       610       620
  NCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYTNYTNGCNGCNGCNTGGTGYYTNCAYTGGCA
   |  || || || || || || || ||  |    ||  | || || || || || ||| |||| | ||||||
  GCTGTTGCTCCTGCTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTGGCA
  600       610       620       630       640       650       660

      630          640       650       660        670       680       690
  RMGNACNMGNMGNM---GNACNCCNMGNCCNGGNGARCARGT-NCCNCCNGTNCCNWSNCCNCARGAYYTNY
  |||  | || || |   |    |  |  || || | ||   |  || ||  | || ||    | || ||| |
  AAGGGCAAGAAGGAGGGGGGAGCTCCACCCTGGGGTGCCCCTCCCCTCCCATCCCTAGGATTCGAGCCTTGT
670       680       690       700       710       720       730        740

        700    X
    TNYTNGTNGARCAY
       | || | || |
    GCATCGTTG-ACTCAGCCAGGGTC
          750    X   760


 4. US-08-162-407-6 (1-705)
    MMU04807     Mus musculus FLT3/FLK2 ligand mRNA, complete cds.

  LOCUS       MMU04807     1152 bp    mRNA            ROD       11-MAY-1994
  DEFINITION  Mus musculus FLT3/FLK2 ligand mRNA, complete cds.
  ACCESSION   U04807
  KEYWORDS    .
  SOURCE      mouse.
    ORGANISM  Mus musculus
              Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
              Eutheria; Rodentia; Myomorpha; Muridae; Mus.
  REFERENCE   1  (bases 1 to 921)
    AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
              Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
              Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
              Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
              Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
    TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
              haematopoietic stem cells and is encoded by variant RNAs
    JOURNAL   Nature 368, 643-648 (1994)
    STANDARD  full automatic
  REFERENCE   2  (bases 1 to 1152)
    AUTHORS   Culpepper,J.A.
    TITLE     Direct Submission
    JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
              Institute, 901 California Avenue, Palo Alto, CA 94304, USA
    STANDARD  full automatic
  COMMENT     NCBI gi: 483846
  FEATURES             Location/Qualifiers
       source          1..1152
                       /clone="mouse Flt3/Flk2 ligand T110"
                       /clone_lib="TA4 cDNA"
                       /organism="Mus musculus"
                       /cell_line="TA4 stroma"
       CDS             256..954
                       /note="NCBI gi: 483847"
                       /codon_start=1
                       /product="FLT3/FLK2 ligand"
                       /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                       KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                       NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQ
                       CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARR
                       RGELHPGVPLPSHP"
  BASE COUNT      238 a    346 c    324 g    244 t
  ORIGIN

 Initial Score     =    427  Optimized Score =     578  Significance = 28.15
 Residue Identity  =    43%  Matches         =     458  Mismatches   =   244
 Gaps              =     21  Conservative Substitutions              =     0

              X       10        20        30           40        50
              ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNACNTAY---YTNYTNYTNYTNYTNYTNYT
              ||||| || || || || || ||||| || |   | | |   || || || || || || ||
    CCCGGCAGAGATGACAGTGCTGGCGCCAGCCTGGAGCCCAAATTCCTCCCTGTTGCTGCTGTTGCTGCTGCT
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    250     X 260       270       280       290       300       310

 60        70        80        90       100       110       120       130
  NWSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAA
   ||  |  | ||  | || || |  |||||||  |||   ||||| || || || ||  |||||   || ||
  GAGTCCTTGCCTGCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAA
  320       330       340       350       360       370       380

        140       150       160       170       180       190       200
  RATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGA
  | | || ||||| || ||| |||| ||  |||||||||| || || || ||    ||||| ||||||||| |
  GTTTAGAGAGTTGACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAA
390       400       410       420       430       440       450       460

      210       220       230       240       250       260       270
  RYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWS
  ||  |||   |  || ||||| ||  | || || ||||| ||||| ||||  || ||||| || || || ||
  GCACTGCAAGGCCTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTC
        470       480       490       500       510       520       530

    280       290       300       310       320       330       340
  NAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCC
   |||||||||   || || |||   || ||||| ||||| |||||||| ||   |||| | |||||||| |
  TAAGATGCAAACGCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCT
      540       550       560       570       580       590       600

  350       360       370       380       390       400       410
  NCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGC
   ||    ||||| || ||||| ||||| ||||| || |  || ||  |||| || ||   ||||||  | |
  ACCAGAATGTCTGCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGG
    610       620       630       640       650       660       670

420       430             440       450       460       470       480
  NYTNAARCCNT------GGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWS
   || ||||| |      |||   |  | ||||||||||| || ||||| ||| | ||||||||||| |||||
  TCTGAAGCCCTGTATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTC
  680       690       700       710       720       730       740

    490       500       510       520       530               540
  NWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNAC--NGCNCCNA------CNGCNC-CNCA
   || || || |  || ||  |||| || |   | || ||||| ||   || || |      | || |   ||
  CTCCACCCTGCTGCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCA
750       760       770       780       790       800       810       820

 550       560       570       580       590       600       610       620
  RCCNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNYTNYTNGCNGCNGCNTGGTGYYTNCAYTG
  ||     || || || || || || || ||  |    ||  | || || || || || ||| |||| | |||
  GCTGTTGCTCCTGCTGCTGCTGCTGCTGCCTCTCACACTGGTGCTGCTGGCAGCCGCCTGGGGCCTTCGCTG
        830       840       850       860       870       880       890

         630       640       650       660       670       680       690
  GCARMGNACNMGNMGNMGNACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNCCNWSNCCNCARGAYYTNYT
  ||||||  | || || ||       |  ||      |   |  || ||  | || |  ||  |||||
  GCAAAGGGCAAGAAGGAGGGGGGAGC-TCCACCCTGGGGTGCCCCTCCCCTCCCAT--CCCTAGGATGCGAG
      900       910        920       930       940         950       960

       700   X
  NYTNGTNGARCAY
   || ||  | | |
  CCTTGTGCATCGTTGACTCAGCC
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      970    X  980


 5. US-08-162-407-6 (1-705)
    SCMIG1       S.cerevisiae MIG1 gene for a C2H2 zinc finger prot

  LOCUS       SCMIG1       2622 bp    DNA             PLN       23-JUL-1991
  DEFINITION  S.cerevisiae MIG1 gene for a C2H2 zinc finger protein involved in
              glucose repression.
  ACCESSION   X55734
  KEYWORDS    glucose repressor; MIG1 gene; zinc-finger protein.
  SOURCE      baker's yeast.
    ORGANISM  Saccharomyces cerevisiae
              Eukaryota; Plantae; Thallobionta; Eumycota; Hemiascomycetes;
              Endomycetales; Saccharomycetaceae.
  REFERENCE   1  (bases 103 to 2622)
    AUTHORS   Nehlin,J.O. and Ronne,H.
    TITLE     Yeast MIG1 repressor is related to the mammalian early growth
              response and Wilms' tumour finger proteins
    JOURNAL   EMBO J. 9, 2891-2898 (1990)
    STANDARD  full automatic
  REFERENCE   2  (bases 1 to 2622)
    AUTHORS   Ronne,H.E.
    TITLE     Direct Submission
    JOURNAL   Submitted (18-JUL-1991) to the EMBL/GenBank/DDBJ databases. H.E.
              Ronne, Ludwig Inst f Cancer Research, Uppsala Branch, Box 595,
              S-751 24 Uppsala, SWEDEN
    STANDARD  full automatic
  COMMENT     NCBI gi: 3962
  FEATURES             Location/Qualifiers
       source          1..2622
                       /organism="Saccharomyces cerevisiae"
                       /strain="W303-1A"
                       /haplotype="haploid"
                       /cell_type="MATa"
                       /clone_lib="pHR81"
                       /chromosome="VII"
                       /map="5.4 cM telomeric to TRP5"
       TATA_signal     780..785
       CDS             943..2457
                       /gene="MIG1"
                       /note="NCBI gi: 3963"
                       /codon_start=1
                       /product="glucose repressor"
                       /translation="MQSPYPMTQVSNVDDGSLLKESKSKSKVAAKSEAPRPHACPICH
                       RAFHRLEHQTRHMRIHTGEKPHACDFPGCVKRFSRSDELTRHRRIHTNSHPRGKRGRK
                       KKVVGSPINSASSSATSIPDLNTANFSPPLPQQHLSPLIPIAIAPKENSSRSSTRKGR
                       KTKFEIGESGGNDPYMVSSPKTMAKIPVSVKPPPSLALNNMNYQTSSASTALSSLSNS
                       HSGSRLKLNALSSLQMMTPIASSAPRTVFIDGPEQKQLQQQQNSLSPRYSNTVILPRP
                       RSLTDFQGLNNANPNNNGSLRAQTQSSVQLKRPSSVLSLNDLLVGQRNTNESDSDFTT
                       GGEDEEDGLKDPSNSSIDNLEQDYLQEQSRKKSKTSTPTTMLSRSTSGTNLHTLGYVM
                       NQNHLHFSSSSPDFQKELNNRLLNVQQQQQEQHTLLQSQNTSNQSQNQNQNQMMASSS
                       SLSTTPLLLSPRVNMINTAISTQQTPISQSDSQVQELETLPPIRSLPLPFPHMD"
  BASE COUNT      864 a    545 c    531 g    682 t
  ORIGIN

 Initial Score    =    173  Optimized Score =     368  Significance = 10.00
 Residue Identity =    28%  Matches         =     341  Mismatches   =   322
 Gaps             =     80  Conservative Substitutions              =     0
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             X       10         20        30         40        50        60
             ATGACNGTNY-TNGCNCCNGCNTGGWSNCCNACNAC-NTAYYTNYTNYTNYTNYTNYTN
             | |   || |   |   | ||   |||     |  |   |||   | ||  | || |  ||
   AGGAGAGTAAAAGCAAGTCCAAAGTAGCTGCGAAGTCAGAGGCGCCAAGACCACATGCTTGTCCTAT--CTG
         1010      1020      1030      1040      1050      1060        1070

           70        80        90       100       110       120       130
   WSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAAR
   || |   | || ||    ||   |||||| |    ||||   || |  || || |   ||   |  |  |||
   TCATAGAGCTTTTC----AC---AGACTGGA-ACATCAGACGAGACACATGAGAATTCATACAGGTGAGAAG
         1080             1090       1100      1110      1120      1130

        140        150          160       170       180       190
   ATNMGNGARY-TNWSNGAY---TAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAY--
      |  | || | ||   |    || | |   ||| ||   | ||    |  || |  ||||  | ||||
   CCTCACGCGTGTGACTTCCCCGGATGTGTGAAAAGGTT---CAGT---AGAAGCGATGAACTGACGAGACAC
     1140      1150      1160      1170            1180      1190      1200

   200        210          220         230       240        250         260
   -GARGARYT-NTGY---GGNGGNYTNTGGMGNY--TNGTNYTNGCNCARMGNTGGATG-GARMGNYTNA--A
    ||||||||  | |         |  | ||| |    |     |    |||  || || | ||  |  |  |
   AGAAGAATTCATACAAACTCCCACCCTCGAGGTAAAAGAGGCAGAAAGAAGAAGGTTGTGGGCTCTCCAATA
         1210      1220      1230      1240      1250      1260      1270

          270       280       290       300       310       320       330
   RACNGTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTG
   ||  || ||  | ||   | ||| |    | |   |||   | ||||| | ||   |||||    |   ||
   AATAGT-GCTAGTTC--TAGTGCTACCAGTATACCAGA-TTTAAATACGGCAA---ATTTTTCACCGCCATT
        1280        1290      1300       1310      1320         1330

        340          350         360         370       380          390
   YGCNTTYCARCCNC---CNCC-NWSNTGYYT-NMGNT-TYG-TNCARACNAAYAT--NWSNMG-NYTNYTNC
     |    ||||  |   | ||  |  | |||   | | ||| | | ||  || ||   || ||  || || |
   ACCACAGCAACACCTATCGCCTTTAATTCCTATTGCTATTGCTCCGAAAGAAAATTCAAGTCGATCTTCTAC
  1340      1350      1360      1370      1380      1390      1400

      400       410       420       430       440       450        460
   ARGARACNWSNGARCARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTYWS-NMGNTGYYTNGAR
   ||||||     ||| |||        |  ||| |   ||  |   |   ||||  | |  |  || ||
   AAGAAAAGGTAGAAAAAC---CAAATTCGAAATCGGCGA-AAGTGGTGGGAATGACCCATATATGGTT---T
1410      1420         1430      1440       1450      1460      1470

     470       480       490       500       510       520       530
   YTNCARTGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCN
   || |  | ||||   ||| | |  |  || ||  | |  || || || |  || |    ||| || |
   CTTC--TCCCAAAACGATGGCT-AAGATTCCCGTCTCGGTGAAG-CCTCCACCTTCTTTAGC-ACTGAATAA
       1480      1490       1500      1510       1520      1530       1540

   540         550       560       570       580       590         600
   ACNG--CNCCNCARCCNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNY--TNYTNGCNGCNGC
      |  |  |  |||  |  |  || |  || || |  || |  || |  |  |  |  |  | || |  |
   TATGAACTACCAAACTTCATCCGCTTCCACTGCTTTGTCTTC--GTTGAGCAATAGCCATAGTGGCAGTAGA
        1550      1560      1570      1580       1590      1600      1610

     610       620       630       640       650       660       670
   NTGGTGYYTNCAYTGGCARMGNACNMGNMGNMGNACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNCCNWS
    | |   ||  ||  |  |    | |  |  |  |   | |  |   |  ||| ||| |  |  |  |  ||
   CT-GAAACTGAACGCGTTATCGTCCCTACAAATGATGACGC-CCATTGCTAGC-AGTGCGCCAAGGAC--TG
         1620      1630      1640      1650       1660       1670
  680         690         700     X
  NCCNCA-RGAY-YTNYT--NYTNGTNGARC-AY
      || ||||   | ||  |      ||| ||
  TTTTCATAGACGGTCCTGAACAGAAACAACTACAACAACAACA
1680      1690      1700      1710      1720


6. US-08-162-407-6 (1-705)
   TAGLUIN1     Wheat Glu-Aly sublocus with Wis-2 insertion 5' end

 LOCUS       TAGLUIN1      794 bp    DNA             PLN       06-JUL-1989
 DEFINITION  Wheat Glu-Aly sublocus with Wis-2 insertion 5' end (0.8 kb Hind III
             fragment).
 ACCESSION   X05995
 KEYWORDS    Glu-Aly gene; glutenin; insertion sequence; retrotransposon;
             Wis-2 insertion sequence.
 SOURCE      wheat.
   ORGANISM  Triticum aestivum
             Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
             Commelinidae; Cyperales; Poaceae.
 REFERENCE   1  (bases 1 to 794)
   AUTHORS   Harberd,N.P., Flavell,R.B. and Thompson,R.D.
   TITLE     Identification of a transposon-like insertion in a Glu-1 allele of
             wheat
   JOURNAL   Mol. Gen. Genet. 209, 326-332 (1987)
   STANDARD  full automatic
 COMMENT     Sequence comparision with Cheyenne
             Glu-Aly sublocus gene has shown that the coding sequence of the
             Chinese Spring sublocus gene is interrupted by a 8.0 kb insertion
             sequence. A DNA duplication and inverted terminal sequences are
             flanking the insertion sequence. See also x05996.
             Data kindly reviewed (18-Apr-1988) by Flavell R.B.

             NCBI gi: 21780
 FEATURES             Location/Qualifiers
      source          1..794
                      /organism="Triticum aestivum"
                      /strain="Chinese spring"
                      /chromosome="chromosome 1a"
      misc_feature    <1..482
                      /note="glutenin homologous seq. (161 AA; includ. stop
                      codon) (1 is 2nd base in codon)"
      misc_feature    478..481
                      /note="DNA duplication"
      intron          483..>794
                      /note="insertion sequence"
      misc_feature    484..493
                      /note="inverted terminal sequence"
 BASE COUNT      290 a    183 c    178 g    139 t      4 others
 ORIGIN

Initial Score    =    164  Optimized Score  =    296  Significance =  9.36
Residue Identity =    25%  Matches          =    283  Mismatches   =   287
Gaps             =     77  Conservative Substitutions             =     0

    90       100        110       120       130           140       150
  YTGYWSNTTYCARC-AYWSNCCNATNWSNWSNGAYTTYGCNGTNA--AR-ATNMGNG-ARYTNWSNGAYTAY
             |||  |||  | |   | ||  |  | ||    |  || |  || | |||  ||  |||||
            AAGCTTCTCCACAACAGCCAGGAAAATGGCAAGAACTAGGACAAGGGCAACAATGGTACTAT
            X       10        20        30        40        50        60
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      160       170       180        190       200       210       220
  YTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNA-AYYTNCARGAYGARGARYTNTGYGGNGGNYTNTG--G
  |     ||  ||| | | |   | |  || || | |    ||| | | || |||   ||     || ||  |
  C-----CA--ACTTCTCTG---CAGCAGCCAGGACAAGGGCAACAAG-GGTACT-ACCGAACTTCTCTGCAG
               70           80         90        100        110       120

       230       240           250       260       270       280       290
  MGNYTNGTNYTNGCNCARMGNTGG----ATGGARMGNYTNAARACNGTNGCNGGNWSNAARATGCARGGNYT
  |  |  |  |     ||||   ||    |  ||||  ||   | | |  ||  | || |||  ||||
  CAGCCAGGACAAAGGCAACAAGGGTACTACCGAAC--TTCTCGGCAGCAGCCAGGAC-AAG-GGCAA--CAG
       130       140       150         160       170        180

         300        310       320       330       340        350       360
  NYTNGARMGNGTNAAY-ACNGARATNCAYTTYGTNACNAARTGYGCNTTYCA-RCCNCCNCCNWSNTGYYTN
   |  || |  |  ||| |  | | | | |  | |  | | | || |   ||| | |     | ||  ||
  ATAGGACAATGGCAACAAGGGTACTACCCAACTTCTCCACA-GCAC---CCAGGACAAGGGCAAC-AACCAG
190      200       210       220        230          240        250

         370       380        390       400       410       420
  MGNTTYGTNCARACNAAYATNWSNM-GNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYTNAARC--CN
   |    || ||||  ||||  || | | |  |  | |||||   |  ||||||   | |  |   |||  |
  -GACAAGTGCAAA-AAATAGGACAAGGGCAACAACCAGAAAAAGGGCAACAAC---TAGGACAAGAGCAACA
     260        270       280       290       300          310       320

430        440        450        460       470       480        490
  TGGATNACNM-GNCAR-AAYTTYWS-NMGNTGYYTNGARYTNCARTGYCARCCNGAY-WSNWSNACNYTNCC
     |  || | | ||| |||  |||  |   | |   |||  |||  | ||    || || || ||     |
  AATAGGACAAGGGCAACAAC--CAGAACAAGGGCAACAAC--CAGGACAAGGGCAACAACCAGGACAAGGGC
       330       340         350       360         370       380       390

  500       510       520       530        540       550       560
  NCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNAC-NGCNCCNCARCCNCCNYTNYTNYTNYTNY
    |     | ||  | |  |  ||    ||  | ||    ||  |  |  |||||     |  |  |  | |
  AAC-AAGGGTACTACCCAAC--TTCTCTGCAGCAGCCAGGACAAGGGCAACAACCAGGACAATGACAACAAC
          400         410       420       430       440       450

570          580       590        600       610       620       630
  TNYTNY--TNCCNGTNGGNYTNYTNYT-NYTNGCNGCNGCNTGGTGYYTNCAYTGGCARMGNACNMGNMGNM
       |     |     |  | || ||         ||  | | | | |   ||    ||   |  |  | |
  CAGGACAAGGGCAACAAGGGTACTGTTGGAAATATGC--CCTAGAGGC--AATAATAAATTGATTATTATTA
460       470       480       490         500         510       520

  640       650       660              670          680       690
  GNACNCCNMGNCCNGGNGARCARGT-----NCC--NCCNG---TNCCNWSNCCNCARGAYYTNYT--NYTNG
       ||  |  |  |  ||  | |      ||    |  |   |    ||     ||  ||   |   | |
  TATTTCCTNGTTCATGATAATCGTTTATTATCCATGCTAGAATTGTATTGATAGGAAACTCAGATACATGTG
  530       540       550       560       570       580       590

  700       X
  TNGA-RCAY
  | || ||||
  TGGATACATAGACAACACC
600       610


7. US-08-162-407-6 (1-705)
   TAGLU1AG     Wheat gene for HMW-glutenin subunit located on chr

 LOCUS       TAGLU1AG     2915 bp    DNA             PLN       06-JUL-1989
```

```
DEFINITION  Wheat gene for HMW-glutenin subunit located on chromosome 1A.
ACCESSION   X03042
KEYWORDS    direct repeat; glutenin; inverted repeat; seed storage protein;
            signal peptide; storage protein.
SOURCE      wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
            Commelinidae; Cyperales; Poaceae.
REFERENCE   1  (bases 1 to 2915)
  AUTHORS   Forde,J., Malpica,J.M., Halford,N.G., Shewry,P.R., Anderson,O.D.,
            Greene,F.C. and Miflin,B.J.
  TITLE     The nucleotide sequence of a HMW glutenin subunit gene located on
            chromosome 1A of wheat (Triticum aestivum L.)
  JOURNAL   Nucleic Acids Res. 13, 6817-6832 (1985)
  STANDARD  full automatic
COMMENT     Though the premature stop codon may not affect gene expression the
            author suggests that the gene is a pseudogene, because no small in
            vivo transcript of chromosome 1A was found. Within the coding
            sequence are two multiple repeated amino acid motifs, PGQGQQ and
            GYYPTSLQQ
            Data kindly reviewed (19-MAR-1986) by J. Forde.

            NCBI gi: 21770
FEATURES             Location/Qualifiers
     source          1..2915
                     /organism="Triticum aestivum"
     repeat_unit     8..24
                     /note="inverted repeat X"
     repeat_region   243..259
                     /note="direct repeat B"
     repeat_region   272..291
                     /note="imp. direct repeat A"
     repeat_region   297..316
                     /note="imp. direct repeat A"
     repeat_region   318..337
                     /note="imp. direct repeat A"
     repeat_region   343..359
                     /note="direct repeat B"
     repeat_unit     419..431
                     /note="inverted repeat Y"
     promoter        582..586
                     /note="pot. CAAT-box"
     promoter        620..624
                     /note="pot. CAAT-box"
     repeat_unit     648..664
                     /note="inverted repeat X"
     promoter        696..699
                     /note="pot. CAAT-box"
     promoter        724..730
                     /note="put. TATA-box"
     CDS             815..2620
                     /note="precursor"
                     /codon_start=1
     CDS             815..877
                     /note="put. signal peptide (aa -21 to -1);  NCBI gi:
                     21771"
                     /codon_start=1
                     /translation="MAKRLVLFATVVIGLVSLTVA"
     CDS             878..2620
                     /note="mature HMW subunit of glutenin (aa 1-581)"
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                     /codon_start=1
     misc_feature    1832..1834
                     /note="premature TAG stop codon"
     repeat_unit     2635..2647
                     /note="inverted repeat Y"
     misc_feature    2678..2683
                     /note="put. polyadenylation signal"
BASE COUNT      977 a    736 c    674 g    528 t
ORIGIN

Initial Score     =    164  Optimized Score  =    362  Significance =  9.36
Residue Identity  =    27%  Matches          =    344  Mismatches   =   326
Gaps              =     98  Conservative Substitutions             =     0

               X       10        20        30          40          50
               ATGACNGTNYTNGCNCCNGCNTGGWSNCCNACNA--CNTAYYT---NYTNYTNYTNYTNYTN
                 |   |  |  ||  | ||    || || || |    |||||       |  || |
     CCTTCTACCATCGCGAGACCACGCCACTGCAGCAACTCCAACAAGGAATATTTGGGGAACATCTTCACAAA
  1110      1120      1130      1140      1150      1160     1170      1180

      60        70                  80        90       100       110
     YTNW-SNWSNGGNYT----NWSNGGNA------CNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNG
     |  | || |  ||     || |  |      | ||| |  | || | | | | ||| || |  |  ||
     CAGTACAAGGGTATTACCCAAGTGTAATATCTCCTCAGCAGGGGTCATATTATC-CAGGCCAAGCTTCTC-C
          1190      1200      1210      1220      1230       1240      1250

    120        130        140       150         160       170       180
     AYTTY-GCNGTNAARAT-NMGNGARYTNWSNGAYTA--YYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSN
     ||  | ||    |||||  |  ||||| || ||| |   |  |    | |||||||     |  | || ||
     ACAACAGCCAGGAAAATGGCAAGAACT-AG-GACAAGGGCAACAATGGTACTATCCAACTTCTCT-GC-AGC
          1260      1270       1280       1290      1300      1310

      190            200        210       220         230       240
     AAYY--TNCARG---AYGARGARYTNT-GYGGNGGNYTNTG--GMGNYTNGTNYTNGCNCARMGNTGG----
     | ||    ||||   ||| ||  |  ||     || ||  ||  |  |  |     ||||   ||
     AGCCAGGACAAGGGCAACAAGGGTACTACCGAACTTCTCTGCAGCAGCCAGGACAAAGGCAACAAGGGTACT
  1320      1330      1340      1350      1360      1370      1380      1390

      250       260       270           280       290         300       310
     ATGGARMGNYTNAARACNGTNGCNGGNWSNA----ARATGCARGGNYTNYTNGA--RMGNGTNAAYACNGAR
     |  ||||  ||     | |  ||  | || |    ||  |  ||| |  |   |  ||| || | |||  ||
     ACCGAAC--TTCTCTGCAGCAGCCAGGACAAGGGCAACAGATAGGACAATGGCAACAAGGGT-ACTACCCAA
            1400      1410      1420      1430      1440      1450       1460

          320       330       340       350       360       370       380
     ATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSN
      | | |  |   ||  || |       ||||  ||    ||  | |  ||   ||  ||||  ||||  ||
     CTTCTCCGCAGCACCCAG-GACAAGGGCAACAACC----AG--GAC-AAG---TG--CAAA-AAATAGGACA
           1470       1480      1490             1500            1510

         390       400       410            420          430       440
     M-GNYTNYTNCARGARACNWSNGARCARYTNG-----TNGCNYTNAA---RCCNTGGATNACNMGNCARAAY
     | | |  |  | |||||   |  ||||||| |       ||    ||   | |  ||   || |  ||||||
     AGGGCAACAACCAGAAAAAGGGCAACAACTAGGACAAGAGCAACAAATAGGACAAGGGCAAC-AACCAGAAC
   1520      1530      1540      1550      1560      1570      1580

     450       460       470          480           490       500       510
     TTYWSNMGNTGYYTNGARYTNCARTGY--CARCC-NGAYW----SNWSNACNYTNCCNCCNCCNTGGWSNCC
         | |    ||   ||    || ||  |||||  ||||    | || |   | |  ||    |  ||  |
     AAGGGCAACAACC---AGGACAAGGGCAACAACCAGGACAAGGGCAACAAGGGTACTACCCAACTTCTCTGC
```

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1590      1600         1610      1620      1630      1640      1650

        520           530        540       550       560       570
   NMGNCCNYTNGA----RGCNACNGCNCCNAC-NGCNCCNCARCCNCCNYTNYTNYTNYTNYTNYTNYTNCCN
    ||    |  ||    ||| ||  |    ||     |  |||||    |     |  |      | || ||
   -AGCAGCCAGGACAAGGGCAACAACCAGGACAATGGCAACAACCAGGACAAGGGCAAC-AAGGGTACTACC-
  1660      1670      1680      1690      1700      1710       1720

 580       590       600       610       620         630       640
   GTNGGNYTNYTNYTNYTNGCNGCNGCNTGGTGYYTNCAYTGGCA--RMGNACNMGNMGNMGNA-CNCCNMGN
         || || || |      | |      | |  ||  ||||  ||  |  |  |  || | |  | ||
   ---CAACTTCT-CTGCAACAGCCAGTACAAGGGCAACAAGGGCACTACCCA-GCTTCTCAGCACCAGCCAGG
     1730       1740      1750      1760      1770       1780      1790

  650        660       670       680       690       700    X
   CCNGGNG-ARCARGTNCCNCCNGTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARCAY
    | || | ||||||  |  |      | || |  ||| | |     |  |   ||||
   GCAGGGGCAACAAGGGCACCAGCCAGCTTCTCTGCAGTAGTCAGGACAAGGGCAACAAGGGCACCACC
     1800      1810      1820      1830      1840      1850 X    1860
```

```
8. US-08-162-407-6 (1-705)
   HSCOL16A     Homo sapiens alpha-1 type XVI collagen (COL16A1) m

ID   HSCOL16A   standard; RNA; PRI; 5387 BP.
XX
AC   M92642;
XX
DT   30-APR-1992 (Rel. 31, Created)
DT   06-JAN-1995 (Rel. 42, Last updated, Version 2)
XX
DE   Homo sapiens alpha-1 type XVI collagen (COL16A1) mRNA, complete
DE   cds.
XX
KW   alpha-1 type XVI collagen; extracellular matrix protein.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC   Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
XX
RN   [1]
RP   1-5387
RA   Pan T.C., Zhang R.Z., Mattei M.G., Timpl R., Chu M.L.;
RT   "Cloning and chromosomal location of human alpha 1(XVI) collagen";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:6565-6569(1992).
XX
CC   NCBI gi: 180757
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..5387
FT                   /organism="Homo sapiens"
FT                   /cell_type="Fibroblasts"
FT                   /sequenced_mol="cDNA to mRNA"
FT   5'UTR           1..153
FT                   /gene="COL16A1"
FT   sig_peptide     154..216
FT                   /gene="COL16A1"
FT                   /codon_start=1
FT   CDS             154..4965
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FT                   /gene="COL16A1"
FT                   /note="NCBI gi: 180758"
FT                   /codon_start=1
FT                   /product="alpha-1 type XVI collagen"
FT   mat_peptide     217..4962
FT                   /partial
FT                   /gene="COL16A1"
FT                   /evidence=EXPERIMENTAL
FT                   /codon_start=1
FT                   /product="alpha-1 type XVI collagen"
FT   3'UTR           4987..5387
FT                   /gene="COL16A1"
XX
SQ   Sequence 5387 BP; 1153 A; 1520 C; 1817 G; 897 T; 0 other;
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Initial Score    =     160  Optimized Score    =     306  Significance =  9.08
Residue Identity =     27%  Matches            =     276  Mismatches   =   296
Gaps             =      62  Conservative Substitutions   =     0
```

```
 100       110       120       130       140       150       160       170
  RCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCC
               ||  | |||  |   |   |||| || ||||     |   ||||     ||||  |||
            GGACCCGTGACCGTCACGGAGAGAT-AGAGAACCCCTAGCGGACCT----GAGGA--ACCT
            X       10        20         30        40            50

         180       190       200       210       220       230       240
  NGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMG
   |   | |   | ||   ||| | |  || |  |||  || | ||     |||  |  |  |   |   ||
  GGGCTCTGCTTCCTC-CGCCTGCTGCCTGGACTGCTCAGT-GAGGTGGGGGATCCCCG-GCCACCGGTGCT
     60        70         80        90        100       110        120

       250       260         270        280       290       300
  NTGGATGGARMGNYTNAARACNGTNG--CNGGNWSNAAR-ATGCARGGNYTNYTNGARMGNGTNAAYAC---
   ||| || ||   || |   |  | |  | || ||   | || | ||| || || |   | |    | |
  GTGGCTGTAG---CTGACCTCTTTGGACCGGGATGTGGGTATCCTGGG-CTCCTGGCCTGTGGCTGCTCGGT
     130          140       150       160        170       180       190

    310       320           330        340       350        360
  ---NGARATNCAYTTYGTNA----CNAARTGYGCNTTY-CARCCNCCNCCNWS-NTGYYTNM--GNTTY--G
      | | | | ||  |  |      |||| |   | | |||   || || ||   ||   |  |  ||
  CTTTGGGCTACCTTCGGCCATGGGGCAAATACAGGTGCACAATGCCCACCTTCACAGCAGGAAGGACTCAAA
       200       210       220       230       240       250       260

  370       380       390       400       410       420       430
  TNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYTNAARCCNTGGATNA--C
  |   |||  |||  || || || |  |||  |||  | ||   |||  |    || |  |   |  | |  |
  TTGGAAC--ACAGTAGTAGCCTGC--CAGCCAAC--GTGACTGGCT--TCAACCTCATCCACCGACTCAGCC
     270         280         290         300         310       320

  440       450       460       470       480            490       500
  NMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAY-----WSNWSNACNYTNCCNCCNCCN
   |   || |  |||| |        || |  |||  ||||   | |     || ||  | |     |  ||
  TCATGAAGAAGTCTGCCATCAAGAAGATCCGCAACCCCAAGGGGCCTCTCATCCTGCGCCTGGGGGCGGCCC
 330       340       350       360       370       380       390       400

     510       520       530       540       550         560       570
  TGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCNCARCCNCCNYT--NYTNYTNYTNYTNYTNY
    ||| || || || |  || |      | |     |   | | |      ||   ||  | ||    || |
  CCGTGACCCAGCCCACGCGACGAGTATTCCCTCGGGGTCTCCCGGAGGAGTTTGCCCTGGTGCTGACACTAC
         410       420       430       440       450       460       470
   580       590       600           610       620        630       640
TNCCNGTNGGNYTNYTNYTNYTNGCNGCNGCNTGG----TGYYTNCAYTGGCARM-GNACNMGNMGNMGNAC
|  | |  |     |  |  |  |  |   | |||    |||||  | || | || | |   |       ||
T-GCTGAAGAAACACACCCACCAGAAG--ACGTGGTATCTGTTTCAAGTGACCGATGCAAATGGGTATCCAC
      480       490         500       510       520       530       540

      650          660       670       680       690       700     X
NCCNMGNCCNG---GNGARCARGTNCCNCCNGTNCCNWSNCCNCARGAYYTNYTNYTNGTNGARC-AY
    |  || |   |  |||||       | |  ||  |  | |||| ||     |  |    || ||
AGATATCCCTGGAAGTCAACAGCCAAGAGCGGAGCCTGGAGCTCAGGGCCCAGGGCCAGGATGGCGACTTTG
      550       560       570       580       590       600       610

TGTCCT


9. US-08-162-407-6 (1-705)
   SCBYP13CS     S.cerevisiae gene for byp1-3 complementing sequenc

 LOCUS       SCBYP13CS     4100 bp    DNA             PLN       24-NOV-1993
 DEFINITION  S.cerevisiae gene for byp1-3 complementing sequence.
 ACCESSION   X55442
 KEYWORDS    byp1-3 complementing sequence.
 SOURCE      baker's yeast.
   ORGANISM  Saccharomyces cerevisiae
             Eukaryota; Plantae; Thallobionta; Eumycota; Hemiascomycetes;
             Endomycetales; Saccharomycetaceae.
 REFERENCE   1  (bases 1 to 4100)
   AUTHORS   Huse,K.
   TITLE     Direct Submission
   JOURNAL   Submitted (05-NOV-1990) to the EMBL/GenBank/DDBJ databases. Huse
             K., Institut fuer Mikrobiologie, TH Darmstadt, Schnittspahnstr. 10,
             D-6100 Darmstadt
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 4100)
   AUTHORS   Huse,K., Hohmannn,S., Valentin,E. and Zimmermann,F.K.
   JOURNAL   Unpublished
   STANDARD  full automatic
 REFERENCE   3  (bases 3841 to 4100)
   AUTHORS   Robison,K.
   TITLE     Direct Submission
   JOURNAL   Submitted (16-FEB-1993) to the EMBL/GenBank/DDBJ databases. Sent to
             EMBL by K. Robison, email:robison@biosun.harvard.edu
   STANDARD  full automatic
 COMMENT     NCBI gi: 3436
 FEATURES             Location/Qualifiers
      source          1..4100
                      /organism="Saccharomyces cerevisiae"
                      /strain="AB 320"
                      /chromosome="VII"
      CDS             2680..3840
                      /note="NCBI gi: 3437"
                      /codon_start=1
                      /product="MIG1"
                      /translation="MQSPYPMTQVSNVDDGSLLKESKSKSKVAAKSEAPRPHACPICH
                      RAFHRLEHQTRHMRIHTGEKPHACDFPGCVKRFSRSDELTRHRRIHTNSHPRGKRGRK
                      KKVVGSPINSASSSATSIPDLNTANFSPPLPQQHLSPLIPIAIAPKENSSRSSTRKGR
                      KTKFEIGESGGNDPYMVSSPKTMAKIPVSVKPPPSLALNNMNYQTSSASTALSSLSNS
                      HSGSRLKLNALSSLQMMTPIASSAPRTVFIDGPEQKQLQQQQNSLSPRYSNTVILPRP
```

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                      RSLTDFQGLNNANPNNNGSLRAQTQSSVQLKRPSSVLSLNDLLVGQRNTNESDSDFTT
                      GGEDEEDGLKDPSNSSIDNLEQDYLQEQSRKKSKTSTPTTMLSRSTGRVWSP"
      misc_feature    3841..4100
                      /note="putative VECTOR sequence pBR322"
                      /citation=[3]
 BASE COUNT     1249 a    821 c    882 g   1148 t
 ORIGIN

Initial Score     =    156  Optimized Score    =    368  Significance =  8.79
Residue Identity  =    28%  Matches            =    341  Mismatches   =   322
Gaps              =     80  Conservative Substitutions                 =     0

             X       10         20        30         40        50        60
             ATGACNGTNY-TNGCNCCNGCNTGGWSNCCNACNAC-NTAYYTNYTNYTNYTNYTNYTNYTN
             | |   || |   |   | ||   |||     |  |   |||   | ||  | || |  ||
   AGGAGAGTAAAAGCAAGTCCAAAGTAGCTGCGAAGTCAGAGGCGCCAAGACCACATGCTTGTCCTAT--CTG
  2740      2750      2760      2770      2780      2790      2800

           70        80        90       100       110       120       130
   WSNWSNGGNYTNWSNGGNACNCARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAAR
   || |   | || ||    ||   |||||| |    ||||   || | || || |   ||   |  |  |||
   TCATAGAGCTTTTC----AC---AGACTGGA-ACATCAGACGAGACACATGAGAATTCATACAGGTGAGAAG
  2810      2820             2830      2840      2850      2860      2870

        140        150          160       170       180       190
   ATNMGNGARY-TNWSNGAY---TAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAY--
      |  | || | ||   |    || | |   ||| ||   | ||    |  || |  ||||  | ||||
   CCTCACGCGTGTGACTTCCCCGGATGTGTGAAAAGGTT---CAGT---AGAAGCGATGAACTGACGAGACAC
        2880      2890      2900         2910         2920      2930

   200        210          220         230       240        250         260
   -GARGARYT-NTGY---GGNGGNYTNTGGMGNY--TNGTNYTNGCNCARMGNTGGATG-GARMGNYTNA--A
    ||||||||  | |         |  | ||| |    |     |    |||  || || | ||  |  |  |
   AGAAGAATTCATACAAACTCCCACCCTCGAGGTAAAAGAGGCAGAAAGAAGAAGGTTGTGGGCTCTCCAATA
  2940      2950      2960      2970      2980      2990      3000

          270       280       290       300       310       320       330
   RACNGTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTG
   ||  || || | ||   | ||| |    | |   |||   | ||||| | ||   |||||    |   ||
   AATAGT-GCTAGTTC--TAGTGCTACCAGTATACCAGA-TTTAAATACGGCAA---ATTTTTCACCGCCATT
3010       3020        3030      3040       3050         3060      3070

        340          350         360         370        380          390
   YGCNTTYCARCCNC---CNCC-NWSNTGYYT-NMGNT-TYG-TNCARACNAAYAT--NWSNMG-NYTNYTNC
     |    ||||  |   | ||  |  | |||   | | ||| | | ||  || ||   || ||  || || |
   ACCACAGCAACACCTATCGCCTTTAATTCCTATTGCTATTGCTCCGAAAGAAAATTCAAGTCGATCTTCTAC
     3080      3090      3100      3110      3120      3130      3140

      400       410       420       430       440       450        460
   ARGARACNWSNGARCARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTYWS-NMGNTGYYTNGAR
   ||||||     ||| |||        |  ||| |   ||  |   |   ||||  | |  |  || ||
   AAGAAAAGGTAGAAAAAC---CAAATTCGAAATCGGCGA-AAGTGGTGGGAATGACCCATATATGGTT---T
   3150      3160         3170      3180       3190      3200      3210

     470       480       490       500       510       520       530
   YTNCARTGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCN
   || |  | ||||   ||| | |  |  || ||  | |  || || || |  || |    ||| || |
   CTTC--TCCCAAAACGATGGCT-AAGATTCCCGTCTCGGTGAAG-CCTCCACCTTCTTTAGC-ACTGAATAA
          3220      3230       3240      3250       3260       3270
  540         550       560       570       580       590         600
  ACNG--CNCCNCARCCNCCNYTNYTNYTNYTNYTNYTNYTNCCNGTNGGNYTNYTNY--TNYTNGCNGCNGC
     |  |  |  |||  |  |  || |  || || |  || |  || |  |  |  |  |  | || |  |
  TATGAACTACCAAACTTCATCCGCTTCCACTGCTTTGTCTTC--GTTGAGCAATAGCCATAGTGGCAGTAGA
3280      3290      3300      3310      3320        3330      3340

    610       620       630       640       650       660       670
  NTGGTGYYTNCAYTGGCARMGNACNMGNMGNMGNACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNCCNWS
   | |   ||  ||  |  |    | |  |  |  |   | |  |   |  ||| ||| |  |  |  |  ||
  CT-GAAACTGAACGCGTTATCGTCCCTACAAATGATGACGC-CCATTGCTAGC-AGTGCGCCAAGGAC--TG
3350       3360      3370      3380       3390       3400      3410

  680         690         700     X
  NCCNCA-RGAY-YTNYT--NYTNGTNGARC-AY
      || ||||  | ||   |      ||| ||
  TTTTCATAGACGGTCCTGAACAGAAACAACTACAACAACAACA
   3420      3430      3440      3450
```

```
10. US-08-162-407-6 (1-705)
    WHTGLIABF    Wheat (T.aestivum) alpha-/beta-gliadin class A-I m

 LOCUS       WHTGLIABF     950 bp ss-mRNA            PLN       02-MAY-1986
 DEFINITION  Wheat (T.aestivum) alpha-/beta-gliadin class A-I mRNA, complete
             cds, clone pA26.
 ACCESSION   M11074
 KEYWORDS    gliadin.
 SOURCE      Wheat (T.aestivum, cv. Cheyenne) seed, cDNA to mRNA, clone pA26.
   ORGANISM  Triticum aestivum
             Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
             Commelinidae; Cyperales; Poaceae.
 REFERENCE   1  (bases 1 to 950)
   AUTHORS   Okita,T.W., Cheesbrough,V. and Reeves,C.D.
   TITLE     Evolution and heterogeneity of the alpha-/beta-type and gamma-type
             gliadin DNA sequences
   JOURNAL   J. Biol. Chem. 260, 8203-8213 (1985)
   STANDARD  full automatic
 COMMENT     Draft entry and sequence in computer readable form for [1] kindly
             provided by T.W.Okita, 25-OCT-1985.
             The alpha-/beta-gliadins can be divided into five homology classes.
             Sequence divergence between the classes is due to single base
             substitutions and to duplications or deletions within or near
             direct repeats.  There are more than a hundred copies of the gene
             encoding alpha-/beta-gliadin per haploid genome.  Amplification or
             rearrangement of DNA does not occur during development, since
             hybridization patterns are the same, whether DNA isolated from
             leaves or seeds is used.

             NCBI gi: 170721
 FEATURES             Location/Qualifiers
      source          1..950
                      /organism="Triticum aestivum"
      mRNA            <1..>950
                      /note="gliadin mRNA"
      sig_peptide     49..108
                      /note="alpha-/beta-gliadin signal peptide"
                      /codon_start=1
      CDS             49..837
                      /note="pre-alpha-/beta-gliadin A-I;  NCBI gi: 170722"
                      /codon_start=1
```

```
                      /translation="MKTFLILALLAIVATTATTAVRVPVPQLQPQNPSQQQPQEQVPL
                      VQQQQFLGQQQPFPPQQPYPQPQPFPSQQPYLQLQPFLQPQLPYSQPQPFRPQQPYPQ
                      PQPQYSQPQQPISQQQQQQQQQQQQQQQQQQIIQQILQQQLIPCMDVVLQQHNIVHG
                      KSQVLQQSTYQLLQELCCQHLWQIPEQSQCQAIHNVVHAIILHQQQKQQQQPSSQVSF
                      QQPLQQYPLGQGSFRPSQQNPQAQGSVQPQQLPQFEEIRNLARK"
      mat_peptide     109..834
                      /note="alpha-/beta-gliadin A-I"
                      /codon_start=1
 BASE COUNT      321 a    296 c    146 g    187 t
 ORIGIN      26 bp upstream of AluI site; chromosome 6.

Initial Score     =    153  Optimized Score  =    227  Significance =  8.58
Residue Identity =    28%  Matches          =    203  Mismatches   =   206
Gaps              =     41  Conservative Substitutions          =     0

260       270       280       290       300       310       320       330
  ARACNGTNGCNGGNWSNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAART
             |   | |  ||  |||     |  |     || |||||  |||| |||  ||     |||
            AGAGCGCATCATTTAAGCCAAGCAAGCTGTGGTCAATAC--AAATCCACCATG-----AAA-
            X       10        20        30          40        50

        340       350       360       370       380       390        400
  GYGCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGAR-ACN
   |   | ||| ||    ||  | ||||      ||||   ||| | |   || |  || |    ||||  |
  ACCTTTCTCATCCTTGCCCTCCTTGCT-----ATCGTGGCGACCACCGCCACAA--CTGCAGTTAGAGTTCC
        60        70        80             90       100         110

        410       420       430        440       450        460       470
  WSNG-ARCARYTNGTNGCNYTNAARCCNT-GGATNACNMGNCARAAYTTYWSNMGNTGY-YTNGARYTNCAR
  || |  ||||||     | |  || || |   |  |  || || ||   ||  || | | || | ||  |||
  AGTGCCACAATTGCAGCCACAAAATCCATCTCAGCAACAGCCACAAGAGCA--AGTTCCATTGGTACAACAA
120       130       140       150       160       170         180

        480       490       500       510       520       530
  TGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNAC----
     ||| |   ||| ||    |  |  |  || |   | || |  |  |    | | || ||  | ||
  ---CAA-CAATTTCTAG--GGCAGCAACAACCATTTCCACCACAACAAC-CATATCCACAGCCGCAACCATT
   190        200         210       220       230        240       250

540       550       560       570         580       590         600
  NGCNCCNCARCCNCCNYTNYTNYTNYTNYTNYTNYTNC--CNGTNGGNYTNYTNY--TNYTNGCNGCNGC-N
    |  | |||| ||  | || |  || |  |  || |  | |  |  |  || |  | ||  | ||  |
  TCCATCACAACAACCATATCTGCAACTGCAACCATTTCTGCAGCCG--CAACTACCATATTCACAGCCACAA
     260       270       280       290       300         310       320

   610        620       630       640       650       660       670
  TGGTGYYTNC-AYTGGCARMGNACNMGNMGNMGNACNCCNMGNCCNGGNGARCARGTNCCNCCNGTNCCNWS
     | ||  | ||    | |  |  |  |  || |  |  ||     |  ||| |   |  ||  |  |
  CCATTTCGACCACAACAACCATATCCACAACCGCAACCACAGTATTCG-CAACCACAACAACCAATTTCACA
     330       340       350       360       370        380       390

  680       690       700     X
  NCCNCARGAYYTNYTNYTNGTNGARCAY
   |  ||| | |  |  |      ||||
  GCAGCAGCAGCAGCAGCAGCAACAACAACAACAACAAC
    400       410       420  X    430
```

maryh@stic **stdin**

NeWSprinter20
Thu Apr 06 10:26:39 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file transl6.res made by maryh on Thu 6 Apr 95 9:48:27-PDT.


Query sequence being compared:US-08-162-407-6 (1-465)
Number of sequences searched:                   313646
Number of scores above cutoff:                    4147

      Results of the initial comparison of US-08-162-407-6 (1-465) with:
   Data bank : EMBL-NEW 1, all entries
   Data bank : GenBank 86, all entries
   Data bank : GenBank-NEW 1, all entries
   Data bank : UEMBL 41_86, all entries

100000-
      -  **
N     -
U50000- *  *
M     -   *
B     -
E     -
R     -
      -*     *
O     -
F10000-       *
      -
S     *
E 5000-
Q     -         *
U     -          *
E     -
N     -
C     -
E     -
S 1000-           *
      -            *
  500-
      -
      -
      -
      -             *
      -
      -
  100-              *
      -
      -               *
   50-
      -
      -
      -
      -
      -                *
      -
```

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    10-                *
      -
      -
     5-                 *
      -
      -
      -                                                *
      -
      -
      -                   * *                                               *
     0---------------------------------------------------------------------
      | |   || |  ||  |   |      |      |      |      |      |      |
SCORE 0 |   50  | 101 | 151     202    252    303    353    404    454
STDEV  -1    1   3   5   7   9

                             PARAMETERS

Similarity matrix       Unitary    K-tuple                   4
Mismatch penalty              1    Joining penalty          30
Gap penalty                1.00    Window size              32
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                             SEARCH STATISTICS

Scores:                    Mean        Median     Standard Deviation
                             32            31        13.51

Times:                     CPU                    Total Elapsed
                       00:27:06.00                00:27:22.00

Number of residues:             288682119
Number of sequences searched:      313646
Number of scores above cutoff:       4147


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                        Init. Opt.
Sequence Name     Description                    Length Score Score   Sig. Frame
-------------------------------------------------------------------------------
                       **** 31 standard deviations above mean ****
  1. HSU03858      Human flt3 ligand mRNA, compl   1080   454   465  31.23   0
  2. HSU04806      Human FLT3/FLK2 ligand mRNA,     859   452   464  31.08   0
                       **** 23 standard deviations above mean ****
  3. MUSLIGAND     Mouse flt3 ligand mRNA, compl    829   345   400  23.16   0
  4. MMU04807      Mus musculus FLT3/FLK2 ligand   1152   343   399  23.01   0
                       ****  9 standard deviations above mean ****
  5. MZEPOD        Maize pyruvate,orthophosphate   3171   161   241   9.55   0
                       ****  8 standard deviations above mean ****
  6. HHU06941      Human herpesvirus 6B R1 repli   1651   145   240   8.36   0
                       ****  7 standard deviations above mean ****
  7. TAGLUIN1     Wheat Glu-Aly sublocus with W    794    134    228    7.55    0
  8. COTMYBA      Cotton DNA-binding domain mRN   1006    134    249    7.55    0
  9. SAUNKORFB    S.ambofaciens ORF, complete C   1449    134    242    7.55    0
 10. TAGLU1AG     Wheat gene for HMW-glutenin s   2915    134    241    7.55    0
 11. MMIGE6H      Mouse mRNA for anti-hPLAP-dir   1579    128    252    7.10    0
 12. MDPMVT10     Aleutian mink disease parvovi   1601    127    239    7.03    0
 13. MDPCGA       Aleutian mink disease parvovi   4801    127    239    7.03    0
                   ****  6 standard deviations above mean ****
 14. BLYSEQ       Hordeum vulgare DNA sequence     830    126    244    6.96    0
 15. DROOTUA      D.melanogaster ovarian tumor    5161    126    249    6.96    0
 16. HSHZF6       H.sapiens HZF6 mRNA for zinc     627    124    227    6.81    0
 17. SCYBR216C    S.cerevisiae chromosome II re   2517    123    238    6.73    0
 18. MZEPPDKA2    Corn pyruvate,orthophosphate    5519    122    239    6.66    0
 19. CHPSZFPA     Pea chloroplast accD gene for   1254    121    241    6.59    0
 20. CHPSZFPG     Pisum sativum chloroplast orf   3240    121    241    6.59    0


1. US-08-162-407-6 (1-465)
   HSU03858     Human flt3 ligand mRNA, complete cds.

 LOCUS       HSU03858     1080 bp    mRNA            PRI       19-JUL-1994
 DEFINITION  Human flt3 ligand mRNA, complete cds.
 ACCESSION   U03858
 KEYWORDS    .
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 1080)
   AUTHORS   Lyman,S.D., James,L., Johnson,L., Brasel,K., de Vries,P.,
             Escobar,S.S., Downey,H., Splett,R.R., Beckmann,M.P. and
             McKenna,H.J.
   TITLE     Cloning of the human homologue of the murine flt3 ligand: a growth
             factor for early hematopoietic progenitor cells
   JOURNAL   Blood 83, 2795-2801 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1080)
   AUTHORS   Lyman,S.D.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-NOV-1993) Stewart D. Lyman, Immunex Research and
             Development Corporation, 51, University St., Seattle, WA 98101, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 494978
 FEATURES             Location/Qualifiers
      source          1..1080
                      /clone_lib="expression, cDNA"
                      /organism="Homo sapiens"
                      /cell_line="clone 22 (T cell)"
      5'UTR           1..83
      CDS             84..791
                      /standard_name="FMS-like tyrosine kinase-3 ligand"
                      /note="ligand for the flt3/flk-2 tyrosine kinase receptor;
                       NCBI gi: 494979"
                      /codon_start=1
                      /function="stimulates proliferation of early hematopoietic
                      cells"
                      /product="flt3 ligand"
                      /translation="MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVK
                      IRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVN
                      TEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
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                     DSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPG
                     EQVPPVPSPQDLLLVEH"
      sig_peptide    84..161
      misc_feature   162..629
                     /note="extracellular domain"
      misc_feature   630..698
                     /note="transmembrane domain"
      misc_feature   699..788
                     /note="cytoplasmic domain"
      3'UTR          792..1080
      misc_feature   1015..1080
                     /note="ATTTA mRNA instability motif"
      polyA_signal   1059..1064
      polyA_site     1080
                     /note="32 A residues"
 BASE COUNT      204 a    384 c    290 g    202 t
 ORIGIN

Initial Score    =    454  Optimized Score  =    465  Significance = 31.23
Residue Identity =    55%  Matches          =    370  Mismatches   =    95
Gaps             =      0  Conservative Substitutions                =     0

             X       10        20        30        40        50        60
             CARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARYT
             ||||||||||| ||||||||||| || || || || |||||||| || ||||| || |||||
    CAGTGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCT
       160   X   170       180       190       200       210       220

          70        80        90       100       110       120       130
    NWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNTGYGGNGG
     || |||||||| || ||||||||||| || || || || || ||||| |||||||||||||| ||||| ||
    GTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGG
     230       240       250       260       270       280       290

       140       150       160       170       180       190       200
    NYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAARATGCARGG
     || ||||| || || || || ||||| ||||||||||| || ||||| || || || || |||||||||||
    CCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGG
   300       310       320       330       340       350       360       370

     210       220       230       240       250       260       270
    NYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCCNWSNTGYYT
     || || ||||| || ||||| ||||| |||||||| || |||||||| |||||||| || || || |||||
    CTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCT
           380       390       400       410       420       430       440

   280       290       300       310       320       330       340       350
    NMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYTNAARCCNTG
     || ||||| ||||| ||||| || || || || |||||||| || |||||||| || || || ||||| ||
    TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTG
         450       460       470       480       490       500       510

           360       370       380       390       400       410       420
    GATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNYTNCCNCCNCC
    ||| || || ||||||||||| || ||||| ||||| ||||||||||| ||||| || || || || || ||
    GATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCC
       520       530       540       550       560       570       580

         430       440       450       460    X
    NTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCN
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     ||||| || || || || ||||| || || || || || ||
    ATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTC
     590       600       610       620       630


2. US-08-162-407-6 (1-465)
   HSU04806     Human FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS       HSU04806       859 bp    mRNA            PRI       11-MAY-1994
 DEFINITION  Human FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION   U04806
 KEYWORDS    .
 SOURCE      human.
   ORGANISM  Homo sapiens
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE   1  (bases 1 to 798)
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 859)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483844
 FEATURES             Location/Qualifiers
     source           1..859
                      /clone="human Flt3/Flk2 ligand S86"
                      /clone_lib="SV48 cDNA"
                      /organism="Homo sapiens"
                      /cell_line="SV48 thymic stroma"
     CDS              93..800
                      /note="NCBI gi: 483845"
                      /codon_start=1
                      /product="FLT3/FLK2 ligand"
                      /translation="MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVK
                      IRELSDYLLQDYPVTVASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVN
                      TEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
                      DSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPG
                      EQVPPVPSPQDLLLVEH"
 BASE COUNT      147 a    318 c    246 g    148 t
 ORIGIN

Initial Score    =    452  Optimized Score  =    464  Significance = 31.08
Residue Identity =    55%  Matches          =    369  Mismatches   =    96
Gaps             =      0  Conservative Substitutions               =     0

             X       10        20        30        40        50        60
             CARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARYT
             ||||||||||| ||||||||||| || || || || |||||||| || ||||| || |||||
    CAGTGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCT
        170  X    180       190       200       210       220       230
```

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          70        80        90       100       110       120       130
    NWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNTGYGGNGG
     || |||||||| || ||||||||||| || || || || || ||||| |||||||||||||| ||||| |
    GTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGC
      240       250       260       270       280       290       300

       140       150       160       170       180       190       200
    NYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAARATGCARGG
     || ||||| || || || || ||||| ||||||||||| || ||||| || || || || |||||||||||
    GCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGG
    310       320       330       340       350       360       370

     210       220       230       240       250       260       270
    NYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCCNWSNTGYYT
     || || ||||| || ||||| ||||| |||||||| || |||||||| |||||||| || || || |||||
    CTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCT
  380       390       400       410       420       430       440       450

   280       290       300       310       320       330       340       350
    NMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYTNAARCCNTG
     || ||||| ||||| ||||| || || || || |||||||| || |||||||| || || || ||||| ||
    TCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTG
          460       470       480       490       500       510       520

           360       370       380       390       400       410       420
    GATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNYTNCCNCCNCC
    ||| || || ||||||||||| || ||||| ||||| ||||||||||| ||||| || || || || || ||
    GATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCACCCCC
        530       540       550       560       570       580       590

         430       440       450       460    X
    NTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCN
     ||||| || || || || ||||| || || || || || ||
    ATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTC
      600       610       620       630       640


3. US-08-162-407-6 (1-465)
   MUSLIGAND    Mouse flt3 ligand mRNA, complete cds.

 LOCUS       MUSLIGAND      829 bp ss-mRNA            ROD       04-JAN-1994
 DEFINITION  Mouse flt3 ligand mRNA, complete cds.
 ACCESSION   L23636
 KEYWORDS    ligand.
 SOURCE      Mus musculus (strain SJL/J) cDNA to mRNA.
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 829)
   AUTHORS   Lyman,S.D., James,L., VandenBos,T., deVries,P., Brasel,K.,
             Gliniak,B., Hollingsworth,L., Picha,K.S., McKenna,H.J.,
             Splett,R.R., Fletcher,F.A., Maraskovsky,E., Farrah,T.,
             Foxworthe,D., Williams,D.E. and Beckmann,M.P.
   TITLE     Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
             receptor -- a proliferative factor for primitive hematopoietic
             cells
   JOURNAL   Cell 75, 1157-1167 (1993)
   STANDARD  full automatic
 COMMENT     NCBI gi: 439441
 FEATURES             Location/Qualifiers
      source          1..829
                      /organism="Mus musculus"
                      /strain="SJL/J"
                      /sequenced_mol="cDNA to mRNA"
      sig_peptide     32..109
                      /codon_start=1
      CDS             32..727
                      /note="NCBI gi: 439442"
                      /codon_start=1
                      /product="flt3 ligand"
                      /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                      KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                      NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQ
                      CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRR
                      GELHPGVPLPSHP"
      mat_peptide     110..724
                      /codon_start=1
 BASE COUNT      163 a    265 c    221 g    180 t
 ORIGIN

Initial Score     =   345  Optimized Score   =   400  Significance = 23.16
Residue Identity  =   46%  Matches           =   322  Mismatches   =   143
Gaps              =     8  Conservative Substitutions              =     0

              X       10        20        30        40        50        60
              CARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARYT
              |  |||||||  |||   ||||| || || || ||  |||||   || ||| | || |||||
    GCGGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTT
      110     X 120       130       140       150       160       170

          70        80        90       100       110       120       130
    NWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNTGYGGNGG
     || ||| |||| ||  |||||||||| || || || ||    ||||| ||||||||| |||  |||   |
    GACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAGCACTGCAAGGC
    180       190       200       210       220       230       240

       140       150       160       170       180       190       200
    NYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAARATGCARGG
     || ||||| ||  | || || ||||| ||||| ||||  || ||||| || || || || |||||||||
    CTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAAC
  250       260       270       280       290       300       310       320

     210       220       230       240       250       260       270
    NYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCCNWSNTGYYT
     || || |||   || ||||| ||||| |||||||| ||   |||| | |||||||| |  ||    |||||
    GCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCT
          330       340       350       360       370       380       390

   280       290       300       310       320       330       340
    NMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYTNAARCCNT-
     || ||||| ||||| ||||| || |  || ||  |||| || ||   ||||||  | || || ||||| |
    GCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGCTCTGAAGCCCTG
        400       410       420       430       440       450       460

       350       360       370       380       390       400       410
    -----GGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNYTNCC
         |||   |  | ||||||||||| || ||||| ||| | ||||||||||| ||||| || || || |
    TATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCT
      470       480       490       500       510       520       530
```

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     420       430       440         450       460    X
    NCCNCCNTGGWSNCCNMGNCCNYTNGARGCNAC--NGCNCCNACNGCNCCN
     || ||  |||| || |   | || ||||| ||   || || |  ||  |
    GCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAG
    540       550       560       570       580       590


4. US-08-162-407-6 (1-465)
   MMU04807     Mus musculus FLT3/FLK2 ligand mRNA, complete cds.

 LOCUS       MMU04807     1152 bp    mRNA            ROD       11-MAY-1994
 DEFINITION  Mus musculus FLT3/FLK2 ligand mRNA, complete cds.
 ACCESSION   U04807
 KEYWORDS    .
 SOURCE      mouse.
   ORGANISM  Mus musculus
             Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
             Eutheria; Rodentia; Myomorpha; Muridae; Mus.
 REFERENCE   1  (bases 1 to 921)
   AUTHORS   Hannum,C., Culpepper,J., Campbell,D., McClanahan,T., Zurawski,S.,
             Bazan,J.F., Kastelein,R., Hudak,S., Wagner,J., Mattson,J., Luh,J.,
             Duda,G., Martina,N., Peterson,D., Menon,S., Shanafelt,A.,
             Muench,M., Kelner,G., Namikawa,R., Rennick,D., Roncarolo,M.G.,
             Zlotnik,A., Rosnet,O., Dubreuil,P., Birnbaum,D. and Lee,F.
   TITLE     Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
             haematopoietic stem cells and is encoded by variant RNAs
   JOURNAL   Nature 368, 643-648 (1994)
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1152)
   AUTHORS   Culpepper,J.A.
   TITLE     Direct Submission
   JOURNAL   Submitted (30-DEC-1993) Janice A. Culpepper, DNAX Research
             Institute, 901 California Avenue, Palo Alto, CA 94304, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 483846
 FEATURES             Location/Qualifiers
      source          1..1152
                      /clone="mouse Flt3/Flk2 ligand T110"
                      /clone_lib="TA4 cDNA"
                      /organism="Mus musculus"
                      /cell_line="TA4 stroma"
      CDS             256..954
                      /note="NCBI gi: 483847"
                      /codon_start=1
                      /product="FLT3/FLK2 ligand"
                      /translation="MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKV
                      KFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDV
                      NTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQ
                      CQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARR
                      RGELHPGVPLPSHP"
 BASE COUNT      238 a    346 c    324 g    244 t
 ORIGIN

Initial Score     =   343  Optimized Score   =   399  Significance = 23.01
Residue Identity  =   46%  Matches           =   321  Mismatches   =   144
Gaps              =     8  Conservative Substitutions              =     0

              X       10        20        30        40        50        60
              CARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARYT
              |  |||||||  |||   ||||| || || || ||  |||||   || ||| | || |||||
    GCGGGGACACCTGACTGTTACTTCAGCCACAGTCCCATCTCCTCCAACTTCAAAGTGAAGTTTAGAGAGTT
  330       340       350       360       370       380       390       400

          70        80        90       100       110       120       130
    NWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNTGYGGNGG
     || ||| |||| ||  |||||||||| || || || ||    ||||| ||||||||| |||  |||   |
    GACTGACCACCTGCTTAAAGATTACCCAGTCACTGTGGCCGTCAATCTTCAGGACGAGAAGCACTGCAAGGC
          410       420       430       440       450       460       470

       140       150       160       170       180       190       200
    NYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAARATGCARGG
     || ||||| ||  | || || ||||| ||||| ||||  || ||||| || || || || |||||||||
    CTTGTGGAGCCTCTTCCTAGCCCAGCGCTGGATAGAGCAACTGAAGACTGTGGCAGGGTCTAAGATGCAAAC
        480       490       500       510       520       530       540

     210       220       230       240       250       260       270
    NYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCCNWSNTGYYT
     || || |||   || ||||| ||||| |||||||| ||   |||| | |||||||| |  ||    |||||
    GCTTCTGGAGGACGTCAACACCGAGATACATTTTGTCACCTCATGTACCTTCCAGCCCCTACCAGAATGTCT
      550       560       570       580       590       600       610

   280       290       300       310       320       330       340
    NMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGTNGCNYTNAARCCNT-
     || ||||| ||||| ||||| || |  || ||  |||| || ||   ||||||  | |  || ||||| |
    GCGATTCGTCCAGACCAACATCTCCCACCTCCTGAAGGACACCTGCACACAGCTGCTTGGTCTGAAGCCCTG
    620       630       640       650       660       670       680

       350       360       370       380       390       400       410
    -----GGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWSNWSNACNYTNCC
         |||   |  | ||||||||||| || ||||| ||| | ||||||||||| ||||| || || || |
    TATCGGGAAGGCCTGCCAGAATTTCTCTCGGTGCCTGGAGGTGCAGTGCCAGCCGGACTCCTCCACCCTGCT
  690       700       710       720       730       740       750       760

     420       430       440       450       460      X
    NCCNCCNTGGWSNCCNMGNCCNYTNGARGCNAC--NGCNCCNACNGCNCCN
     || ||  |||| || |   | || ||||| ||   || || |  ||  |
    GCCCCCAAGGAGTCCCATAGCCCTAGAAGCCACGGAGCTCCCAGAGCCTCGGCCCAGGCAG
          770       780       790       800       810 X     820
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5. US-08-162-407-6 (1-465)
   MZEPOD        Maize pyruvate,orthophosphate dikinase mRNA, compl

 LOCUS       MZEPOD       3171 bp ss-mRNA            PLN       30-SEP-1988
 DEFINITION  Maize pyruvate,orthophosphate dikinase mRNA, complete cds.
 ACCESSION   J03901
 KEYWORDS    pyruvate orthophosphate dikinase.
 SOURCE      Maize (strain Golden Cross Bantam) green leaf, cDNA to mRNA, clones
             pPPD[71,1067].
   ORGANISM  Zea mays
             Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
             Commelinidae; Cyperales; Poaceae.
 REFERENCE   1  (bases 1 to 3171)
   AUTHORS   Matsuoka,M., Ozeki,Y., Yamamoto,N., Hirano,H., Kano-Murakami,Y. and
             Tanaka,Y.
   TITLE     Primary structure of maize pyruvate,orthophosphate dikinase as
             deduced from cDNA sequence
   JOURNAL   J. Biol. Chem. 263, 11080-11083 (1988)
   STANDARD  full automatic
```

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 COMMENT     Draft entry and printed copy of sequence for [1] kindly provided by
             M.Matsuoka, 18-MAY-1988.

             NCBI gi: 168579
 FEATURES             Location/Qualifiers
      source          1..3171
                      /organism="Zea mays"
      mRNA            <1..3171
                      /note="PODK mRNA"
      CDS             114..2957
                      /note="pyruvate,orthophosphate dikinase (EC 2.7.9.1);
                      NCBI gi: 168580"
                      /codon_start=1
                      /translation="MAASVSRAICVQKPGSKCTRDREATSFARRSVAAPRPPHAKARR
                      RHPLRLRRGTGPHCSPLRAVVDAAPIQTTKKRVFHFGKGKSEGNKTMKELLGGKGANL
                      AEMASIGLSVPPGFTVSTEACQQYQDAGCALPAGLWAEIVDGLQWVEEYMGATLGDPQ
                      RPLLLSVRSGAAVSMPGMMDTVLNLGLNDEVAAGLAAKSGERFAYDSFRRFLDMFGNV
                      VMDIPRSLFEEKLEHMKESKGLKNDTDLTASDLKELVGQYKEVYLSAKGEPFPSDPKK
                      QLELAVLAVFNSWESPRAKKYRSINQITGLRGTAVNVQCMVFGNMGNTSGTGVLFTRN
                      PNTGEKKLYGEFLVNAQGEDVVAGIRTPEDLDAMKNLMPQAYDELVENCNILESHYKE
                      MQDIEFTVQENRLWMLQCRTGKRTGKSAVKIAVDMVNEGLVEPRSAIKMVEPGHLDQL
                      LHPQFENPSAYKDQVIATGLPASPGAAVGQVVFTAEDAEAWHSQGKAAILVRAETSPE
                      DVGGMHAAVGILTERGGMTSHAAVVARWWGKCCVSGCSGIRVNDAEKLVTIGSHVLRE
                      GEWLSLNGSTGEVILGKQPLSPPALSGDLGTFMAWVDDVRKLKVLANADTPDDALTAR
                      NNGAQGIGLCRTEHMFFASDERIKAVRQMIMAPTLELRQQALDRLLTYQRSDFEGIFR
                      AMDGLPVTIRLLDHPSYEFLPEGNIEDIVSELCAETGANQEDALARIEKLSEVNPMLG
                      FRGCRLGISYPELTEMQARAIFEAAIAMTNQGVQVFPEIMVPLVGTPQELGHQVTLIR
                      QVAEKVFANVGKTIGYKVGTMIEIPRAALVADEIAEQAEFFSFGTNDLTQMTFGYSRD
                      DVGKFIPVHLAQGILQHDPFEVLDQRGVGELVKFATERGRKARPNLKVGICGEHGGEP
                      SSVAFFAKAGLDFVSCSPFRVPIARLAAAQVLV"
 BASE COUNT      691 a    852 c    971 g    657 t
 ORIGIN      1 bp upstream of EcoRI site.

Initial Score    =    161  Optimized Score  =    241  Significance =  9.55
Residue Identity =    28%  Matches          =    224  Mismatches   =   222
Gaps             =     46  Conservative Substitutions           =     0
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              X            10        20        30         40        50
              CA--RGAYTGY---WSNTTYCARCAYWSNCCNATNWSNWSNGA-YTTYGCNGTNAARATNMG
              ||  || ||||   ||   ||||  |||  |  | || || ||    |||    |  |  ||
    AGATGGCGAGCATCGGGCTGTCGGTGCCGCCAGGGTTC-ACGGTGTCGACGGAGGCGTGCCAGCAGTACCAG
        430   X   440       450       460       470       480       490

      60        70        80          90       100       110         120
    NGARYTNWSNGAYTAYYTNYTNCARGAYTAY--CCNGTNACNGTNGCNWSNAAYYTNCA--RGAYGARGARY
       ||   | |    ||  |  | || || |   | |  |  ||  | ||   ||| ||  || || || |
    GACGCCGGGTGCGCCCTCCCCGCGGGGCTCTGGGCCGAGATCGT--CGAC-GGCCTGCAGTGGGTGGAGGAG
       500       510       520       530         540        550       560

       130       140       150       160       170          180       190
    TNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNY---TNAARACNGTNGCNGGNW
    |   |||  | |     |  || |      | |||||   | |   ||  |   |     | |  || |
    TACATGGGCGCC-----ACCCTGGGCGATCCGCAGCGCCCGCTCCTGCTCTCCGTCCGCTCCGGCGCCGCCG
        570            580       590       600       610       620       630

        200       210       220       230       240       250         260
    SNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTG--YGCNTTYCARCC
         ||||  ||  |  | || |  ||   ||    |   | |  ||  || |||||  |||    | | |
    TGTCCATGCCCGGCATGATGGACACGGTGCTCAACCTGGGGCTCAACG--ACGAAGTGGCCGCCGGGCTGGC
           640       650       660       670         680       690       700
        270       280       290       300       310       320       330
    NCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNGT
      |    ||  |    || ||||  |  || | |   || || |  || |  || |  |  | |||||  ||
    GGCCAAGAGCGGGGAGCGCTTCG--CCTACGACTCCTTC-CGCCGCTTCCTCGACATGTTCG-GCAAC--GT
           710       720         730        740       750        760

       340        350           360        370       380       390
    NG-CNYTNA-ARCCNTGGATNAC---NMG-NCARAA-YTTYWSNMGNTGYYTNGARYTNCARTGYC---ARC
     | | |  | | ||   | | ||    ||   |||| ||| || |  ||    ||||   || | |   ||
    CGTCATGGACATCCCCCGCTCACTGTTCGAAGAGAAGCTTGAGCACATG-AAGGAATCCAAGGGGCTGAAGA
     770       780       790       800       810        820       830

    400        410        420       430       440       450       460    X
    CNGAYW-SNWSNACNYTNCCNC-CNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCN
      |||| | ||  | |  || |   ||    ||  | ||    |  | | | |      | ||  | |
    ACGACACCGACCTCACGGCCTCTGACCTCAAAGAGCTCGTGGGTCAGTA-CAAGGAGGTCTACCTCTCAGCC
    840       850       860       870       880        890       900     X

    AAGGGAGA
   910
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6. US-08-162-407-6 (1-465)
   HHU06941     Human herpesvirus 6B R1 replication origin (oriLyt

 LOCUS       HHU06941     1651 bp    DNA             VRL       02-MAY-1994
 DEFINITION  Human herpesvirus 6B R1 replication origin (oriLyt).
 ACCESSION   U06941
 KEYWORDS    .
 SOURCE      Human herpesvirus 6B.
   ORGANISM  Human herpesvirus 6B
             Vira; Viruses; dsDNA enveloped viruses; Herpesviridae;
             Betaherpesvirinae.
 REFERENCE   1  (bases 1 to 1651)
   AUTHORS   Dewhurst,S., Krenitsky,D. and Dykes,C.
   TITLE     Human herpesvirus 6B origin: sequence diversity, requirement for
             two binding sites for origin-binding protein and enhanced
             replication from naturally occurring origin multimers
   JOURNAL   Unpublished
   STANDARD  full automatic
 REFERENCE   2  (bases 1 to 1651)
   AUTHORS   Dewhurst,S.
   TITLE     Direct Submission
   JOURNAL   Submitted (18-FEB-1994) Stephen Dewhurst, Microbiology and
             Immunology, University of Rochester Medical Center, 575 Elmwood
             Avenue, Rochester, NY 14642, USA
   STANDARD  full automatic
 COMMENT     NCBI gi: 476271
 FEATURES             Location/Qualifiers
      source          1..1651
                      /clone="RC3 clone"
                      /strain="R1 isolate"
                      /organism="Human herpesvirus 6B"
                      /map="approx. 75-80kb on R1 genome"
                      /note="HHV-6B"
      rep_origin      394..761
      misc_binding    618..640
                      /bound_moiety="OBP"
      misc_binding    674..696
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                      /bound_moiety="OBP"
      repeat_unit     873..1065
                      /note="type 1 repeat (exactly as Z29)"
                      /rpt_type=DIRECT
      repeat_unit     1066..1252
                      /note="type 1 repeat"
                      /rpt_type=DIRECT
 BASE COUNT      555 a    264 c    296 g    536 t
 ORIGIN

Initial Score      =     145  Optimized Score   =     240  Significance =  8.36
Residue Identity   =     27%  Matches           =     223  Mismatches   =   231
Gaps               =      43  Conservative Substitutions                =     0

              X         10        20        30        40        50
              CAR--GAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARAT--NMGNG
              |||  |||||||  |   |   ||| |   | || ||  ||  | |    |||||   |  |
    GTAGGCACCTCAAACGATTGCAAGTGAAATTTTTGTCTGGTTTGCTCACATAAT-CGAATAAGATCACCATG
          30  X     40        50        60        70         80        90

    60         70         80          90       100        110       120
    ARYTNWSNGAY-TAYYTNYT-NCAR--GAYTAYCCNGTNACNGTNGC-NWSNAAYYTNCARGAYGARGARYT
    | || || | | ||||  ||  | |   | | ||  |  |      |  ||   | |  |||||| | | ||
    ATCT-TCGGCCATACCAACTAACTGCTCAGTTCCATGAAAAAAAAACACACGGGCATAAAAGACGTA-ATTT
         100       110       120       130       140       150        160

      130       140       150       160       170          180       190
    NTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGA--RMGNYTNA-ARACNGTNGCNGGNWS
      ||   |  || | ||  |     || |   | || ||  |  |  | | |  | |||  ||        |
    TAGT-TAGAATTGT-GCCTCCAAAATTAG-TGATAGGTGTTTTAACCGTGGTCGAGAAATCGTTTTCTACGG
         170        180       190        200       210       220       230

       200       210        220        230         240       250       260
    NAARATGCARGGNYTNY-TNGARMGNGTNAAYAC-NGARA--TNCAYTTYGTNACNAARTGYGCNTTYCARC
      |||| ||    |  |   ||||   | | |||  ||||  | | || | | |   |     |   | ||
    TCAAATTCATTAACAACGGCGAAA---TAACTACAGGAGAATTTCTCTCCATTAACGATAAAACAGATAAAA
         240       250          260       270       280       290       300

         270       280       290         300       310        320       330
    CNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYAT--NWSNMGNYTNYTNCARGA-RACNWSNGARCARY
    |  |    || | |||    ||||   ||||  | ||   || || |  |   || | ||  ||  | || |
    CATCCAAAAGTTCTTTCTCTTTTGGAAAAACATAGATCCAAGCAG-CAGTAGAAACAGGAGCAGAAACCACC
          310       320       330       340        350       360       370

          340               350       360       370          380       390
    TNGTNGCNYTNA--ARCC------NTGGATNACNMGNCARAAYTTYWSNMGNTG---YYTNGARYTNCARTG
       | |  || |  ||||       |||||       |||||    ||    ||   ||| | | |  |||
    GTTTCGTTTTCATCAGCCATCTTTGTGGATTCGATCACAAAAACAAAGATAATGGGTTTTTGTGGTGAAATC
         380       390       400       410       420       430       440

         400        410       420       430       440        450       460
    YCARCCNGAY-WSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNG-ARGCNACNGCNCCNACNGCN
    |  |     | || |  ||  |  |    |    |||  | |        | || | ||       |
    CTTATATATTATGTTTGAC-GTAACATAACACGCGTCATCAAACATAAAAGTAAACCACAAGTTGAAATATA
       450       460        470       480       490       500       510

      X
    CCN
    ||
    CCGTTTTCTATAT
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      520

   7. US-08-162-407-6 (1-465)
      TAGLUIN1     Wheat Glu-Aly sublocus with Wis-2 insertion 5' end

    LOCUS       TAGLUIN1     794 bp    DNA             PLN       06-JUL-1989
    DEFINITION  Wheat Glu-Aly sublocus with Wis-2 insertion 5' end (0.8 kb Hind III
                fragment).
    ACCESSION   X05995
    KEYWORDS    Glu-Aly gene; glutenin; insertion sequence; retrotransposon;
                Wis-2 insertion sequence.
    SOURCE      wheat.
      ORGANISM  Triticum aestivum
                Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
                Commelinidae; Cyperales; Poaceae.
    REFERENCE   1  (bases 1 to 794)
      AUTHORS   Harberd,N.P., Flavell,R.B. and Thompson,R.D.
      TITLE     Identification of a transposon-like insertion in a Glu-1 allele of
                wheat
      JOURNAL   Mol. Gen. Genet. 209, 326-332 (1987)
      STANDARD  full automatic
    COMMENT     Sequence comparision with Cheyenne
                Glu-Aly sublocus gene has shown that the coding sequence of the
                Chinese Spring sublocus gene is interrupted by a 8.0 kb insertion
                sequence. A DNA duplication and inverted terminal sequences are
                flanking the insertion sequence. See also x05996.
                Data kindly reviewed (18-Apr-1988) by Flavell R.B.

                NCBI gi: 21780
    FEATURES             Location/Qualifiers
         source          1..794
                         /organism="Triticum aestivum"
                         /strain="Chinese spring"
                         /chromosome="chromosome 1a"
         misc_feature    <1..482
                         /note="glutenin homologous seq. (161 AA; includ. stop
                         codon) (1 is 2nd base in codon)"
         misc_feature    478..481
                         /note="DNA duplication"
         intron          483..>794
                         /note="insertion sequence"
         misc_feature    484..493
                         /note="inverted terminal sequence"
    BASE COUNT     290 a    183 c    178 g    139 t      4 others
    ORIGIN

   Initial Score    =    134  Optimized Score  =    228  Significance =  7.55
   Residue Identity =    28%  Matches          =    224  Mismatches   =   196
   Gaps             =     64  Conservative Substitutions              =     0

       10     X   20        30        40          50          60        70
    YTGYWSNTTYCARC-AYWSNCCNATNWSNWSNGAYTTYGCNGTNA--AR-ATNMGNG-ARYTNWSNGAYTAY
               |||  |||  | |   | ||  |  ||    |  || |  || | |||  ||  |||||
              AAGCTTCTCCACAACAGCCAGGAAAATGGCAAGAACTAGGACAAGGGCAACAATGGTACTAT
              X       10        20        30        40        50        60

          80        90        100        110       120       130       140
    YTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNA-AYYTNCARGAYGARGARYTNTGYGGNGGNYTNTG--G
    |     ||  ||| | | |   | |  || || | |    ||| | | || |||   ||     || ||  |
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      C-----CA--ACTTCTCTG---CAGCAGCCAGGACAAGGGCAACAAG-GGTACT-ACCGAACTTCTCTGCAG
                     70           80        90        100        110       120

            150       160           170       180       190       200
      MGNYTNGTNYTNGCNCARMGNTGG----ATGGARMGNYTNAARACNGTNGCNGGNWSNAARATGCARGGNYT
      |  |  |  |     ||||   ||    |  ||||  ||   | | |  ||  | || |||  ||||
      CAGCCAGGACAAAGGCAACAAGGGTACTACCGAAC--TTCTCGGCAGCAGCCAGGAC-AAG-GGCAA--CAG
           130       140       150         160       170        180

    210       220        230       240       250       260        270
      NYTNGARMGNGTNAAY-ACNGARATNCAYTTYGTNACNAARTGYGCNTTYCA-RCCNCCNCCNWSNTGYYTN
       |  || |  |  ||| |  | | | | |  | |  | | | || |   ||| | |     | ||   ||
      ATAGGACAATGGCAACAAGGGTACTACCCAACTTCTCCACA-GCAC---CCAGGACAAGGGCAAC-AACCAG
     190       200       210       220        230          240        250

    280       290       300        310       320       330            340
      MGNTTYGTNCARACNAAYATNWSNM-GNYTNYTNCARGARACNWSNGARCARYTNG-----TNGCNYTNAA-
       |    || ||||  ||||  || | | |  |  | |||||   |  ||||||| |       ||    ||
      -GACAAGTGCAAA-AAATAGGACAAGGGCAACAACCAGAAAAAGGGCAACAACTAGGACAAGAGCAACAAAT
         260        270       280       290       300       310       320

           350       360       370       380       390          400
      --RCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCARTGY--CARCC-NGAYW----SNWS
        | |  ||   || |  ||||||    | |    ||   ||    |  ||  |||||  ||||    | ||
      AGGACAAGGGCAAC-AACCAGAACAAGGGCAACAACC---AGGACAAGGGCAACAACCAGGACAAGGGCAAC
        330        340       350       360          370       380       390

      410       420       430       440           450       460    X
      NACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGA----RGCNACNGCNCCNACNGCNCCN
       |   | |  ||    |  ||  | ||    |  ||    ||| ||  |    ||     |
      AAGGGTACTACCCAACTTCTCTGC-AGCAGCCAGGACAAGGGCAACAACCAGGACAATGACAACAACCAGGA
            400       410        420       430       440       450   X   460


   8. US-08-162-407-6 (1-465)
      COTMYBA      Cotton DNA-binding domain mRNA.

    LOCUS       COTMYBA      1006 bp ss-mRNA           PLN       31-DEC-1993
    DEFINITION  Cotton DNA-binding domain mRNA.
    ACCESSION   L04497
    KEYWORDS    .
    SOURCE      Gossypium hirsutum (cultivar Acala SJ-2) 3-day pre-anthesis ovule
                cDNA to mRNA.
      ORGANISM  Gossypium hirsutum
                Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida;
                Dilleniidae; Malvales; Malvaceae.
    REFERENCE   1  (bases 1 to 1006)
      AUTHORS   Wilkins,T.A. and Lu,C.-C.
      JOURNAL   Unpublished (1993)
      STANDARD  full automatic
    COMMENT     NCBI gi: 437326
    FEATURES             Location/Qualifiers
         source          1..1006
                         /organism="Gossypium hirsutum"
                         /cultivar="Acala SJ-2"
                         /dev_stage="3-day pre-anthesis"
                         /sequenced_mol="cDNA to mRNA"
                         /tissue_type="ovule"
         mRNA            1..1006
         CDS             59..943
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                      /note="MYB A; putative;  NCBI gi: 437327"
                      /codon_start=1
                      /translation="MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEGCWRSLPKAA
                      GLLRCGKSCRLRWINYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDN
                      EIKNYWNTHIKRKLISRGIDPQTHRPLNQTANTNTVTAPTELDFRNSPTSVSKSSSIK
                      NPSLDFNYNEFQFKSNTDSLEEPNCTASSGMTTDEEQQEQLHKKQQYGPSNGQDINLE
                      LSIGIVSADSSRVSNANSAESKPKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRN
                      CQNSNSNGFYSYCRPLDS"
      protein_bind    92..403
                      /note="putative"
                      /bound_moiety="MYB"
      repeat_region   107..133
                      /note="MYB DNA-binding domain repeat signature 1;
                      putative"
 BASE COUNT      323 a    209 c    204 g    270 t
 ORIGIN

Initial Score     =    134  Optimized Score =    249  Significance =  7.55
Residue Identity  =    27%  Matches         =    231  Mismatches   =   217
Gaps              =     49  Conservative Substitutions             =     0

              X       10          20         30          40          50
              CARGAYTGYW--SNTTYCARCAYWSNCC-NATNWSNWSNG--AYTTYGCNGT--NAARATNM
               ||| |||||  | ||||    ||| ||  |  || || |   ||| |  ||   ||||
    TGTCCATGGTGAAGGCTGCTGGCGTTCC----CTCCCCAAAGCTGCTGGGCTGCTTAGATGTGGTAAGAGTT
    150       160       170           180       190       200       210

       60          70        80          90       100       110       120
    GNGARYTNWS--NGAYTAYYTNYTNCARGAYT-AYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARY
    |   ||| ||   ||| | || ||  ||| || |||     |  |     |  | |    |||| || ||||
    GCAGATTAAGATGGATAAACTACTTGAGGCCTGATCTTAAGAGAGGAAATTTCACTGAAGAAGAAGATGAGC
      220       230       240       250       260       270       280

       130       140       150       160         170       180       190
    TNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGG--ATGGARMGNYTNAARACNGTNGCNGGNWS
    |   |      ||    || ||  | |     ||||  |||  || ||  | |  ||||   |  | || ||
    TTATCATCAAGCTTCACAGTTTACT-TGGAAACAAA--TGGTCATTGATTGCTGGAAGA--TTACCAGGAAG
    290       300       310        320         330       340         350

        200              210       220       230       240       250
    NA-ARAT-------GCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTY
     | ||||         |||  || || ||||      |||   |||   |  || | |  | | |      |
    AACAGATAATGAGATAAAGAACTACTGGAAC--ACACACATCAAAAGAAAGCTTATAAGCAGAGGAATTGAT
       360       370       380         390       400       410       420

   260         270       280       290         300       310          320
    CARCCNCCNC--CNWSNTGYYTNMGNTTYGTNCAR-ACNAAYA-TNWSNMGNYTNYTNCARGA---RACNWS
    | ||   | |  | || | ||       ||  ||| || ||||   || |  |  |  | | |   ||  ||
    CCACAAACTCATCGTCCTCTCAATCAAACGGCCAATACCAACACAGTCACAGCCCCCACCGAATTGGATTTC
       430       440       450       460       470       480       490

        330       340            350       360       370       380       390
    NGARCARYTNGTNGCNYTNAAR---CC--NTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCAR
      || |||| |   | |    |   ||   |  |   | |   |||||   || |   | ||  |||| |||
    --AGAAACTCG-CCCACATCCGTTTCCAAATCCAGTTCCATCAAAAACCCGTCTC-TGGATTTCAATTACAA
       500        510       520       530       540        550       560

           400       410       420       430       440       450       460
    TGYCARCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCN
    ||  |     |||| ||  |    |     || | ||     |   |  |  || |  | |   | |   |
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    TG-AATTTCAATTCAAGTCCAACACAGATTCCCTTGAAGAACCCAACTGTACAGCCAGCAGTGGC-ATGACT
        570       580       590       600       610       620        630

      X
    CCN
     |
    ACAGATGAAGAGC
       640


9. US-08-162-407-6 (1-465)
   SAUNKORFB    S.ambofaciens ORF, complete CDS.

 LOCUS        SAUNKORFB    1449 bp    DNA             BCT       02-NOV-1993
 DEFINITION   S.ambofaciens ORF, complete CDS.
 ACCESSION    Z22675
 KEYWORDS     .
 SOURCE       Streptomyces ambofaciens.
   ORGANISM   Streptomyces ambofaciens
              Prokaryota; Bacteria; Firmicutes; Streptomycetaceae.
 REFERENCE    1  (bases 1 to 1449)
   AUTHORS    Aubert,M., Weber,E., Schneider,D., Simonet,J.M. and Decaris,B.
   TITLE      Primary structure analysis of a duplicated region in the
              amplifiable AUD6 locus of Streptomyces ambofaciens DSM40697
   JOURNAL    FEMS Microbiol. Lett. 113, 49-56 (1993)
   STANDARD   full automatic
 REFERENCE    2  (bases 1 to 1449)
   AUTHORS    AUBERT,M.
   TITLE      Direct Submission
   JOURNAL    Submitted (05-MAY-1993) to the EMBL/GenBank/DDBJ databases. Martine
              AUBERT, Laboratoire Genetique et Microbiologie, Universite Nancy I
              Faculte des Sciences, Boulevard des Aiguillettes,
              Vandoeuvre-ls-Nancy, 54506, France
   STANDARD   full automatic
 COMMENT      NCBI gi: 297826
 FEATURES              Location/Qualifiers
      source           1..1449
                       /organism="Streptomyces ambofaciens"
                       /strain="DSM40697"
      CDS              375..1373
                       /note="NCBI gi: 581595"
                       /codon_start=1
                       /translation="MTRRLAQVAKKVGVSEATVSRVLNDKPGVSEATRQSVLSALDVL
                       GYERPTQLRGERARLVGLVLPELQNPIFPAFAEVIGGALAQQGLTPVLCTQTKGGVSE
                       ADYVELLLQQQVSGVVFAGGLFAQADAPHDHYRLLAERNIPVVLINAAIADLDFPCIA
                       CDDAVAVEQSWRHLTSLGHERIGLVLGPGDHLPSRRKLAAVRAAGGSLGDDLVERSMF
                       SLEGGQAAASRLLERGVTGIICASDPLALGAVRAARRRGLHVPRDVSVVGYDDSAFMT
                       CTEPPLTTVRQPIEAMGRAAVDLLWAQIQGTEVPHSELLFEPELVVRGSTAQASAK"
 BASE COUNT      233 a    541 c    454 g    221 t
 ORIGIN

Initial Score     =    134  Optimized Score =    242  Significance =  7.55
Residue Identity  =    27%  Matches         =    225  Mismatches   =   215
Gaps              =     44  Conservative Substitutions             =     0

              X       10        20          30        40        50        60
              CARGAYTGYWSNTTYCARCA-YWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARY
              | || ||||||  ||||||| |||        | || | |||||| |    | |    |  |
    CCGACTACGTCGAG-CTGCTG-CTCCAGCAGCAGGTGTCGGGCGTC-GTCTTCGCCGGCGGACTGTTCGCCC
          690 X      700        710       720        730       740       750
       70        80        90       100       110       120       130
    TNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNTGYGGNG
       | |||  ||  |   |  ||||||   |    |  |   | ||| | |  |  |    | |   ||  |
    AGGCGGACGCCCCCCACGACCACTACCGGCTGCTCGCCGAACGCAACATCCCCGTGGTCCTGATCAACGCCG
           760       770       780       790       800       810       820

        140         150       160       170       180       190        200
    GNYTNTGGMG--NYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNA-ARATGC
      |  | |||   || |  ||  | | ||   |  ||  |||    | | | || || |  || |  | | |
    --CCATCGCGGACCTCG-ACTTCCCCTGCATCGCCTGCGACG----ACGCC-GTCGCCG--TCGAGCAGTCC
           830        840       850       860            870         880

          210       220       230       240       250           260
    ARG-GNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTY----CARCCNCC-NC
     || | |  ||        |   |   |||   | | |||   |   || | |   |    | ||| ||  |
    TGGCGCCACCTCACCTCCCTGGGCCACGAG---CGCATCG--GCCTGGTCCTCGGCCCCGGCGACCACCTCC
       890       900       910          920         930       940       950

   270        280        290       300        310        320         330
    CNWSNTGYY-TNMGNT-TYGTNCARACNAAYATNWSNMGNYT-NYTNCARGA-RACNWS--NGARCARYTNG
    | ||  |||   || |  |   |   |   |    | || ||  ||   ||| ||| ||   |||| ||| |
    CCTCCCGCCGGAAGCTGGCCGCCGTGCGGGCCGCGGGAGGCTCACTCGGGGACGACCTCGTGGAACGCTCG
          960       970       980       990      1000      1010       1020

       340       350       360         370       380       390       400
    TNGCNYTNAARCCNTGGATNACNMGNCA--RAAYTTYWSNMGNTGYYTNGARYTNCARTGYCARCCNGAYWS
      |  ||    || ||||   |  |  |  |  |  ||| ||    || ||||  | | ||| ||| |  ||
    ATGTTCT----CCCTGGAGGGCGGGCAAGCGGCCGCCTCCCGCCTGCTGGAAC-GCGGCGTC-ACCGGCATC
            1030      1040      1050      1060      1070        1080

       410       420       430       440       450       460     X
    NWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNACNG-CNCCN
     ||  | |   |  | || | | |  |    || |  | | |  | ||     | | | ||
    ATCTGCGCCAGCGACCCCCTCGCCCTCGGCGCCGTCCGCGCCGCCCGCAGGCGCGGACTCCACGTACCCCGC
  1090      1100      1110      1120      1130      1140      1150      1160

10. US-08-162-407-6 (1-465)
    TAGLU1AG     Wheat gene for HMW-glutenin subunit located on chr

 LOCUS       TAGLU1AG     2915 bp    DNA             PLN       06-JUL-1989
 DEFINITION  Wheat gene for HMW-glutenin subunit located on chromosome 1A.
 ACCESSION   X03042
 KEYWORDS    direct repeat; glutenin; inverted repeat; seed storage protein;
             signal peptide; storage protein.
 SOURCE      wheat.
   ORGANISM  Triticum aestivum
             Eukaryota; Plantae; Embryobionta; Magnoliophyta; Liliopsida;
             Commelinidae; Cyperales; Poaceae.
 REFERENCE   1  (bases 1 to 2915)
   AUTHORS   Forde,J., Malpica,J.M., Halford,N.G., Shewry,P.R., Anderson,O.D.,
             Greene,F.C. and Miflin,B.J.
   TITLE     The nucleotide sequence of a HMW glutenin subunit gene located on
             chromosome 1A of wheat (Triticum aestivum L.)
   JOURNAL   Nucleic Acids Res. 13, 6817-6832 (1985)
   STANDARD  full automatic
 COMMENT     Though the premature stop codon may not affect gene expression the
             author suggests that the gene is a pseudogene, because no small in
             vivo transcript of chromosome 1A was found. Within the coding
```

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             sequence are two multiple repeated amino acid motifs, PGQGQQ and
             GYYPTSLQQ
             Data kindly reviewed (19-MAR-1986) by J. Forde.

             NCBI gi: 21770
 FEATURES             Location/Qualifiers
      source          1..2915
                      /organism="Triticum aestivum"
      repeat_unit     8..24
                      /note="inverted repeat X"
      repeat_region   243..259
                      /note="direct repeat B"
      repeat_region   272..291
                      /note="imp. direct repeat A"
      repeat_region   297..316
                      /note="imp. direct repeat A"
      repeat_region   318..337
                      /note="imp. direct repeat A"
      repeat_region   343..359
                      /note="direct repeat B"
      repeat_unit     419..431
                      /note="inverted repeat Y"
      promoter        582..586
                      /note="pot. CAAT-box"
      promoter        620..624
                      /note="pot. CAAT-box"
      repeat_unit     648..664
                      /note="inverted repeat X"
      promoter        696..699
                      /note="pot. CAAT-box"
      promoter        724..730
                      /note="put. TATA-box"
      CDS             815..2620
                      /note="precursor"
                      /codon_start=1
      CDS             815..877
                      /note="put. signal peptide (aa -21 to -1);  NCBI gi:
                      21771"
                      /codon_start=1
                      /translation="MAKRLVLFATVVIGLVSLTVA"
      CDS             878..2620
                      /note="mature HMW subunit of glutenin (aa 1-581)"
                      /codon_start=1
      misc_feature    1832..1834
                      /note="premature TAG stop codon"
      repeat_unit     2635..2647
                      /note="inverted repeat Y"
      misc_feature    2678..2683
                      /note="put. polyadenylation signal"
 BASE COUNT      977 a    736 c     674 g     528 t
 ORIGIN

Initial Score    =    134  Optimized Score  =    241  Significance =  7.55
Residue Identity =    28%  Matches          =    238  Mismatches   =   199
Gaps             =     70  Conservative Substitutions             =     0

              X       10        20        30        40         50         60
              CARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTY-GCNGTNAARAT-NMGNGAR
              ||| |  | || | | | | ||| || |  |  ||  ||  | ||    |||||  |  |||
    AATATCTCCTCAGCAGGGGTCATATTATC-CAGGCCAAGCTTCTC-CACAACAGCCAGGAAAATGGCAAGAA
    1210      1220      1230       1240      1250       1260      1270

            70          80        90       100         110          120
    YTNWSNGAYTA--YYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYY--TNCARG---AYGARGARYT
    || || ||| |   |  |    | |||||||     |  | || || | ||    ||||   |  ||| ||
    CT-AG-GACAAGGGCAACAATGGTACTATCCAACTTCTCT-GC-AGCAGCCAGGACAAGGGCAACAAGGGTA
     1280       1290      1300      1310        1320      1330      1340

       130       140         150       160           170       180       190
    NT-GYGGNGGNYTNTG--GMGNYTNGTNYTNGCNCARMGNTGG----ATGGARMGNYTNAARACNGTNGCNG
     |  ||     || ||  ||  |  |  |     ||||   ||    |  ||||  ||     | |  ||
    CTACCGAACTTCTCTGCAGCAGCCAGGACAAAGGCAACAAGGGTACTACCGAAC--TTCTCTGCAGCAGCCA
      1350      1360      1370      1380      1390        1400      1410

               200       210         220       230       240       250
    GNWSNA----ARATGCARGGNYTNYTNGA--RMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNT
    | || |    ||  |  ||| |  |   |  ||| || | |||  || | | |  |   ||  || |
    GGACAAGGGCAACAGATAGGACAATGGCAACAAGGGT-ACTACCCAACTTCTCCGCAGCACCCAG-GACAAG
      1420      1430      1440      1450       1460      1470       1480

     260       270       280       290       300        310       320
    TYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNM-GNYTNYTNCARGARACNWSNGAR
      ||||  ||    ||  | |  ||   ||  ||||  ||||  || | | |  |  | |||||   |  ||
    GGCAACAACC----AG--GAC-AAG---TG--CAAA-AAATAGGACAAGGGCAACAACCAGAAAAAGGGCAA
      1490             1500            1510      1520      1530      1540

    330            340          350       360       370       380       390
    CARYTNG-----TNGCNYTNAA---RCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCART
    ||||| |       ||    ||   | |  ||   || |  ||||||    | |    ||   ||    ||
    CAACTAGGACAAGAGCAACAAATAGGACAAGGGCAAC-AACCAGAACAAGGGCAACAACC---AGGACAAGG
       1550      1560      1570      1580       1590      1600         1610

             400          410       420       430       440           450
    GY--CARCC-NGAYW----SNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGA----RGCNACNGC
    ||  |||||  ||||    | || |   | |  ||    |  ||  | ||    |  ||    ||| ||  |
    GCAACAACCAGGACAAGGGCAACAAGGGTACTACCCAACTTCTCTGC-AGCAGCCAGGACAAGGGCAACAAC
         1620      1630      1640      1650       1660      1670      1680

         460    X
    NCCNACNGCNCCN
        ||     |
    CAGGACAATGGCAACAACCAGGA
        1690    X 1700
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file translnsq6.res made by maryh on Thu 6 Apr 95 10:02:19-PDT.


Query sequence being compared:US-08-162-407-6 (1-465)
Number of sequences searched:                57621
Number of scores above cutoff:                4579

      Results of the initial comparison of US-08-162-407-6 (1-465) with:
   Data bank : N-GeneSeq 17, all entries
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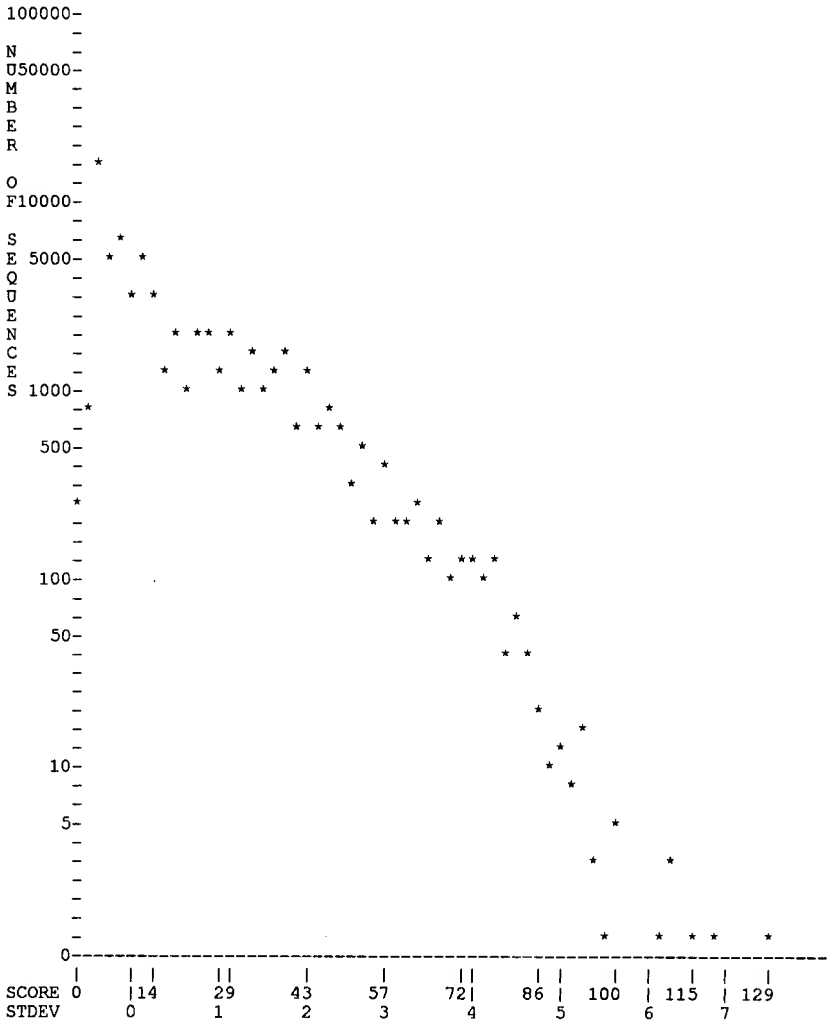

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                            PARAMETERS

Similarity matrix      Unitary     K-tuple                      4
Mismatch penalty             1     Joining penalty             30
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Gap penalty                 1.00     Window size                  32
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                         SEARCH STATISTICS

Scores:                 Mean        Median      Standard Deviation
                          18          14          15.49

Times:               CPU                        Total Elapsed
                  00:02:36.05                   00:02:37.00

Number of residues:               24347505
Number of sequences searched:        57621
Number of scores above cutoff:        4579


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:

                                                           Init. Opt.
Sequence Name     Description                       Length Score Score   Sig. Frame
------------------------------------------------------------------------------------
                       ****  7 standard deviations above mean ****
   1. Q14532        T cell protein 19.1 cDNA (par    1301   129   243    7.16   0
                       ****  6 standard deviations above mean ****
   2. Q54029        Flocculation protein coding s    2685   117   249    6.39   0
   3. Q45455        Sequence encoding murine bone    2373   114   246    6.20   0
                       ****  5 standard deviations above mean ****
   4. Q25812        Clone 45-A.                      4300   110   252    5.94   0
   5. Q15174        Plasmid pAMVBT4.                 4583   109   236    5.87   0
   6. N90183        DNA sequence of plant vector     4583   109   236    5.87   0
   7. Q63241        Crucifer 1-aminocyclopropane-    5613   108   236    5.81   0
   8. N30044        Sequence encoding bovine leuk    1162   100   251    5.29   0
   9. Q14235        A.faecalis penicillin acylase    2451   100   246    5.29   0
  10. Q03661        Maize C3 sequence encoding ac    2546   100   203    5.29   0
  11. Q11176        Clone encoding recombinant hu    4569   100   239    5.29   0
  12. N70607        Sequence encoding the melanom    2362    97   240    5.10   0
  13. Q55768        Human melanoma-associated ant    2368    96   240    5.03   0
  14. N60847        Human pre-prolactin gene.        3621    96   236    5.03   0
                       ****  4 standard deviations above mean ****
  15. Q46099        A. rhizogenes NIAES1724 megal    5893    95   239    4.97   0
  16. Q49206        Golden hamster Aphrodisin cod     501    93   236    4.84   0
  17. Q49205        Field hamster Aphrodisin codi     501    93   236    4.84   0
  18. Q49210        Hamster Aphrodisin coding seq     713    93   211    4.84   0
  19. Q48773        Aphrodisine.                      713    93   211    4.84   0
  20. Q49207        Field hamster Aphrodisin codi     747    93   237    4.84   0


1. US-08-162-407-6 (1-465)
   Q14532        T cell protein 19.1 cDNA (partial).

 ID    Q14532 standard; DNA; 1301 BP.
 AC    Q14532;
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DT    29-JAN-1992  (first entry)
DE    T cell protein 19.1 cDNA (partial).
KW    Multiple membrane spanning protein; T cell; development; ss.
OS    Mus musculus.
PN    WO9116430-A.
PD    31-OCT-1991.
PF    12-APR-1990; U02518.
PR    13-APR-1990; US-509684.
PA    (REDE-) RES DEV FOUND.
PI    Macleod CL;
DR    WPI; 91-339818/46.
PT    New recombinant polypeptide comprising a T-cell protein - used to
PT    regulate T-cell development and tumorigenic phenotype and to
PT    block T-cell activation in auto:immune disease
PS    Disclosure; Fig 20; 98pp; English.
CC    An SL 12.4 cDNA library was constructed from which six cDNAs were
CC    isolated via subtractive hybridisation against a related sister
CC    lymphoma cell line, SL 12.3.  Five clones were obtd. representing
CC    genes which are preferentially expressed in the SL 12.4 T cell
CC    clone, and are undetectably or weakly expressed in SL 12.3.
CC    These clones are 19.5 (Q14534), 20.5 (Q14533), 19.1 (Q14532),
CC    19.2 (Q14531) and 19.4 (Q14530).
CC    No predicted protein sequence is given, incomplete cDNA clone,
CC    therefore, no long ORF.
CC    See also Q14530-34.
SQ    Sequence   1301 BP;    380 A;    291 C;    241 G;    389 T;

Initial Score     =    129  Optimized Score   =    243  Significance =  7.16
Residue Identity  =    26%  Matches           =    224  Mismatches   =   221
Gaps              =     44  Conservative Substitutions              =     0

              X          10         20        30         40        50
              CARGA---YTGYWSNTTYCA-RCAYWSNCCNATNWSNWS-NGAYTTYGCNGTNAARATNMGN
              | |||   |||||| ||  | || |||     | |  ||   |  || | ||  |||  |
    TCCCTACCAACTGGAAAGTTGTTGTTTAAATACCCTGTTGGTTAAAATGTCAAACTTACTGTTTAAA--CAC
          620 X     630       640       650       660       670         680

     60        70        80        90       100         110       120
    GARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNA-AYY-TNCARGAYGARGARYTNT
      ||| ||  ||  ||  ||  ||   ||| |  |  |  | |  || | |||   | ||||   |||||
    TCATT-AGCCATATCCAACTTGAAACATATGCTATTGC--TTG--ACCATATTAAGCCAGACTTTGAACTAG
           690       700       710         720         730       740

    130       140       150       160       170       180       190
    GYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAARA
    ||    | |  |||||  |     |  |  |||| |   | |     |  ||||      | ||  | || |
    GTCAATGTCCCTGGAGTATAAATGTACCATAGAGCTTCCTTGCTTCTTGCAAAAGTCCTCAGG--CGAACA
   750       760       770       780       790       800       810

  200        210          220       230       240       250       260
    T-GCARGGNYTNYTNGARMG---NGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCN
    |  |   | |  |   ||||     | | | |  | |  | |  | |  |  ||    | |||  |||
    TAACTTTGACCCCCATAAAGGTCCCTCACTTCTCACAGCCTTGATTTTGCTGAA--GACCTTCACACCCTGG
   820       830       840       850       860       870         880

    270       280       290       300       310        320          330
    CCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNY-TNCARGARACNWSNGARCA---RYTNGT
    || |    |||  |   ||| |  ||  || | || |  || | |       || ||  ||||   ||   |
    CCCA---ATCTAGGAAATGTTC-TACTCATGTAAGAATTCTTCATCTCTCCCACCTCATAACAAGTGTCCTT
   890          900        910       920       930       940       950
   340       350        360       370           380       390       400
NG-CNYTNAARCCNTGG-ATNACNMGNCARAAYTTTYWSNMGNTGYY---TNGARYTNCARTGYCARCCNGA-
 | | ||  ||   ||| ||    ||  |||||  ||| |    ||    | | ||  |||| |  | | ||
TGTCCCTATAATAATGGCAT----AG-AAAAATCCCTGAAAGACCCAAATTGGGCAACAATACAGATCAGAT
 960       970             980       990      1000      1010      1020

       410       420          430       440       450       460    X
YWS-NWSNACNYTNCCNCCNCCNTGGWS--NCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCN
|||   |  | |   | |  |  |||||      |    | |   |||     |  |  |     |
CAGAGCCTTCATGGGCCCGACAATGGAGAATTGTATTTCTTAAAAAGTGTGTGATCATATTTGTCTGAGCTG
   1030      1040      1050      1060       1070      1080      1090

CAATA
 1100


2. US-08-162-407-6 (1-465)
   Q54029       Flocculation protein coding sequence of Saccharomy

 ID   Q54029 standard; DNA; 2685 BP.
 AC   Q54029;
 DT   19-JUL-1994  (first entry)
 DE   Flocculation protein coding sequence of Saccharomyces cerevisiae.
 KW   Immobilisation; enzyme; cell wall; alpha agglutinin; AGA 1; FLO 1;
 KW   Major cell wall protein; glycosyl-phosphatidyl-inositol;
 KW   anchoring protein; alpha factor; alpha-agglutinin; invertase;
 KW   inulinase; alpha-amylase; Saccharomyces cerevisiae;
 KW   floculation protein; enzymatic process; fermentation;
 KW   biodegradation; catalysis; ss.
 OS   Saccharomyces cerevisiae.
 FH   Key             Location/Qualifiers
 FT   CDS             1..2685
 FT   /*tag=  a
 FT   /product= Flocculation protein.
 PN   WO9401567-A.
 PD   20-JAN-1994.
 PF   07-JUL-1993; E01763.
 PR   08-JUL-1992; EP-202080.
 PR   14-DEC-1992; EP-203899.
 PA   (UNIL ) UNILEVER NV.
 PA   (UNIL ) UNILEVER PLC.
 PI   Klis FM,  Schreuder MP,  Toschka H,  Verrips CT;
 DR   WPI; 94-035071/04.
 DR   P-PSDB; R47578.
 PT   Immobilisation of enzymes to microbial cell wall - by prodn. of
 PT   fusion protein of enzyme linked to anchoring protein
 PS   Claim 6; Page 59-64; 99pp; English.
 CC   The flocculation protein is used in a method to immobilise enzymes
 CC   to a microbial cell wall.  The coding sequence (FLO 1) is used in
 CC   the production of a recombinant polynucleotide which comprises a
 CC   structural gene encoding a protein with catalytic activity and at
 CC   least part of a gene encoding at least the C-terminus of a protein
 CC   capable of anchoring in a eukaryotic or prokaryotic cell wall.   The
 CC   anchoring fragment or protein is selected from alpha agglutinin,
 CC   AGA 1, FLO 1, major cell wall protein of lower eukaryotes or a
 CC   proteinase of lactic acid bacteria.  The recombinant polynucleotide
 CC   preferably also comprises a sequence encoding a signal peptide to
 CC   ensure secretion of the expressed product.  The signal peptide is
 CC   preferably derived from glycosyl-phosphatidyl-inositol, anchoring
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 CC   protein, alpha factor, alpha-agglutinin, invertase or inulinase,
 CC   alpha-amylase of Bacillus or proteinases of lactic acid bacteria.
 CC   The host microorganism can be used for performing enzymatic
 CC   processes on an industrial scale.
 SQ   Sequence   2685 BP;    751 A;    699 C;    492 G;    743 T;

Initial Score     =     117  Optimized Score    =     249  Significance =  6.39
Residue Identity  =     28%  Matches            =     242  Mismatches   =   203
Gaps              =      69  Conservative Substitutions           =     0

            X           10             20            30         40
            CARGAYT----GYWSNT--TYCA---RCAYWSNCCNAT----NWSNWSNGAYTTYGCNGTNA
            |||  ||    |||| |  | ||   || |||  |  |     || || |    ||| |
  GACGACTCTGCAATTCTATCAGTAGGTGGTGCAACCGCGTTCAACTGTTGTGCTCAACAGCAACCGCCGATC
  480       490       500       510       520       530       540

 50        60        70        80        90       100       110
  ARATNMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGA-YGA-
  | || |  ||||| |   |||  |  |  |||| | ||   ||    |  |  ||  ||||  || | |||
  ACATCAACGAACTTTACCATTGACGGTATCAAG-CCATGGGGT---GGAAGTTTGCCACCT--AATATCGAA
 550      560       570       580        590          600         610

 120      130       140       150       160       170       180
  RGARYTNTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGC---
  ||||| | |    |  |  |  | ||  | ||  | ||| |  || ||   |  |  ||  | ||  |
  GGAACCGTCTATATG--TACGCTGGCTACTATTATC-CAATGAAGGTTGTTTA-CTCGAACGCTGTTTCTTG
    620       630         640        650       660        670       680

 190           200       210       220       230       240       250
  NGGNWS----NAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNT
   || ||      || |   | | |  ||  |||  || | ||| | ||   ||  | |  | ||| || | |
  GGGTACACTTCCAATTAGTGTGACACTTCCAGATGGT-ACCACTGTAAGTGATGACTT--CGAAGGTACGT
      690       700       710       720         730       740        750

   260       270        280       290       300        310        320
  TYCARCCNCCNCCNWSNTG-YYTNMGNTTYGTNCARACNAAYATNWSNM-GNYTNYTNCARGAR-AC-NWSN
   |   ||     |  | || ||| ||  ||   | |||     | || | | |  ||  ||  |  |  ||
  CTATTCCTTTGAC--GATGACCTAAG--TCAATCTAACTGTACTGTCCCTGACCCTTCAAATTATGCTGTCA
       760         770         780       790       800       810       820

     330         340       350              360        370       380
  GARCARYT--NGTNGCNYTNAARCCNTGGA-------TNACNMGNC-ARAAYTTYWSNMGNTGYYTNGARYT
  | || |||       |     |||| ||||       |  | |  | | | || ||| |    ||     |
  GTACCACTACAACTACAACGGAACCATGGACCGGTACTTTCACTTCTACATCTACTGAAATGACCACCGTCA
         830       840       850       860       870       880       890

  390              400       410       420         430       440
  NCARTGYCARC------CNGAYWSNWSNACNYTNCCNCCNCCNT--GGWSNCCNMGNCCNYTNGARG-CNA-
   | || |||||      |  |||| || |  |   |     | |  | || || |  ||  |  ||| | |
  CCGGTACCAACGGCGTTCCAACTG-ACGAAACCGTCATTGTCATCAGAACTCCAA--CCAGTGAAGGTCTAA
      900       910        920       930       940         950       960

 450         460    X
  -CNGCNC--CNACNGCNCCN
   | || |  | || |  ||
  TCAGCACCACCACTGAACCATGGACTGGCA
       970       980       990


3. US-08-162-407-6 (1-465)
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 Q45455       Sequence encoding murine bone-related sulphatase 1

ID    Q45455 standard; cDNA to mRNA; 2373 BP.
AC    Q45455;
DT    12-OCT-1994  (first entry)
DE    Sequence encoding murine bone-related sulphatase like  precursor
DE    protein OSF-8.
KW    OSF-8; bone-related sulphatase-like protein; osteoporosis;
KW    Paget's disease; osteomalacia; therapy; diagnosis; ss.
OS    Mus musculus osteoblastic cell line MC3T3-E1.
FH    Key                Location/Qualifiers
FT    CDS                150..1820
FT    /*tag=  a
PN    AU9344921-A.
PD    03-MAR-1994.
PF    27-AUG-1993; 044921.
PR    28-AUG-1992; JP-230030.
PR    03-DEC-1992; JP-324034.
PA    (FARH ) HOECHST JAPAN LTD.
PA    (FARH ) HOECHST JAPAN KK.
PI    Amann E,  Ito T,  Otawara-hamamoto Y,  Takeshita S;
DR    WPI; 94-109856/14.
DR    P-PSDB; R51355.
PT    Bone-related sulphatase-like protein, OSF-8 - degrades sulphate
PT    groups of proteoglycan sugar chains, useful for treating bone
PT    metabolic diseases
PS    Claim 3; Page 17-22; 29pp; English.
CC    cDNA of mouse OSF-8 (mOSF-8) was isolated from mouse osteoblastic
CC    cell line MC3T3-E1 cDNA library by a combination of PCR and the
CC    subtraction method, and by the differential screening method. OSF-8
CC    has homology with known representative sulphatase molecules but
CC    belongs to a new subclass different from those so far reported.
CC    The inventors claim the precursor protein (R51355 AAs 1-556) which
CC    includes the signal peptide(AAs 1-18),and they also claim a protein
CC    comprised of residues 19-556. They also claim DNA or RNA encoding
CC    the claimed proteins.
SQ    Sequence   2373 BP;    697 A;    547 C;    466 G;    663 T;

Initial Score    =    114  Optimized Score  =    246  Significance =  6.20
Residue Identity =    29%  Matches          =    236  Mismatches   =   202
Gaps             =     53  Conservative Substitutions            =     0

           X       10        20          30        40          50
           CARGAYTGYWSNTTYCARCAYWS--NCCNATNWSNWSNGAYTTYGC--NGTNAARATNM-GN
            ||||||  || ||||||| |||      |  |  |   ||||| |    | ||  | | |
 TCCTTCGATGGAAGACT-AACATTTCAAC-CAGGAAGTCAGGTAGTAAAACTTCCCTTCATTAACTTCATGA
280       290        300        310       320       330       340

  60         70         80        90       100       110       120
 GARY-TNWSNGAYTA-YYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNT
 ||||   ||  || | ||| ||  | | |||| |  | |      | ||   | | ||  ||| | |||  |
 GAGCACATGGCACCACCTTCCTAAATGCCTACAC--TAATTCACCCATCTGCTGTCCATCACGTGCAGCAAT
350       360       370       380         390       400       410

 130         140       150       160       170        180       190
 GYG--GNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGAR-MGNYTNAARACNGTNGCNGGNWSNA
 |||  | || || |  |  ||    || |  ||||  |   ||||| |  || |||   ||  | || || |
 GTGGAGTGGCCTCTTCA--CT--CACTTG-ACAGA-ATCT-TGGAATAATTTTAAG--GGT--CTGGATCCA
420       430           440         450        460         470
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   200       210       220       230        240       250       260
  ARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAY-TTYGTNACNAARTGYGCNTTYCARCCNCCN
  || |  |    |  |  | | | |  | ||  ||||  |||   | | |   |  |    ||  ||
  AATTATA----CGACATGGATG-GACATCATGGAGAAGCATGGCTATCAGACACAGAAATTTGGAAAAGTGG
480           490        500       510       520       530       540

  270       280         290          300       310       320       330
  CCNWSNTGYYTNMG--NTTYGTNCAR--ACNAA-YATNWSNMGNYTNYTNCARGARACNWSNGARCARYTNG
   | |  | ||| ||    || | | |  |  || | | || |  |     |||||||  ||   || |||
  ACTA--TACTTCAGGACATCATTCCATTAGTAACCGTGTGGAAGCATGGACAAGAGA--TG-TTGC-ATTCT
   550         560       570       580       590       600           610

     340       350       360         370          380       390
  TNGCNYTNAARCCNTGGATNACNMGNCA--RAAYTTYWSNM-GNT--GYYTNGARYTNCARTGYCARCC--N
  | || |  | |    ||   || |   |  || ||| || | | |  |  |||    ||||   |||
  T-GCTCCGACAAGAAGGCAGACCCATAATTAATCTTATCCCTGATAAGAATAGAAGGAGAGTGATGACCAAG
        620       630       640       650       660       670       680

400        410       420         430       440       450       460    X
  GAYW-SNWSNACNYTNCCNCCNCCNTGG--WSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCN
  |||| | || |  |   |    |  | |  || |  || |   |  |    ||    ||    |  |
  GACTGGCAGAATACAGACAAAGCAATCGAATGGCTAAGACAGGTTAACTACACCAAGCCATTTGTCCTTTAC
      690       700       710       720       730       740       750 X

  TTGGGAT
    760


4. US-08-162-407-6 (1-465)
   Q25812       Clone 45-A.

 ID    Q25812 standard; cDNA; 4300 BP.
 AC    Q25812;
 DT    04-JAN-1993  (first entry)
 DE    Clone 45-A.
 KW    GLU-G-R; Xenopus oocyte; cerebellum sublibrary; voltage clamp assay;
 KW    neurotransmitter; glutamate; neuronal excitation; ss.
 OS    Synthetic.
 FH    Key                Location/Qualifiers
 FT    CDS                377..3676
 FT    /*tag=  a
 FT    /label= Subtype_1a
 PN    WO9210583-A.
 PD    25-JUN-1992.
 PF    12-DEC-1991; U09422.
 PR    12-DEC-1990; US-626806.
 PR    30-JAN-1991; US-648481.
 PR    18-MAR-1991; US-672007.
 PA    (UNIW ) UNIV WASHINGTON.
 PA    (ZYMO ) ZYMOGENETICS INC.
 PI    Almers W, Hagen FS, Houamed KM, Mulvihill ER;
 DR    WPI; 92-234638/28.
 DR    P-PSDB; R25080.
 PT    Mammalian G protein-coupled glutamate receptors - activate
 PT    phospholipase C or stimulate inositol phospholipid metabolism,
 PT    for use in diagnosis and identification of receptor agonists and
 PT    antagonists
 PS    Disclosure; Fig 5; 144pp; English.
 CC    The sequence given encodes mammalian G protien-coupled glutamate
 CC    receptor (GLU-G-R) subtype 1a.  The clone was isolated from Xenopus
 CC   oocyte cultures which had been injected with RNA extracted from a
 CC   cerebellum sublibrary.  Expression of GLU-G-R activity was assessed by
 CC   voltage clamp assay.  Plasmid DNA encoding GLU-G-R activity was
 CC   isolated by replica-plating experiments.  The protein encoded by clone
 CC   45-A was found to act as a receptor for the neurotransmitter glutamate,
 CC   and may play a critical role in the control of neurons.  GLU-G-R and
 CC   antibodies may be used to identify agonists and antagonists of
 CC   GLU-G-R-mediated neuronal excitation and in diagnosis.
 SQ   Sequence   4300 BP;    1038 A;    1191 C;    1148 G;    923 T;

Initial Score    =     110  Optimized Score  =     252  Significance =  5.94
Residue Identity =     29%  Matches          =     241  Mismatches   =   196
Gaps             =      56  Conservative Substitutions            =     0

              X       10        20          30        40        50
              CARGAYTGYWSNTTYCARCAY--WSNCCNATNWSNWSNGAYTTYGCNGTNAA--RATNMGNG
              ||| ||||| | | || || |  || ||    || ||  ||||| | |  ||  ||  |  |
    TCGGTGATGGCAA-ACTGC-CGTGCC-GCTCCAACACCTTCCTCAAC--ATTTTCCGGAGAAAGAAGCCCGG
      2960    X  2970        2980      2990        3000      3010      3020

    60        70        80         90       100          110       120
    ARYTNWSNGAYTAYYTNYTNCAR-GAYTAYCCNGTNACNGTNGCNWSNAAYY---TNCARGAYGARGARYTN
     ||  || || | ||  ||  || | | |  | ||  |  | |  || ||||   |  ||||| ||| ||
    GGC--AGGGAATGCCAATTCTAACGGCAAGTCTGTGTC-ATGGTCTG-AACCAGGTGGAAGAC-AGGCGCCC
           3030      3040      3050       3060       3070      3080

     130          140       150       160       170       180       190
    TGYGGNGGNY---TNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSN
       ||    |   | ||||  |   | |  |  | ||| || |  || |  |   |||| |   | |  ||
    AAGGGACAGCACGTGTGGCAGCGCCTCTCTGTGC-ACG-TGAA--GACCAAC--GAGACGG--CCTGTAACC
  3090      3100      3110      3120          3130        3140        3150

      200       210       220       230         240        250         260
    AARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNC--AYTTYGTNACNA-ARTGYG--CNTTYCA--
    |||  || |    |  |  |||   | | ||   || | |  |   | |  | | ||  ||  | |||||
    AAACAGCCG----TAATCAAACCCCTCACTA-AAAGTTACCAAGGCTCTGGCAACAGCCTGACCTTTTCAGA
        3160          3170       3180      3190      3200      3210

            270       280       290       300       310       320       330
    -RCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAYATNWSNMGNYTNYTNCARGARACNWSNGARCARY
     |||  | || ||   ||| |    |||   ||  || |  || |  |  || | |   || || |  |  |
    TGCCAGCACCAAGACCCTTTA-CAATGT--GGAAGAAGAGGACAATACCCCTTCTGCTCACTTCAGCCCTCC
 3220      3230      3240         3250      3260      3270      3280

          340       350       360       370       380         390
    TNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGA-RY-TNCARTGYCA----RC
      |  || ||   |   |||   || || | |     ||| ||  |||.. | ||   |  |||||    |
    CAGCAGCCCTTCTATGGTGGTGCAC-CGAC-GCGGGCCACCCGTGGCCACCACACCACCTCTGCCACCCCAT
  3290      3300      3310        3320      3330      3340      3350

    400       410         420        430       440       450       460    X
    CNGAYWSNWSNACNYTNCCNCC--NCCNTGG-WSNCCNMGNCCNYTNGARGCNACNGCNCCNACNGCNCCN
    | ||| | || |     || ||    | ||| ||    || |  |   |||     ||  |  |  | ||
    CTGACCGCAGAAGAGACCCCCCTGTTCCTGGCTGATTCCGTCATCCCCAAGGGCTTGCCTCCTCCTCTCCCG
  3360      3370      3380      3390      3400      3410      3420      3430

    CAGCAGCAG
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5. US-08-162-407-6 (1-465)
   Q15174         Plasmid pAMVBT4.

 ID   Q15174 standard; DNA; 4583 BP.
 AC   Q15174;
 DT   11-MAR-1992  (first entry)
 DE   Plasmid pAMVBT4.
 KW   Bacillus thuringiensis; transgenic; tree; poplar; ss.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   CDS             482..2427
 FT   /*tag=  a
 FT   misc_feature    480..897
 FT   /*tag=  b
 FT   /note= "altered synthetic sequence "
 PN   WO9118094-A.
 PD   28-NOV-1991.
 PF   23-MAY-1991; U03629.
 PR   24-MAY-1990; US-530133.
 PA   (AGRA-) AGRACETUS INC.
 PA   (WISC ) WISCONSIN ALU RES FOUND.
 PI   McCabe DE, McCown BH.
 DR   WPI; 91-369248/50.
 DR   P-PSDB; R15356.
 PT   Particle-mediated transformation of woody plants - for
 PT   construction of trangenics(s) expressing high levels of Bacillus
 PT   toxin
 PS   Example; Fig 6,7; 43pp; English.
 CC   The sequence is that of plasmid pAMVBT4 which encodes a wild type
 CC   Bacillus thuringiensis (Bt) gene from Bt strain HD-1-Dipel. This
 CC   codes for an insect toxin amino-terminal of the delta endotoxin
 CC   crystal protein, the synthetic sequence was used as substitution of
 CC   the first 138 codons has previously been found to enhance expression
 CC   of the protein in plant cells. It can be used in a method of particle
 CC   mediated transformation which is effective with various tissue types
 CC   of poplar, incl. protoplasts, internode and petiole segments and, more
 CC   efficiently with nodule cultures. Transgenic trees produced express
 CC   sufficient levels of toxin to provide toxicity to feeding insects.
 SQ   Sequence   4583 BP;    1279 A;    1061 C;    1003 G;    1240 T;

Initial Score    =     109  Optimized Score  =     236  Significance =  5.87
Residue Identity =     26%  Matches          =     225  Mismatches   =   219
Gaps             =      56  Conservative Substitutions            =     0

              X        10        20        30        40        50
              CARGAYTG-YWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAAR--ATNMGNG-
               |   ||| |||   | ||  ||| ||    || |   || ||   || | |  |  |  |
    TCGGTCCTCCGATCGTTGTCAGAAGTAAG--TTGGCCGCAGTGTTATCAC-TCATGGTTATGGCAGCACTGC
      3940    X 3950      3960        3970      3980       3990      4000

      60        70             80          90       100        110
    --ARYTNWSNGAYTAYY-TNY--TNC--ARGA--YTAYCCNGTNACNGTNGCNWSNAAYY-TNCARGAY---
      |||| ||  ||| || | |  | |  ||||  || | | || ||  | |  || | ||   |||| |
    ATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGAC--TGGTGAGTACTCAACCAAGTCATT
       4010      4020      4030      4040        4050      4060      4070

        120        130        140       150       160       170       180
    ----GARGARY-TNTGYGGNGGNY-TNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACN
        ||| ||| | ||||| |  |   | ||  || |  |     ||||   ||||   ||  |   | |
    CTGAGAATAGTGTATGCGGCGACCGAGTTGC-TCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACA--
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     4080      4090      4100       4110      4120      4130      4140

      190         200       210       220       230       240       250
  GTNGCNG-GNWSNAARA-TGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAART--G
   | || |   |  |||| |||     |  || ||||  ||   | | | |    |  ||   |  |  |
  -TAGCAGAACTTTAAAAGTGC--TCATCATTGGAAAACGT-TCTTCGGGGCGAAAACTCTCAAGGATCTTAC
       4150      4160        4170       4180      4190      4200      4210

        260       270       280       290        300       310       320
  YGCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAY-ATNWSNMGNYTNYTNCARGARACNW
  |||  || ||   ||     | |||   |   |||| ||  | | | || |  || |  ||   |    |
  CGCTGTTGAG-ATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAG-CATCTTTTACTTTCAC
        4220       4230      4240      4250      4260       4270      4280

       330       340       350       360           370       380       390
  SNGARCARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTY----WSNMGNTGYYTNGARYTNCAR
  | | |   || |  |  |  ||||   |||     || ||||||  |    |  ||    |  | ||  ||
  CAGCGTTTCTGGGTGAGCAAAAAC--AGGA-----AGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACAC
        4290      4300             4310      4320      4330      4340

          400       410       420       430         440       450
  TGYCA-RCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNY--TNGARGCNACNGCNCCNACN
   |  | |    ||||    || || ||     |    |     |  |  |  |   ||  |  |   |
  GGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGA
   4350      4360      4370      4380      4390      4400      4410

460    X
  GCNCCN
  ||
  GCGGATACATATTTGA
 4420  X   4430
```

6. US-08-162-407-6 (1-465)
N90183 DNA sequence of plant vector pAMVBTS

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ID   N90183 standard; DNA; 4583 BP.
AC   N90183;
DT   1-NOV-1989  (first entry)
DE   DNA sequence of plant vector pAMVBTS
KW   Chimeric gene; transgenic plants; Bacillus thuringiensis;
KW   delta-endotoxin; promoter; translational enhancer; polyadenylation
KW   sequence; tobacco plant; cotton plant; Lepidoptera; Diptera; Coleoptera.
KW   vector; pAMVBTS.
PN   WO8904868-A.
PD   01-JUN-1989.
PF   17-NOV-1988; U04107.
PR   19-NOV-1987; US-123054.
PA   (AGRA) Agracetus.
PI   Barton KA, Umbeck PF;
DR   WPI; 89-178387/24.
PT   Chimeric gene construct for producing transgenic plants - contains
PT   delta-endotoxin of Bacillus thuringiensis for toxicity to, eg
PT   lepidoptera sp.
PS   Disclosure; fig. 4a-b; 55pp; English.
CC   The sequence is of vector pAMVBTS (ATCC 53637), comprising ampicillin
CC   resistance plasmid replicon derived from pMT21, and a chimeric gene which
CC   consists of, in order from the 5' end, a DNA fragment corresp. to
CC   cauliflower mosaic virus 35S transcription promoter, DNA leader fragment
CC   corresp. to alfalfa mosaic virus coat protein mRNA 5' noncoding region, a
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CC   DNA fragment corresp. to N-terminal of B. thuringiensis delta-endotoxin,
CC   and a DNA fragment corresp. to polyadenylation region of nopaline
CC   synthase. The vector is used to transform plants, esp. tobacco and
CC   cotton, which then produce the toxin which is active against
CC   Lepidopteran, Dipteran and Coleopteran pests. This trait is then
CC   transmitted by Mendelian inheritance.
SQ   Sequence   4583 BP;   1316 A;   991 C;   977 G;   1299 T;

Initial Score     =    109  Optimized Score  =    236  Significance =  5.87
Residue Identity  =    26%  Matches          =    225  Mismatches   =   219
Gaps              =     56  Conservative Substitutions              =     0

            X        10        20        30        40        50
            CARGAYTG-YWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAAR--ATNMGNG-
             |   ||| |||   | ||  ||| ||    || |   || ||   || | |  |  |  |
  TCGGTCCTCCGATCGTTGTCAGAAGTAAG--TTGGCCGCAGTGTTATCAC-TCATGGTTATGGCAGCACTGC
    3940    X 3950      3960        3970      3980       3990      4000

    60        70             80           90        100        110
  --ARYTNWSNGAYTAYY-TNY--TNC--ARGA--YTAYCCNGTNACNGTNGCNWSNAAYY-TNCARGAY---
    |||| ||  ||| || | |  | |  ||||  || | | || ||  | |  || | ||   |||| |
  ATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGAC--TGGTGAGTACTCAACCAAGTCATT
     4010      4020      4030      4040        4050      4060      4070

      120        130        140       150       160       170       180
  ----GARGARY-TNTGYGGNGGNY-TNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACN
      ||| ||| | ||||| |  |   | ||  || |  |     ||||   ||||   ||  |   | |
  CTGAGAATAGTGTATGCGGCGACCGAGTTGC-TCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACA--
     4080      4090      4100       4110      4120      4130      4140

      190         200       210       220       230       240       250
  GTNGCNG-GNWSNAARA-TGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAART--G
   | || |   |  |||| |||     |  || ||||  ||   | | | |    |  ||   |  |  |
  -TAGCAGAACTTTAAAAGTGC--TCATCATTGGAAAACGT-TCTTCGGGGCGAAAACTCTCAAGGATCTTAC
       4150      4160        4170       4180      4190      4200      4210

        260       270       280       290        300       310       320
  YGCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARACNAAY-ATNWSNMGNYTNYTNCARGARACNW
  |||  || ||   ||     | |||   |   |||| ||  | | | || |  || |  ||   |    |
  CGCTGTTGAG-ATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAG-CATCTTTTACTTTCAC
        4220       4230      4240      4250      4260       4270      4280

       330       340       350       360           370       380       390
  SNGARCARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTY----WSNMGNTGYYTNGARYTNCAR
  | | |   || |  |  |  ||||   |||     || ||||||  |    |  ||    |  | ||  ||
  CAGCGTTTCTGGGTGAGCAAAAAC--AGGA-----AGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACAC
        4290      4300             4310      4320      4330      4340

          400       410       420       430         440       450
  TGYCA-RCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNY--TNGARGCNACNGCNCCNACN
   |  | |    ||||    || || ||     |    |     |  |  |  |   ||  |  |   |
  GGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGA
   4350      4360      4370      4380      4390      4400      4410

460    X
  GCNCCN
  ||
  GCGGATACATATTTGA
 4420  X   4430
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7. US-08-162-407-6 (1-465)
   Q63241       Crucifer 1-aminocyclopropane-1-carboxylate (ACC) s

ID   Q63241 standard; DNA; 5613 BP.
AC   Q63241;
DT   14-DEC-1994  (first entry)
DE   Crucifer 1-aminocyclopropane-1-carboxylate (ACC) synthase.
KW   Crucifer 1-aminocyclopropane-1-carboxylate (ACC) synthase;
KW   Arabidopsis thaliana; transgenic plant; ethylene; ripening;
KW   maturation; senescence; inhibition; ss.
OS   Arabidopsis thaliana.
FH   Key             Location/Qualifiers
FT   GC_signal       340..345
FT   /*tag=  a
FT   CAAT_signal     709..715
FT   /*tag=  b
FT   /note= "Putative CAAT signal."
FT   CAAT_signal     723..729
FT   /*tag=  c
FT   /note= "Putative CAAT signal."
FT   CAAT_signal     993..996
FT   /*tag=  d
FT   /note= "Putative CAAT signal."
FT   CAAT_signal     1151..1154
FT   /*tag=  e
FT   /note= "Putative CAAT signal."
FT   TATA_signal     1310..1315
FT   /*tag=  f
FT   /note= "Putative TATA signal."
FT   exon            1432..1603
FT   /*tag=  g
FT   /label= Exon 1.
FT   intron          1604..1777
FT   /*tag=  h
FT   /label= Intron 1.
FT   exon            1778..1909
FT   /*tag=  i
FT   /label= Exon 2.
FT   intron          1910..2161
FT   /*tag=  j
FT   /label= Intron 2.
FT   exon            2162..2322
FT   /*tag=  k
FT   /label= Exon 3.
FT   intron          2323..2595
FT   /*tag=  l
FT   /label= Intron 3.
FT   exon            2596..3621
FT   /*tag=  m
FT   /label= Exon 4
FT   polyA_signal    3926..2931
FT   /*tag=  n
FT   /note= "Putative polyadenylation signal."
PN   WO9408449-A.
PD   28-APR-1994.
PF   13-OCT-1993; U09816.
PR   15-OCT-1992; US-962481.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYGE-) RIJKSUNIV GENT.
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PI   Goodman H,  Van DER STRAETEN D,  Van MONTAGUE M;
DR   WPI; 94-150818/18.
DR   P-PSDB; R53114.
PT   DNA encoding crucifer ACC synthase - used for prodn. of
PT   recombinant polypeptide(s) or regulating ethylene-inducible
PT   events in a plant.
PS   Claim 1; Figure 1A; 54pp; English.
CC   The crucifer 1-aminocyclopropane-1-carboxylate (ACC) synthase coding
CC   sequence can be used to produce transgenic plants in which ethylene
CC   inducible events such as fruit ripening, fruit maturation or
CC   senescence are inhibited.
SQ   Sequence   5613 BP;    1794 A;    959 C;    960 G;    1900 T;

Initial Score      =    108  Optimized Score  =    236  Significance =  5.81
Residue Identity =     28%  Matches          =    228  Mismatches   =   215
Gaps               =     64  Conservative Substitutions              =     0

              X       10        20        30        40         50        60
              CARGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNA-ARATNMGNGARY
              ||| || | |    |||| | |     |  || ||  ||   |  || | || | |   |||
    TGTATAAGATCAATATCGATACCCCCAAAAAAAAAAAAAAAC-AGCTACAAAGAAGTGAGAATTGACACAGC
 1360      1370      1380      1390      1400       1410      1420      1430

           70        80           90             100       110       120
    TNWSNGAYTAYYTNYTNCARGAYTA---YCCNGT------NACNGTNGCNWSNAAYYTNCARGAYGARGARY
      |  | |  ||      || || |   | | ||       |   | || || |||   ||| ||| ||||
    AAATGGGTCTTCCGGGAAAAAATAAAGGTGCAGTTTTGTCGAAGATAGCGACTAACAATCAACACGGAGAGA
          1440      1450      1460      1470      1480      1490      1500

       130       140         150        160       170       180       190
    TNTGYGGNGGNYTNTGGMGNYTNG--TNYTNGC-NCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNW
      | | | |  || ||  |  | |    ||  |  ||||| |   |   |   ||     | ||  |    |
    ACT-CAGAGTACTTTGATGGATGGAAAGCTTACGACAAAGATCCTTTTCATCTTT----CCCGTAACCCCCA
         1510      1520      1530      1540      1550          1560

          200        210       220        230        240         250
    --SNAARATGC-ARGGNYTNYTNGARMGNGTNA-AYACNGA-RATNCAYTTYGTNACNAA--RTGYGCNTTY
      | |  || | || |  | ||  ||||  | |  ||| ||  ||  ||  |   |  ||  ||||   | |
    TGGGATCATCCAAATGGGTCTTGCAGAGAATCAGGTACAGATTATATATAATCCAATAAATCATGT---TAT
 1570      1580      1590      1600      1610      1620      1630

   260       270       280          290         300       310       320
    CARCCNCCNCCNWSNTGYYTNMGNTT---YGTNCARACNA--AYATNWSNMGNYTNYTNCARGARACNWSNG
      |       | |  ||| | |  ||   | |   | | |  |||| || |  |   | ||   | | ||
    ATGTTGTTGTCGTTGTGCATGAACTTCCATCTATTAGCTATTATATATGAACACGTATACA--CATCAAGCT
  1640      1650      1660      1670      1680      1690        1700

      330       340       350       360          370       380        390
    ARCARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARA-AYTT--YWSNMGNTGYYT-NGARYTNCARTGY
    || | ||  |    ||    |  |  |   | ||  ||| ||||  ||  |  | |||   |||| |  |
    AATACCTTTT----TTTCTTCTTTTCAAGTCAAGTTAAATACTTAATAACACATTTTTCTAAACTTC--TTA
  1710          1720      1730      1740      1750      1760      1770

        400       410       420         430       440           450
    CARCCNGAYWSNWSNACNYTNCCNCCNCCNT--GGWSNCCNMGNCCNYTNGARGCNAC----NGCNCC---N
    ||||    ||| |  |  ||    |     |  ||||    ||  | |  |||||  |     || ||
    CAGC---TTTGCT-TAGATTTGATCAAAGATTGGGTCAAAGAGAAC-CCAGAAGCTTCTATTTGCACCCTTG
         1780       1790      1800      1810       1820      1830      1840

     460        X
    ACNG----CNCCN
    |  |    |  |
    AAGGTATTCATCAGTTTAGCGAC
         1850   X  1860

8. US-08-162-407-6 (1-465)
   N30044        Sequence encoding bovine leukocyte interferon (IFN

 ID  N30044 standard; DNA; 1162 BP.
 AC  N30044;
 DT  25-MAY-1992  (first entry)
 DE  Sequence encoding bovine leukocyte interferon (IFN) -beta-2.
 KW  Antiviral; cancer; therapy; immunosuppression; tumour; ss.
 OS  Bos taurus.
 FH  Key               Location/Qualifiers
 FT  sig_peptide       320..382
 FT  /*tag=  a
 FT  mat_peptide       383..880
 FT  /*tag=  b
 PN  EP--88622-A.
 PD  14-SEP-1983.
 PF  08-MAR-1983; 038114.
 PR  08-MAR-1982; US-355298.
 PR  01-NOV-1982; US-438128.
 PA  (GETH ) GENENTECH INC.
 PI  Capon DJ, Goeddel DV;
 DR  WPI; 83-766437/38.
 DR  P-PSDB; P30078.
 PT  Polypeptide(s) with amino acid sequence of an animal interferon -
 PT  useful as antiviral, anticancer and immuno-modulator agents
 PS  Disclosure; Fig 9b; 62pp; English.
 CC  A bovine genomic DNA library was screened for IFN genes.  Four
 CC  bovine leukocyte IFN genes were identified (see N30039, N30040,
 CC  N30041, N30042).  Whereas the BoIFN-alpha-2 and -3 genes encode
 CC  peptides with only minor apparent differences to BoIFN-alpha-1, the
 CC  BoIFN-alpha-4 protein is as distinct from the other bovine peptides
 CC  as are any two bovine and human leukocyte interferons.  Three
 CC  distinct bovine fibroblast IFN genes were also identified (see
 CC  N30043, N30044, N30045).  The bovine proteins are quite distinct
 CC  from one another but show an even greater difference with the human
 CC  peptide.
 SQ  Sequence   1162 BP;    371 A;    257 C;    234 G;    300 T;

Initial Score    =    100  Optimized Score  =    251  Significance =  5.29
Residue Identity =    31%  Matches          =    242  Mismatches   =   187
Gaps             =     64  Conservative Substitutions             =     0

          10  X     20        30        40        50        60
    RGAYTGYWSNTTYCARCAYWSNCCNATNWSNWSNGAYTTYGCNGTNAARATNMGNGARYTNW--SNGAY---
              ||| ||||||   | ||    ||  | ||| |    || || ||  ||||  |  | |||
              TTTTAGCATTTAGCAATTCACTGAAAATTTAC-AAAAACATTAG-AAATTCTCCCAGACTGT
              X       10        20        30         40         50        60

    70             80         90       100       110       120        130
    -TAYYTNYTNC-----ARGAY-TAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYTNT-GYGGNG
     ||||| || |     || || |||    | |     || || | ||   ||||  ||||||| | | ||
    ATATCTTTTTCCCCTTAATACATATAAAATCA-AAAAGCAAGGAGCTAAAAAGAAAAAGAGTTTTAGAGGTA
            70        80        90        100       110       120       130
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        140       150       160          170       180       190        200
    GNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGA---TGGARMGNYTNAARACNGTNGCNGGNWSNAA-RATG
      |  |  |  |  |     |  | ||   |||   |||||||    |||    |  |    || || ||||
    ACTAATCAACACAGG----AGAACTAAAAAGGAAACTGGAAAGTGGGAAATTCCTCTCCAATAGAAAGAATG
          140           150       160       170       180       190

           210       220       230       240       250       260       270
    CARGGNY-TNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNACNAARTGYGCNTTYCARCCNCCNCCNWS
     |||| | | || | |   || | | |  | |  ||    |  |    || | |  | ||| |    || ||
    GAGGGCCATGCT-GTATAAGT-AGCCC--ACACTCAAGAAGGAAGGCCATTCACTCTGCAAAC----CCTTG
  200       210         220         230       240       250           260

         280        290       300           310       320        330
    NTGYYTNMGNTTY-GTNCARACNAAYATNW---SNMGNY-TNYTNCARGARACNWS-NGARCARYTNGTNGC
      | || || ||| |  |  || | ||  |   | || | | |  | |    | ||  || | ||  ||  |
    AAGACTCAGCTTCAGCACCTACTAGCAGAACAGGCAGCCCTGTGCCTGATTTCATCATGACCCACCGGTGCC
        270       280       290       300       310       320       330

    340       350       360       370            380          390       400
    -NYTNAARCCNTGGATNACNMGNCARAAYTTYWS-----NMGNTGYYT---NGARYTNCARTGYCARCCNGA
      ||  ||   ||| |  | |  | |  ||||||      ||  | |||    |||||  ||| |    | ||
    TCCTCCAG--ATGGTTCTC-CTGCTGTGTTTCTCCACCACAGCTCTTTCCAGGAGCTACAGCTTGCTTC-GA
      340         350        360       370       380       390       400

          410       420           430       440          450       460    X
    YWSNWSNACNYTNCCNCCNCCNTG-GW---SNCCNMGNCCNYTNGARGC---NACNGCNCCNACNGCNCCN
    |||  | ||     |    || || ||   | |  |  |  || |||||    ||  |  | ||  | |
    TTC--CAACAAAGGCGGAGCCTTGAGTTATGTCAGAAACTCCT-GAGGCAGTTAC--CTTCAACTCCTCAAC
          410       420       430       440        450         460       470

    ATTGCCTCG


9. US-08-162-407-6 (1-465)
   Q14235        A.faecalis penicillin acylase coding sequence.

 ID  Q14235 standard; DNA; 2451 BP.
 AC  Q14235;
 DT  10-JAN-1992  (first entry)
 DE  A.faecalis penicillin acylase coding sequence.
 KW  antibiotic; pac gene; beta-lactam acylase; EC.3.4.1.11;
 KW  ss.
 OS  Alcaligenes faecalis ATCC 19018.
 FH  Key               Location/Qualifiers
 FT  sig_peptide       1..78
 FT  /*tag=  a
 FT  /evidence= experimental
 FT  mat_peptide       79..708
 FT  /*tag=  b
 FT  /label= alpha-subunit
 FT  mat_peptide       709..2448
 FT  /*tag=  c
 FT  /label= beta-subunit
 PN  EP-453047-A.
 PD  23-OCT-1991.
 PF  18-APR-1991; 200929.
 PR  18-APR-1990; EP-200962.
 PR  20-DEC-1990; EP-203483.
 PR  18-APR-1991; EP-200929.
 PA   (KONN ) GIST-BROCADES NV.
 PI   Quax WJ;
 DR   WPI; 91-312307/43.
 DR   P-PSDB; R14444.
 PT   Penicillin G acylase gene - isolated from Alcaligenes faecalis,
 PT   used to produce recombinant enzyme for prodn. of penicillin(s)
 PT   and cephalosporin(s)
 PS   Claim 1; Page 8; 23pp; English.
 CC   An A.faecalis ATCC 19018 genomic DNA library was constructed from
 CC   4-7kb fragments of a partial Sau3A digest. A probe was designed from
 CC   the N-terminal sequence of the beta-subunit which had been isolated
 CC   from A.faecalis cells. Two positive clones were isolated. Acylase
 CC   activity was assigned to a subclone of one of the positive clones.
 CC   The subclone was sequenced and the ORF is given here.
 SQ   Sequence   2451 BP;    534 A;    680 C;    739 G;    498 T;

Initial Score    =    100  Optimized Score  =    246  Significance =  5.29
Residue Identity =    30%  Matches          =    246  Mismatches   =   188
Gaps             =     71  Conservative Substitutions           =     0

              X              10         20        30        40        50
              CARGA-YTGY------WSNTT-YCARCAYWSNCCNATNWSNWSNGAYTTYG--CNGTNAARA
              ||| | ||||      ||  |  ||||| || |     || || ||| |||  |      ||
    AAAGCTGGCGCAACAGCTGCCGGCCGACGATAGCAGCA-AGGCGGCGCTG-AC-GATGTTGCTCGCCTGGGA
          1710      1720      1730       1740       1750       1760

            60        70        80        90       100       110
    T--NMGNGARYTNWSNGAYTAYYTNYTNCARGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAY-----
    |   |  ||||  || ||| |       ||| ||   || |  || |  ||  |   ||| ||||||
    TGGAATGGAAC--AG-GATCAGGGAGGGCAAAAT--GCCGG--ACCGGCGCGGGTGCTCTTCAAGACCTGGC
 1770      1780         1790      1800          1810      1820      1830

      120         130       140       150       160       170        180
    --GARGARYTNTGY--GGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNY-TNAARACNG
      |||||| | | |  |  || || || |  |  ||  | || | ||   | || | ||  | |  || | |
    TGGAAGAAATGTACAAGCAGGTCT-TG-ATGCCGGTGGT-GC-CTGAATCGCATCGCGCCATGTATAGCCAG
      1840      1850       1860       1870        1880      1890      1900

       190          200       210       220       230        240       250
    TNGCNGGNW---SNAARATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCA-YTTYGTNACNAARTGY
       | || |   | | |  |||||| |  |     ||  |  ||    || |  | | | |  || ||| ||
    --ACTGGTTTTGCCACGCAGCAAGG-TCCCAACCCCGGTTCCAT---CAACTTGAGCATGGGCACCAAG-GT
          1910      1920       1930      1940         1950      1960

         260       270       280       290          300       310
    GCNTTYCARCCNCCNCCNWSNTGYYTNMGNTTYGTNCARA--CNAA-YATNWSNM-GNYTNYTNCARGAR-A
     | ||   ||     || || ||||  |    | | | ||  | || | | || | | || |    || |
    -C-TTGTTGC--GTGCCTTGGTGCTGGAAGCCCATCCCGATCCCAAGCGTGTGAATGTCTTTGGTGAGCGTT
     1970        1980      1990      2000      2010      2020      2030

  320       330       340       350       360       370       380       390
    CNWSNGARCARYTNGTNGCNYTNAARCCNTGGATNACNMGNCARAAYTTYWSNMGNTGYYTNGARYTNCART
    | ||  || || |  | || |   |||  || |  |  || |||  |  ||  |   |||  ||||
    CGTCTCAGGAAATCAT-GCAC-ACAGCTTTGCAAAATGCG-CAGGCCCGCTTGA---GCCAGGAGCAGGGCG
     2040      2050        2060      2070       2080         2090      2100

          400       410        420           430          440        450
    GYCARCCNGAYWSNWSNACNYTNCC-NCCNCCNTG----GWSNCCNMGNC---CNYTNGA-RGCNACNGCNC
     ||||   |   | || ||  | ||  || || ||    ||  |  || |     ||  | ||  ||  | |
    CTCAGATGGCGCGCTGGACCATGCCGACCTCCGTGCATCGTTTCAGCGACAAGAACTTCACGGGAACCCCGC
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         2110      2120      2130      2140      2150      2160      2170

       460    X
    CNACNGCNCCN
      ||    ||
    AGACGATGCCTGGCAATACCT
       2180   X  2190


10. US-08-162-407-6 (1-465)
    Q03661        Maize C3 sequence encoding acetohydroxy acid synth

 ID   Q03661 standard; DNA; 2546 BP.
 AC   Q03661;
 DT   08-AUG-1990  (first entry)
 DE   Maize C3 sequence encoding acetohydroxy acid synthetase (AHAS) gene.
 KW   acetohyroxy acid synthetase; AHAS; sulphonylurea;
 KW   herbicide; ds.
 OS   Zea sp.
 FH   Key               Location/Qualifiers
 FT   CDS               256..2169
 FT   /*tag=  a
 PN   EP-360750-A.
 PD   28-MAR-1990.
 PF   13-SEP-1989; 810685.
 PR   22-SEP-1988; US-248000.
 PR   06-JAN-1989; US-294530.
 PR   08-JUN-1989; US-363663.
 PA   (CIBA) Ciba Geigy AG.
 PI   Montoya A, Jen G, Harms C, Carswell G, Armour S, Volrath S;
 DR   WPI; 90-093264/13.
 DR   P-PSDB; R05589.
 PT   Plant cell tolerating herbicidal aceto:hydroxy acid synthase inhibitor -
 PT   producing increased levels of enzyme, obtd. by selection
 PT   processes or genetic engineering.
 PS   Disclosure;  64pp; English.
 CC   Using DNA confering tolerance to the effects of AHAS inhibitors such as
 CC   sulphonurea herbicide allows for the control of weeds using these
 CC   compounds. The tolerance may also be used as a selectable marker in
 CC   somatic hybrids and transgenic plants.
 SQ   Sequence   2546 BP;    544 A;    717 C;    680 G;    605 T;

Initial Score    =    100  Optimized Score  =    203  Significance =  5.29
Residue Identity =    27%  Matches          =    195  Mismatches   =   179
Gaps             =     47  Conservative Substitutions           =     0

        60    X   70        80         90       100       110       120
    MGNGARYTNWSNGAYTAYYTNYTNCA-RGAYTAYCCNGTNACNGTNGCNWSNAAYYTNCARGAYGARGARYT
              | |   |||| || || | ||| |   ||    ||    || ||| | | ||  |||  |||
              CCGTAAATCTCTTCCACGCACTCTGTCGT----GT----ACCAACGTGC-AGTGGAAACGCT
              X       10        20            30            40         50

      130       140       150       160       170       180       190
    NTGYGGNGGNYTNTGGMGNYTNGTNYTNGCNCARMGNTGGATGGARMGNYTNAARACNGTNGCNGGNWSNAA
       ||     || || |  |  || |     | |    | |  | ||  ||   ||| ||  | |  ||  |
    -CACGTACCTTTGTGTA-TTATGTACGGATTCGG----GCAACGGACATTT--CGAC-GT--CGGTTTGCGA
          60         70        80            90         100          110

    200       210       220       230       240           250          260
    RATGCARGGNYTNYTNGARMGNGTNAAYACNGARATNCAYTTYGTNA----CNAART-GY--GCNTTYCARC
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  | | | |   |  |  ||||     | | | |||    | |  |  |    |   || ||   | |||| ||
  G-TCCCATTCCCATCTGAACCACACATCTCTGAACAAAAGTAGGGGAGGCGCCCGGTAGCCCCCTTTCCCAC
      120       130       140       150       160       170       180

        270       280        290       300       310         320
  -CNCCNCCNWSNTGYYTNMGNT-TYGTNCARACNAAYATNWSNMGNYTNYTNCARG--ARACNWSNG-ARCA
     ||  |  | ||||  || |  |   |   | ||    || || |  || | ||  || |  | | |||
  AATCCCACTCCGTGCC--AGGTGCCACCCTCCCCAAGCCCTCGCGCCGCCTCCGAGACAGCCGCCCGCAACC
    190       200         210       220       230       240       250

330       340       350        360          370        380       390
  RYTNGTNGCNYTNAARCCNTGGATNACNMG-NCA---RAAYTTYWSNMGNTGY-YTNGARYTNCARTGYC-A
  ||      | |    |||  ||    | ||  ||   |  |  ||  || | | |   |||    | ||| |
  ATGGCCACCGCCGCCACCGCGGCGGCCGCGCTCACCGGCGCCACTACCGCTACGCCCAAGTCGAGGCGCCGA
    260       270       280       290       300       310       320

    400       410       420       430       440       450        460    X
  RCCNGAYWSNWSNACNYTNCCNCCNCCNTGGWSNCCNMGNCCNYTNGARGCNACNGCNCCNAC-NGCNCCN
  |||   ||| ||  | |  ||  |  |    || || || || |  |  ||  | ||     |  || ||
  GCCCACCACTTGGCCAC--CCGGC-GCGCCCTCGCCGCGCCCATCAGGTGC-TCAGCGTTGTCACGCGCCAC
  330       340          350       360       370        380       390   X

  GCCGACGGC
    400
```

maryh@stic **stdin**

NeWSprinter20
Thu Apr 06 10:28:18 1995

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

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